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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                     Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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Pred. No. 5e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 94311; 29pp + Sequence Listing; German.
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                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                    Oligonucleotide SEQ ID NO 234733 for detecting SNP TSC0057297.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99889, ABF00010-ABF99889, ABF00010-ABF89989, ABF00010-ABF89989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                              Claim 1; SEQ ID NO 6146; 29pp + Sequence Listing; German
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represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences
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                                                        ABF41880 standard; DNA; 13 BP
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nes 10; Conservative
2 AGGAGAAGATA 13
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                                                                                                                                                                                               Homo sapiens
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire.wipo.int/pub/published_pct_sequences
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 141878; 29pp + Sequence Listing; German.
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Piepenbrock C,

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Sequence 13 BP; 5 A; 0 C; 5 G; 3 T; 0 U; 0 Other;
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Best Local Similarity 83.3
Matches 10; Conservative
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     (EPIG-) EPIGENOMICS AG
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                             WPI; 2001-657177/75
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Berlin K;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 the represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                          was obtained in electronic format from Wl
ftp.wipo.int/pub/published_pct_sequences
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Conservative
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nes 10; Conserv
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                                                                                                                                                                                                                                                                                                                                              This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligoners are also used for detecting cell type differentiation. ABC0010-ABC99989, ABPR0010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic discorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABC0010-ABC99889, ABC0010-ABC99889 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                          Oligonucleotide SEQ ID NO 127765 for detecting SNP TSC0031989.
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ABF27768 standard; DNA; 13 BP.
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                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                               Query Match
40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels
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BP; 8 A; 4 C; 0 G; 1 T; 0 U; 0 Other;
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Best Local Similarity
Matches 10; Conserv
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Sequence 13
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Berlin K;

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SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                           Oligonucleotide SEQ ID NO 148662 for detecting SNP TSC0037536.
                                                        12 GAAACCGAAAAC 1
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728 GCCAGGAGAAC 739

12 GCCACGAAAAC 1

RESULT 574 ABF27768/c

Gaps

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                                                                                                                                                                              This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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cytosine
                                         Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                      Claim 1; SEQ ID NO 224295; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 40.0%; Score 8.8; DB 1; Length 13; Local Similarity 83.3%; Pred. No. 5e+02; les 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 240240; 29pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Set of oligonucleotides, useful for diagnosis and cell designed to detect single-nucleotide polymorphisms and methylation status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13 BP; 1 A; 0 C; 6 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences
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WPI; 2001-657177/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 148662; 29pp + Sequence Listing; German.
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0; Mismatches
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central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC399889, ABF00010-ABF99889, ABF00010-ABF99899 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format from WIPO at fitted the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at
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                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                Oligonucleotide SEQ ID NO 67872 for detecting SNP TSC0017721.
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                              ABC67855 standard; DNA; 13
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              methylation status.
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三十八年一日日 田子東江 湯

Gaps

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DB 1; Length 13;

Query Match 40.0%; Score 8.8; DB 1; Length 13 Best Local Similarity 83.3%; Pred. No. 5e+02; Matches 10; Conservative 0; Mismatches 2; Indels

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                        SNP; single nuclectide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                         Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
            Oligonucleotide SEQ ID NO 94313 for detecting SNP TSC0023541.
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Gaps ô 40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 5e+02; tive 0; Mismatches 2; Indels Sequence 13 BP; 1 A; 0 C; 6 G; 6 T; 0 U; 0 Other; Local Similarity 83.

736 AAACAGAACACC 747 AAACACATCACC 1 21-FEB-2002 (first entry)

ВЪ

Oligonucleotide SEQ ID NO 69714 for detecting SNP TSC0018143.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

W0200177384-A2

18-OCT-2001

This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99999, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at Set of oligonuclectides, useful for diagnosis and cell typing, idesigned to detect single-nuclectide polymorphisms and cytosine methylation status. . 0 Query Match

40.0%; Score 8.8; DB 1; Length 13;

Best Local Similarity 83.3%; Pred. No. 5e+02;

Matches 10; Conservative 0; Mismatches 2; Indels Claim 1; SEQ ID NO 69714; 29pp + Sequence Listing; German. Sequence 13 BP; 0 A; 5 C; 0 G; 8 T; 0 U; 0 Other; Berlin K; 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173. Piepenbrock C, (EPIG-) EPIGENOMICS WPI; 2001-657177/75. olek A, δ

Berlin K;

Gaps

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ABC76055 standard; DNA; 13 ABC76055; ABC76055 

RESULT 582

BP

21-FEB-2002 (first entry)

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Oligonucleotide SEQ ID NO 76072 for detecting SNP TSC0019478.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2

18-OCT-2001

06-APR-2001; 2001WO-IB000713

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG

Berlin K; Piepenbrock C, olek A,

WPI; 2001-657177/75.

Set of oligonuclectides, useful for diagnosis and cell typing, is designed to detect single-nuclectide polymorphisms and cytosine methylation status.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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            Claim 1; SEQ ID NO 76072; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                              Sequence 13 BP; 6 A; 5 C; 0 G; 2 T; 0 U; 0 Other;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cycosine methylation status in chemically pretraated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting call type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABIS2073 trepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                        DB 1; Length 13;
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                                                  Sequence 13 BP; 11 A; 2 C; 0 G; 0 T; 0 U; 0 Other;
was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                    40.0%; Score 8.8; DB 1;
83.3%; Pred. No. 5e+02;
iive 0; Mismatches
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Best Local Similarity
                                                                                                        Local Similarity
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(EPIG-) EPIGENOMICS AG
Homo sapiens
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ABF73773/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo int/pub/published_pct_sequences
                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                Oligonucleotide SEQ ID NO 88825 for detecting SNP TSC0022318.
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               ABC88808 standard; DNA; 13 BP
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Best Local Similarity 83.3
Matches 10; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 124590; 29pp + Sequence Listing; German
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Best Local Similarity 83.3%;
Matches 10; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but fip.wipo.int/pub/published_pot_sequences
                                                                                                           Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                      Claim 1; SEQ ID NO 173770; 29pp + Sequence Listing; German.
                        Berlin K;
                        Olek A, Piepenbrock C,
                                                                  WPI; 2001-657177/75
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Sequence 13 BP; 2 A; 2 C; 0 G; 9 T; 0 U; 0 Other;

Gaps . 40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 5e+02; 2; Indels cive 0; Mismatches 2; Indels Local Similarity 83.3 les 10; Conservative Query Match

ઠે 엄 RESULT 588 ABH25373 ABH25373;

22-FEB-2002 (first entry)

BP.

ABH25373 standard; DNA; 13

Oligonucleotide SEQ ID NO 225350 for detecting SNP TSC0054939.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG.

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 225350; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH999989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at 8888888888888

Seguence 13 BP; 10 A; 2 C; 0 G; 1 T; 0 U; 0 Other;

Gaps ö 40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 5e+02; ive 0; Mismatches 2; Indels Best\_Local Similarity 83.3
Matches 10; Conservative Query Match

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734 AGAAACAGAACA 745 1 ATAAACAAAACA 12 ਨੇ 셤

RESULT 589 ABF56044

BP. ABF56044 standard; DNA; 13

ABF56044;

21-FEB-2002 (first entry)

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonucleotide SEQ ID NO 156041 for detecting SNP TSC0039372.

Homo sapiens.

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 156041; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cycosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABF99989, abmoost of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at 

Sequence 13 BP; 7 A; 0 C; 5 G; 1 T; 0 U; 0 Other;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, certical nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 5e+02;
0; Mismatches 2; Indels
   DB 1; Length 13;
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Score 8.8; DB 1;
Pred. No. 5e+02;
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Best Local Similarity 83.3%;
Matches 10; Conservative
Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
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                                                                       731 AGGAGAAACAGA 742
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                              Oligonucleotide SEQ ID NO 235977 for detecting SNP TSC0005750.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 235977; 29pp + Sequence Listing; German.
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Best Local Similarity 83.3
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es 10; Conservative
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ABH42948/
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleitde polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI32073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                               Claim 1; SEQ ID NO 242925; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fit, wipo.int/pub/published_pct_sequences
  -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
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40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                  Oligonucleotide SEQ ID NO 229461 for detecting SNP TSC0055973.
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                                  ABH29484 standard; DNA; 13
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Matches 10; Conservative
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Oligonucleotide SEQ ID NO 182669 for detecting SNP TSC0045147.

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40.0%; Score 8.8; DB 1; Length 13; ilarity 83.3%; Pred. No. 5e+02; Conservative 0; Mismatches 2; Indels

Query Match Best Local Similarity Matches 10; Conserv

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                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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83.3%; Pred. No. 5e+02;
cive 0; Mismatches
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Best Local Similarity 83.3
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40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 5e+02; ive 0; Mismatches 2; Indels

734 AGAAACAGAACA 745

Sequence 13 BP; 0 A; 0 C; 3 G; 10 T; 0 U; 0 Other;

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Berlin K;

Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG

WPI; 2001-657177/75.

07-APR-2000; 2000DE-01019173

Claim 1; SEQ ID NO 240295; 29pp + Sequence Listing; German.

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                   ABH40319 standard; DNA; 13
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           This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                              40.0%; Score 8.8; DB 1; Length 13; llarity 83.3%; Pred. No. 5e+02; Conservative 0; Mismatches 2; Indels
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Sequence 13 BP; 2 A; 5 C; 0 G; 6 T; 0 U; 0 Other;
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Best Local Similarity 84....
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RESULT 602

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                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                          Oligonucleotide SEQ ID NO 67871 for detecting SNP TSC0017721.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 5e+02; tive 0; Mismatches 2; Indels
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               ABC67854 standard; DNA; 13
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Best Local Similarity
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE09989, ABF00010-ABE99989, ABF00010-ABE99989 and ABI00010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pot_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 219382; 29pp + Seguence Listing; German.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status; in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cantral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but fep.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                   set or oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  set of oligonucleotides, useful for diagnosis and cell typing, : designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                              Claim 1; SEQ ID NO 242776; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             40.0%; Score 8.8; DB 1; Length 13;
ilarity 83.3%; Pred. No. 5e+02;
Conservative 0; Mismatches 2; Indels
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                                                    central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989 and ABI00010-ABF9989 and ABI00010-ABF9999 and ABI00010-ABF99999 and ABI00010-ABF9999 and ABI00010-ABF999 
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                           gastrointestinal, respiratory
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range of diseases including immune system, central nervous system.
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Best Local Similarity 83.3
Matches 10, Conservative
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40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 5e+02;

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                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
  Gaps
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Mismatches
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10; Conservative
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                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonucleotide SEQ ID NO 39734 for detecting SNP TSC0012134.
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                                                                                      This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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Claim 1; SEQ ID NO 219968; 29pp + Sequence Listing; German.
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40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonucleotide SEQ ID NO 159004 for detecting SNP TSC0040037.

(first entry)

21-FEB-2002

ABF59007;

BP.

ABF59007 standard; DNA; 13

RESULT 613 ABF59007

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data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Best Local Similarity 83.3
Matches 10; Conservative
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Berlin K;

Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG

WPI; 2001-657177/75.

designed to detect methylation status.

Set of old

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173.

WO200177384-A2. Homo sapiens.

18-OCT-2001

Claim 1; SEQ ID NO 159004; 29pp + Sequence Listing; German.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
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peptide nucleic acid, cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Matches 10, Conservative
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                                 Berlin K;
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(EPIG-) EPIGENOMICS AG.
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This invention describes novel oligonucleotide primers or peptide nucleic

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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretracted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABE9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                               40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 5e+02; tive 0; Mismatches 2; Indels
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Best Local Similarity 83.3
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; 88; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                  Oligonucleotide SEQ ID NO 202491 for detecting SNP TSC0049770.
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Pred. No. Se+02;
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40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 5e+02;
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Matches 10; Conservative
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ABF82675
ID ABF8267
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Sequence 13 BP; 9 A; 2 C; 0 G; 2 T; 0 U; 0 Other;

ABF82675

WO200177384-A2.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99899, ABH0010-ABF99989, ABH0010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but typo.int/pub/published_pct_sequences
                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                   Oligonucleotide SEQ ID NO 182672 for detecting SNP TSC0045147.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99999, ABH00010-ABH99989 and ABI00010-AB182073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at the printed specification, but fip.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 249209; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 5e+02;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligoners for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, candra system, ardiovascular and metabolic disorders. The oligoners are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABE99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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              Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                          Claim 1; SEQ ID NO 23161; 29pp + Sequence Listing; German
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ABC37604/c
ID ABC37604 standard; DNA; 13
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oligomers are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99889, ABH00010-ABH99989 and ABI00010-ABI82073
represent the Oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic forms from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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to detect single-nuclectide polymorphisms and cytosine
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40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                    Score 8.8; DB 1; Length 13;
Pred. No. 5e+02;
0; Mismatches 2; Indels
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                                                                                                                                   Sequence 13 BP; 1 A; 0 C; 2 G; 10 T; 0 U; 0 Other;
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Best Local Similarity 83.3%;
Matches 10; Conservative
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Oligonucleotide SEQ ID NO 94312 for detecting SNP TSC0023541.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, artdiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE9989, ABF00010-ABE9989, ABH00010-ABH99989 and ABI00010-ABI82073 data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide SEQ ID NO 242913 for detecting SNP TSC000966.
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40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels
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736 AAACAGAACACC 747
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99889, ABH00010-ABF99889 and ABI00010-ABF8073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                          SNP; single nuclectide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Local Similarity 83.3%; Pred. No. 5e+02;
les 10; Conservative 0; Mismatches 2; Indels
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06-APR-2001; 2001WO-IB000713.

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schultz1-727.rng

Claim 1; SEQ ID NO 31769; 29pp + Sequence Listing; German.

Page 283

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABF8073 arepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                  Berlin K;
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                                                                                                               This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA: The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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Pred. No. 5e+02;
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Best Local Similarity 83.3
Matches 10; Conservative
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ABC32872/c
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acid (FNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABC0010-ABC99989 ABC0010-ABC99899 ABC0010-ABC99899 ABC0010-ABC9989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                              Oligonucleotide SEQ ID NO 130656 for detecting SNP TSC0032625.
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                                           ABF30659 standard; DNA; 13 BP
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Best Local Similarity 83.3
Matches 10; Conservative
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Pred. No. 5e+02;
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                                              Sequence 13 BP; 1 A; 0 C; 2 G; 10 T; 0 U; 0 Other;
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ftp.wipo.int/pub/published_pct_sequences
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Olek A, Piepenbrock C,

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels
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                                                                                                                                          Claim 1; SEQ ID NO 219381; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
40.0%; Score 8.8; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13 BP; 2 A; 0 C; 3 G; 8 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         736 AAACAGAACACC 747
                                                                   Set of oligonucleotides, designed to detect single methylation status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 AAACATAAAACC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Olek A, Piepenbrock C,
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                                WPI; 2001-657177/75.
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ABH19406/c
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Gaps

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Pred. No. 5e+02;

83.3%;

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Seguence 13 BP; 1 A; 4 C; 1 G; 7 T; 0 U; 0 Other;
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ABH43253;

DB 1; Length 13;

40.0%; Score 8.8;

Query Match

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              range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC09989, ABF00010-ABF99889, ABF00010-ABH99889 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire printed specification, but fire wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory. Central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABR99889, ABF00010-ABR99899, ABF00010-ABR99899 ABF00010-ABR99899 and ABI00010-ABR82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPD at the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes novel oligonuclectide primers or peptide nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ligonuclectides, useful for diagnosis and cell typing, is to detect single-nuclectide polymorphisms and cytosine
                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide SEQ ID NO 233768 for detecting SNP TSC0057055.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 233768; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                    40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. Se+02; 1ive 0; Mismatches 2; Indels
                                                                                                                                                                                               Sequence 13 BP; 1 A; 0 C; 4 G; 8 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                       ilarity 83.3%;
Conservative
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Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     methylation status.
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ABH33791/c
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                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                   Gaps
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                     Indels
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                   5;
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                     Mismatches
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                   0;
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                                                                                                                                                                       ABH10381 standard; DNA; 13 BP
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Best Local Similarity 83.3
Matches 10; Conservative
                     10; Conservative
                                                                                     12 AGAAACGGAAGA 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EPIG-) EPIGENOMICS AG
                                                     734 AGAAACAGAACA
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                           WO200177384-A2
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ABH10381/c
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                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; leukocyte antigen; HLA; typing; sequence specific probe; SSOPH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                               Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                               Oligonucleotide SEQ ID NO 243230 for detecting SNP TSC0059331.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 243230; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 5e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13 BP; 8 A; 4 C; 1 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                        06-APR-2001; 2001WO-IB000713
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Conservative
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               22-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                   Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HLA-DR typing probe #34.
                                                                                                                                                                                                                                                                                                     (EPIG-) EPIGENOMICS
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Matches 10; Conserv
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                                                                                                                                                                          WO200177384-A2
                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                            The present invention relates to human leukocyte antigen (HLA) typing. The method involves detecting polymorphic residues by sequence specific oligonucleotide probe hybridization (SSOPH) with labeled oligonucleotide
                                                                                                                                                              Human leukocyte antigen typing by amplifying a sample followed by sequence specific oligonucleotide hybridization with labeled oligonucleotide probes that hybridize with a series of known control DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New mammalian agouti polypeptide useful to identify molecules that control agouti polypeptide and as immunogen to produce antibodies usefu for treating, preventing diabetes, hyperamylinemia, neoplasms, obesity.
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murine, agouti, fatty acid synthetase, intracellular calcium level, diabetes; neoplasm; hyperinsulinaemia, obesity, cancer; tumour; anorectic; antidiabetic, cytostatic; mouse; ss.
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                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Exonl-exon2 junction of wild type mouse agouti cDNA clone.
                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                  Sequence 13 BP; 4 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                             40.0%; Score 8.8; DB 1;
83.3%; Pred. No. 5e+02;
iive 0; Mismatches
                                                                                                                                                                                                                                    Disclosure; Col 11-14; 16pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Fig 9B; 140pp; English.
                                                                              (BLOO-) BLOOD CENT RES FOUND INC.
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           97US-00000805
                                      90US-00544218.
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                                                                                                         Baxter-Lowe LA, Gorski JA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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nes 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTGGAGAGACA 13
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                                                                                                                                  WPI; 2001-217923/22.
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           30-DEC-1997;
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                                     27-JUN-1990;
08-APR-1993;
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AAS17271/c
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methods, compositions and kits for identifying compounds which are inhibitors of agouti activity, and for altering fatty acid synthetase activity and intracellular calcium levels in transformed cells. The sequences and methods of the invention are useful in the detection and treatment of diabetes, neoplasms, hyperinsulinaemia, obesity, and various forms of cancer including tumours. The present sequence representing the exon1-exon2 junction of the wild type mouse agouti cDNA clone is compared to the same junction in the agouti Ay (lethal yellow) cDNA clone
                                                                                                                                                                                                                                                                                                     Sequence 13 BP; 0 A; 3 C; 3 G; 7 T; 0 U; 0 Other;
          88666666668
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40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. 5e+02; tive 0; Mismatches 2; Indels 734 AGAAACAGAACA 745 Query Match
Best Local Similarity 83.3
Matches 10; Conservative 13 AGAAGCAGCACA 2 ઠ

; 0

Gaps

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Wild-type human agouti cDNA fragment. ABX11332 standard; cDNA; 13 (first entry) 30-APR-2003 ABX11332; RESULT 639 CCCCCCXXXXLLTHXXBXXBXXBXXBXXLLHHHXXXXXAXAXAXBXXBXXBX

Human, ss, agouti, chromosome 20, black pigment, yellow pigment, agouti coat colour; obesity; non-insulin dependent diabetes; obesity-associated diabetes; intracellular calcium level, hyperinsulinaemia; hyperglycaemia; fatty acid synthetase; metabolism; adipocyte cell; diabetes; hyperamylinaemia; cancer; gene therapy; cytostatic; antidiabetic; anorectic; intron/exon structure; AY.

Homo sapiens

/\*tag= a /note= "DNA break point" Location/Qualifiers misc feature

US2002151463-A1

17-OCT-2002

93US-00064385 98US-00034088 12-FEB-2001; 2001US-00781811 21-MAY-1993; 03-MAR-1998;

(WOYC/) WOYCHIK R P. (BULT/) BULTMAN S J. (MICH/) MICHAUD E J.

Michaud EJ; foychik RP, Bultman SJ,

WPI; 2003-198329/19.

New polynucleotide comprising an isolated agouti gene, useful for diagnosing, preventing and/or treating diabetes, hyperamylinemia, cancer obesity

Example 1; Fig 9B; 152pp; English.

The invention discloses a polynucleotide comprising an isolated agoutingene and the polypeptide it encodes. The agoutincts in chromosome 20, regulates the differential production of black and yellow pigment granules that give rise to the agoutine colour of mice. Obesity and non-insulin dependent diabetes are genetically inherited disorders in humans and mice. The obesity-associated diabetes of the mutant agouti

The invention relates to an isolated nucleic acid (NI) comprising at least 20 but not more than 1500 consecutive nucleotides of the optineurin promoter appearing as ADE13890. Also included are the optineurin promoter operably linked to a hererologous nucleic acid, a nucleic acid capable of detecting a single nucleotide polymorphism (SNP) in the optineurin

Claim 11; SEQ ID NO 199; 159pp; English.

disorders.

New nucleic acid sequences of the optineurin gene are useful to detect polymorphisms particularly single nucleotide polymorphisms in the optineurin promoter to diagnose, prognose and treat glaucoma and related

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Raymond V, Morissette J,

WPI; 2003-864168/80.

(MORI/) MORISSETTE J.

humans. Also disclosed are methods for detecting proteins which interact with the agouti polypeptide, for generating an immune response, for increasing or decreasing the intracellular calcium level in a cell, for increasing or decreasing the intracellular calcium level in a cell, for promoting obesity, hyperinsulinaemia or hyperglycaemia in an animal and for altering fatty acid synthetase activity in a cell or increasing the metabolism in an adipocyte cell. The polymucleotide is useful in detecting and cloning of the gene in which expression of the gene product correlates with the development of diabetes, hyperamylinaemia, cancer and obesity in animals, in detecting the agouti gene and homologous DNA sequences, in detecting mutations in the gene, in early detection of animals at risk of deflicted animals. The antibody is used in isolating and regulating the activity of agouti proteins. The sequence presented is the wild-type human agouti cDNA fragment showing the DNA break point at the exon I boundary compared to the agouti AY mutation cDNA sequence (ABX11334) ö Human, optineurin, ds. ophthalmological, single nucleotide polymorphism; SNP; glaucoma; progressive ocular hypertensive disorder; glaucoma related disorder; motif; repeat element; regulatory region. Gaps Optineurin promoter motif, repeat element or regulatory region #197. ô 40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. Se+02; cive 0; Mismatches 2; Indels Sequence 13 BP; 0 A; 3 C; 3 G; 7 T; 0 U; 0 Other; 06-MAR-2002; 2002US-00091281. 06-MAR-2002; 2002US-00091281 ADE14088 standard; DNA; 13 29-JAN-2004 (first entry) 734 AGAAACAGAACA 745 Conservative 13 AGAAGCAGCACA 2 Local Similarity nes 10; Conserv (SIEE/) SI E. (RAYM/) RAYMOND V. US2003190617-A1 Homo sapiens. ADE14088; Query Match Best Loca Matches RESULT 640 ADE14088 \$ ò g

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promoter, a host cell comprising the promoter operably linked to a heterologous sequence, diagnosing or prognosing glaucoma in a sample obtained from a cell or bodily fluid (comprising detecting a polymorphism in a promoter region of the optimeurin gene, associated with a glaucoma phenotype), detecting a SNP sequence variation in a sample containing a SNP sequence variation in a sample containing DNA, determining the presence of an optimeurin promoter sequence variation in a sample containing DNA, determining the presence or increased susceptibility to glaucoma or to a progressive ocular hypertensive or progression of glaucoma or to a progressive ocular hypertensive or progression of glaucoma in a patient, comprising providing a muglification reaction primers that direct amplification of a selected nucleic acid region containing the variation within the optimeurin promoter and amplifying the DNA) and detecting a polymorphism (comprising capable of detecting a SNP located within an optimeurin promoter, and detecting the polymorphism). The invention is used to diagnose and present sequence is an optimeurin promoter motif, repeat element or putative regulatory region.
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Seguence 13 BP; 6 A; 2 C; 5 G; 0 T; 0 U; 0 Other;

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      40.0%; Score 8.8; DB 1; Length 13; 83.3%; Pred. No. Se+02; tive 0; Mismatches 2; Indels
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Best Local Similarity 83.35
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Oligonucleotide SEQ ID NO 145514 for detecting SNP TSC0036638. BP. ABF45517 standard; DNA; 13 21-FEB-2002 (first entry) ABF45517; RESULT 641 ABF45517/c 

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2.

18-OCT-2001,

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 145514; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The

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oligomers are also used for detecting cell type differentiation. ABC00010 -ABC9989, ABF0010-ABF99889, ABH0010-ABH99989 and ABI00010-ABF8273 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fig. wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                            Oligonucleotide SEQ ID NO 145513 for detecting SNP TSC0036638.
                                                                                                     39.1%; Score 8.6; DB 1; Length 13; 88.9%; Pred. No. 5.4e+02; arive 1; Mismatches 0; Indels
                                                                                 Sequence 13 BP; 1 A; 5 C; 0 G; 6 T; 0 U; 1 Other;
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Best Local Similarity 88.9
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Claim 1; SEQ ID NO 145513; 29pp + Sequence Listing; German.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Berlin K;

Olek A, Piepenbrock C,

WPI; 2001-657177/75.

(EPIG-) EPIGENOMICS AG

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99899 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 13 BP; 6 A; 0 C; 5 G; 1 T; 0 U; 1 Other;

.. 0 Gaps .. 0 Query Match
39.1%; Score 8.6; DB 1; Length 13;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 8; Conservative 1; Mismatches 0; Indels

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Oligonucleotide SEQ ID NO 116959 for detecting SNP TSC0029279.
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ABP 48268

IID ABP 4

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Claim 1; SEQ ID NO 116960; 29pp + Sequence Listing; German.

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligoners are also used for detecting cell type differentiation. ABC00010 ABC099999, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                       Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                    07-APR-2000; 2000DE-01019173
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                                                          (EPIG-) EPIGENOMICS AG
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0; Gaps Query Match 39.1%; Score 8.6; DB 1; Length 13; Best Local Similarity 88.9%; Pred. No. 5.4e+02; Matches 8; Conservative 1; Mismatches 0; Indels

731 AGGAGAAAC 739 AGGAGAAAY 1 σ à 원

963/c ABF16963 standard; DNA; 13 BP. 21-FEB-2002 (first entry) ABF16963; RESULT 646 ABF16963/ 

Oligonucleotide SEQ ID NO 116960 for detecting SNP TSC0029279.

SNP, single nucleotide polymorphism, human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG.

봈 Berlin Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metebolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99899 and ABI00010-ABI82073 tepsesm the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences 

Sequence 13 BP; 2 A; 3 C; 0 G; 7 T; 0 U; 1 Other;

Gaps . 0 39.1%; Score 8.6; DB 1; Length 13; 88.9%; Pred. No. 5.4e+02; Attive 1; Mismatches 0; Indels Query Match
Best Local Similarity 88.5-

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g 8

RESULT 647

AAL37783 standard; RNA; 13 BP.

AAL37783;

05-AUG-2002 (first entry)

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5' conserved RNA region of wild-type influenza B virus.

Cytostatic; antiviral; tumour associated antigen; TAA; dendritic cell; virus-associated antigen; VAA; recombinant influenza virus; vaccine; viral infection; immune; wild-type; influenza B virus; ss.

Influenza virus.

EP1201760-A1.

02-MAY-2002.

30-OCT-2000; 2000EP-00123687

30-OCT-2000; 2000EP-00123687.

(ARTE-) ARTEMIS PHARM GMBH.

α Schuler G, Hobom G, Steinkasserer A, Strobel I, Grassmann

WPI; 2002-418777/45.

Expressing tumor or viral associated antigens by dendritic cells, use for treating tumors or viral infections, comprises using recombinant influenza virus containing nucleic acid encoding the antigens.

Disclosure; Page 6; 33pp; English

The invention relates to a method for the expression of tumour associated antigens (TRA) by dendritic cells comprising: preparing a recombinant influenza virus containing a nucleotide sequence coding for the TRA or VAA; and infecting dendritic cells with the recombinant virus. The method is used for expressing TRA or VAA in dendritic cells. The cells are used for expressing TRA for treating tumours or viral infections. A vaccine can be created by using dendritic cells presenting tumour antigens to induce an immune response. This polynucleotide sequence represents a 5' conserved RNA region of the wild-type influenza B virus of the invention ALIJ7783

ALIJ7783

ALIJ7783

ALIJ783

AND A

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The present invention describes a human influenza virus (I) comprising an RNA-sequence encoding a modified RNA-polymerase that differs from the wild-type RNA-polymerase of the human influenza virus in that at least 1 of the amino acid residues distinguishing the wild-type RNA-polymerase of the human influenza virus from FPV Bratislava RNA-polymerase of the human influenza virus from FPV Bratislava RNA-polymerase of Extinguishing amino acid residue(s) as present in FPV Bratislava RNA-polymerase of Extislava RNA-polymerase or double-strand sequences relative to the target cellular mRNA molecules, and continual viruses can be expresent of Extislava RNA interference mechanisms such as ribozyme cleavages of target RNAs. The recombinant viruses can be made for use in vaccines against HIV, hepatitis B or C virus, herpes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human influenza virus comprising an RNA-sequence encoding a modified RNA-polymerase, useful for preparing agents for therapeutic and prophylactic vaccination, or treating a growing tumor or a chronic infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                              Influenza virus; transcription; replication; RNA polymerase; vaccine; gene therapy; cytostatic; anti-HIV; hepatotropic; antiinflammatory; immunomodulator; virucide; infectious disease; ss.
                                                                          Gaps
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0
                                    Score 8.6; DB 1; Length 13;
Pred. No. 5.4e+02;
2; Mismatches 1; Indels
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Sequence 13 BP; 5 A; 1 C; 2 G; 0 T; 1 U; 4 Other;
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                                                                                                                                                                                                                                                 ABQ75466 standard; RNA; 13 BP
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                                                                            Conservative
                                                                                                                731 AGGAGAAACAG 741
                                                                                                                                                     1 AGUAGWAACAR 11
                    Query Match
Best Local Similarity
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The invention describes a recombinant influenza virus (I), stable in the absence of any helper virus, that has a viral RNA segment being a biscistronic RNA molecule coding for two genes in tandem arrangement (and mean that are segment and the segment TRS). (I) is useful for expression of incorporated foreign gene(s) and RNA molecules in cells. (I), preferably a recombinant influenza A virus is useful for: preventing and/or treating influenza, and for preparing a medicament for vaccination purposes; somatic gene therapy, and as immunogen for inducing antibodies; as an expression vector for producing proteins or glycoproteins; preparing agents for somatic gene therapy; immunotherapy, preferably autologous immunotherapy; transfer and expression of foreign genes and RNA molecules into cells infected by such viruses, where the RNA molecules into cells infected by such viruses, where the RNA molecules into cells cartisense or double-stranded sequences relative to the target cell callular mRNA molecules, and/or the agent is suitable for sequence specific gene silencing, preferably by antisense RNA or RNA interference sequence represents the S' conserved region of influenza B virus, conserved region of influenza B virus,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant influenza virus for transfer and expression of foreign genes and RNA molecules into cells and for preventing, treating influenza, has biscistronic viral RNAs coding for two genes in tandem arrangement.
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viruses or papilloma viruses. The present sequence represents conserved region of a wild type influenza virus, given in the exemplification of the present invention
                                                                                                                         39.1%; Score 8.6; DB 1; Length 13; llarity 72.7%; Pred. No. 5.4e+02; Conservative 2; Mismatches 1; Indels
                                                                               Sequence 13 BP; 5 A; 1 C; 2 G; 0 T; 1 U; 4 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wild type influenza B, 5' conserved region.
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                                                                                                                                                                                                                                                                                                                                                       ABK15502 standard; RNA; 13 BP
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                                                                                                                                          Best Local Similarity
Matches 8; Conserv
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39.1%; Score 8.6; DB 1; Length 13;

Query Match

Sequence 13 BP; 5 A; 1 C; 2 G; 0 T; 1 U; 4 Other;

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Human dendritic cell SAGE tag, SEQ ID NO:1175.
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19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
19-JUN-1998;
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19-JUN-1998;
19-JUN-1998;
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19-JUN-1998;
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                                                                          Homo sapiens
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19-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or more decanuclectides (AAQ96406-Q97018) from the nef gene and/or 1 or more decanuclectides (AAQ97019-Q97166) from the LTR region; the sequence of AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The response in humans, and enable the generation of therapeutic, diagnostic and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                        New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or LTR region - can be used in a vaccine to inhibit/reduce productive infection in an individual by a pathogenic strain.
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 Pred. No. 5.4e+02;
2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                     Crowe S,
                                                                                                                                                         HIV-1 NL4-3 nef gene nucleotide deletion 477.
                                                                                                                                                                                                                                                                                                         (MACF-) MACFARLANE BURNET CENT MEDICAL. (AURE-) AUSTRALIAN RED CROSS SOC.
                                                                                                                                                                                                                                                                                                                                     Mcphee DA,
                                                                                                                                                                                                                                                                                                                                                                                                            Claim 13; Page 194; 301pp; English.
                                                                                                                                                                                              Human immunodeficiency virus 1.
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94AU-00000284.
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 72.78;
                                                                                           AAQ96882 standard; DNA; 10
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(first entry)
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                                                                                                                                                                                                                                                                                                                                     Deacon NJ, Learmont JC,
Best Local Similarity 72.7
Matches 8, Conservative
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                                             1 AGUAGWAACAR 11
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les 9; Conserv
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21-FEB-1994;
23-DEC-1994;
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26-MAR-1996
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                                                                                  AAZ78747
ID AAZ7
XX AZ
AC AAZ7
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Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene expression) tags used to identify mRNA transcripts encoding the munostimulatory cofactor proteins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTS (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while other transcripts correspond to novel genes. Antigen-presenting cell (APC)-associated costimulatory factors play an important role in the activation of the cytotoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MMC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytotoxic immune response that can lyse tumour cells, immunostimulatory cofactors also being required for
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SAGE tag; serial analysis of gene expression; antigen-presenting cell; APC; monocyte-derived dendritic cell; differential gene expression; immunostimulatory cofactor; costimulatory factor; CTL; cytocoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
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98US-0089981P
98US-0089991P
98US-0089992P
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98US-0089997P
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98US-009904P
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efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid sequences identified using the SAGE tags have several potential uses. They may be used in vaccines to induce an immune response, particularly against a tumour antigen; to modulate the genotype of an APC; to screen for agents that modulate expression of differentially expressed genes in an APC; and APC; and APC; and as hybridisation probes/amplification primers for the diagnosis, prognosis and monitoring of diseases related to abnormal expressed genes. Detection of the dendritic cell differentially cypressed genes. Detection of the dendritic cell differentially calls as belonging to the monocyte lineage. Calls containing these genes can be used in active immunotherapy (or to stimulate production of a population of antigen-specific effector cells) and vectors containing them are used in gene therapy. Co-administration of tumour antigens and APC-associated costimulatory factors ensures adequate antigen presentation to endogenous APCs and upregulates the APCs for the presentation of co-stimulatory signals, migration to T cell-rich sites, secretion of I cell growth factors and secretion of chemokines for recruitment of immune effector cells
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Expression) tagg used to identify mRNA transcripts encoding immunostimulatory cofactor proteins which are preferentially or differentially expression monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTs (expressed sequence tags) which were previously unknown to be the preferentially or differentially expressed in dendritic cells, while cother transcripts correspond to novel genes. Antigen-presenting cell other transcripts correspond to novel genes. Antigen-presenting cell or the cytocxic immune response, particularly against tumour cells. Tumour antigen presentation via the MRIC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytotoxic immune response that can lyse complex) and subsequent recognition by T-cell receptors is alone insufficient activation of cytotoxic Immune response that can lyse complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytotoxic immune response that can lyse the tumour cells, immunostimulatory cofactors also being required for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid sequents that modulate to immune response, particularly against a tumour antigen; to modulate the genotype of an APC; to screen for agents that modulate expression of differentially expressed genes in an APC; and as hybridisation probes amplication primers for the diagnosis, prognosis and monitoring of diseases related to abnormal companies, or of their encoded proteins, can be used to identify expressed genes complexion of a because of the manulation of the demonstration of tumour antigens and the manulatory factors entities and entities a pelonging to the monocyte lineage. Cells and vectors containing these genes complex in munophenial and upper particularly and vectors containing of them are used in gene therapy. Co-administration of tumour antigens and processed appears the pagenter as the page to be admini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated polynucleotides differentially expressed in antigen-presenting cells, useful in gene vaccines against cancer.
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ID AAZ77903 standard; DNA; 10 BP.
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Best Local Similarity 90.0
Matches 9; Conservative
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08 - DEC - 1998;
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(ROBE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated polynucleotides differentially expressed in antigen-presenting cells, useful in gene vaccines against cancer.
                                      SAGE tag, serial analysis of gene expression, antigen-presenting cell, APC; moncoyte-derived dendritic cell; differential gene expression; immunostimulatory cofactor, costimulatory factor; CTL; cytotoxic T-lymphocyte, tumour antigen; immunotherapy; anticancer; ss.
                    Human dendritic cell SAGE tag, SEQ ID NO:331.
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(first entry)
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 10-APR-2000
                                                                                         Homo sapiens
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the tumour cells, immunostimulatory cofactors also being required for efficient activation of cytotoxic T-lymphocytes (CTLS). Nucleic acid consequences identified using the SAGE tags have several potential uses. They may be used in vaccines to induce an immune response, particularly capainst a tumour antigen; to modulate the genotype of an APC; to screen for agents that modulate expression of differentially expressed genes in an APC; and as hybridisation probes/amplification primers for the diagnosis, prognosis and monitoring of diseases related to abnormal expression of these genes. Detection of the dendritic cell differentially cells as belonging to the monocyte lineage. Calls containing these genes or of their encoded proteins, can be used to identify cells as belonging to the monocyte lineage. Calls containing these genes can be used in active immunotherapy (or to stimulate production of a copulation of antigen-specific effector cells) and vectors containing them are used in gene therapy. Co-administration of tumour antigens and APC-associated costimulatory factors ensures adequate antigen presentation of co-stimulatory signals, migration to T cell-rich sites, secretion of T cell growth factors and secretion of chemokines for recruitment of immune effector cells
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90.0%; Pred. No. 5.2e+02;
iive 0; Mismatches 1;
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98US-0089997P.
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Best Local Similarity 90..v
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Claim 1; Page 59; 219pp; English.
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SHANKARA S.
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that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for disgnosis, prognosis, monitoring and transcripts can be used for disgnosis, prognosis, monitoring and transcripts can be used for hybridisation/amplification reactions. by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic and isolate populations of educated, and these used for adoptive cells, educated, and these used for adoptive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.2%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 5.2e+02;
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98US-0090040P.
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ROBERTS B L.
SHANKARA S.
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(ROBE/) 1
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                                      AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic Diagnosis is by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic and isolate populations of educated, antigen-specific immune effecter cells.
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                     Claim 1; Page 131; 219pp; English.
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treatment of cancer
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Compounds that modulate expression of the transcribts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also riboxymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines, for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
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Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and
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                                                                                                                                      Claim 1; Page 66; 219pp; English.
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(ROBE/) ROBERTS B L.
(SHAN/) SHANKARA S.
                                                                    treatment of cancer.
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Best Local Similarity 90.v-
Best Local Similarity
Conservative
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ROBERTS B L.
SHANKARA S.
             treatment of cancer.
                                                                                            immunotherapy
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19-JUN-1998;
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(ROBE/)
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AAZ80767 to AAZ893941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregalated in metastatic breast tumour cells). AAZ89342 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). These tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts are modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), c.g. therapeutic genes (also ribozymes or antisense sequences), c.g. vaccines, for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter cells, e.g. cytocoxic T lymphocytes, and these used for adoptive immunotherapy
                                                                                                   Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and
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Shankara
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                                                   Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and
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                                                                                                                                                            Claim 1; Page 80; 219pp; English.
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98US-0090039P.
98US-0090040P.
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WPI; 2000-106079/09.
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98US-0089853P. 98US-0089997P. 98US-0090039P. 98US-0090040P.

19-JUN-1998; 19-JUN-1998; 19-JUN-1998;

19-JUN-1998;

CORP

(GENZ ) GENZYME CORP (ROBE/) ROBERTS B L.

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(GENZ ) GENZYME CORP.
(ROBE/) ROBERTS B L.
(SHAN/) SHANKARA S.
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                                                         Roberts BL,
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                                                                                                                                                              that are preferentially transcribed in the metastatic breast tumour cliss. AAZ860767 to AAZ83941 represent tags corresponding to distinct transcripts tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells. These transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for hybridisation/amplification reactions. Or standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for trearment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines, for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides or as therapeutic and isolate populations of educated, and these used for adoptive community.
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                                                                                Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence 10 BP; 2 A; 3 C; 2 G; 3 T; 0 U; 0 Other;
                                                                                                                                        Claim 1; Page 87; 219pp; English.
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98US-0089937P.
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Best Local Similarity 90.05
Matches 9, Conservative
                             Roberts BL, Shankara S;
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                                                        WPI; 2000-106079/09.
 (SHAN/) SHANKARA S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunotherapy
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19-JUN-1998;
19-JUN-1998;
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that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ80767 to AAZ80677 represent tags corresponding to distinct transcripts that are preferentially transcribed in metastatic breast tumour cells). AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). These can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and compounds that modulate expression of the transcripts are potentially compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of c.g. therapeutic genes (also riboxymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines, for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic and isolate populations of educated, antigen-specific immune effecter cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter.
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                                                                                                                                                                                               Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and
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                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 108; 219pp; English.
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                                                                                                                                                                                                                                                                                                          treatment of cancer.
                                                                                               WPI; 2000-106079/09.
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XX AAZ82
DE Metaa.
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non-metastatic breast tumour tissue, gene therapy, anticancer,
antimetastatic, vaccine, diagnosis, ss.
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                                                                                                                                                                        Claim 1; Page 114; 219pp; English.
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Best Local Similarity 90.0
Matches 9; Conservative
                                                                        Roberts BL, Shankara S;
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                       (GENZ ) GENZYME CORP. (ROBE/) ROBERTS B L.
                                                                                                WPI; 2000-106079/09
                                                                                                                                               treatment of cancer
                                                SHANKARA S.
19-JUN-1998;
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that are preferentially transcribed in the metastatic breast tumour cells. AA280767 to AA280941 represent tags corresponding to distinct transcripts that are upregulated in metastatic breast tumour cells). AA280942 to AA280677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells) these crisses (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from casful for treatment of direct expression, in selected cell types, of the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines, Polypeptides encoded by the transcripts are also useful in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter cells, e.g. cytocxic T lymphocytes, and these used for adoptive immunetherapy immunetherapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 211; 219pp; English.
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Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                                                       GENZYME CORP
                                                                                                                                                                                   (ROBE/) ROBERTS B L. (SHAN/) SHANKARA S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treatment of cancer.
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19-JUN-1998;
19-JUN-1998;
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99JP-00095481.

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The present invention describes a method of identifying the type of cell in a sample, involving determining which of the sequences AAR63161-AAR64724 is expressed by the cell. The transcriptomes described in the invention are cell-type specific, cancer specific or ubiquitously expressed in humans. They can also be used to screen for drugs, reduce cancer specific agene expression, standardise expression and restore the function of a diseased cell or tissue. The present sequence is one of the transcriptomes described in the exemplification of the invention

Sequence 10 BP; 4 A; 2 C; 4 G; 0 T; 0 U; 0 Other;

AAH64523 standard; cDNA; 10

729 CCAGGAGAAA 738

(first entry)

20-SEP-2001

AAH64523;

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Query Match 38.2%; Score 8.4; DB 1; Length 10; Best Local Similarity 90.0%; Pred. No. 5.2e+02; Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                         RESULT 666
                                                                                                                                                                                                                                                                     AAH64523/c
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                                                                                                                                                    The present invention describes a group of genes consisting of 100 genes which are highly expressed in human dendritic cells, a group of genes which are expressed at a higher frequency in human dendritic cells than in human monocytes; and a group of genes which are expressed at lower frequency in human dendritic cells than in human monocytes. Each group of genes are characterised in that cDNAs of these genes respectively have the base sequences of SEQ ID NO:10 to 100 (AAC74014 to AAC74113) and SEQ ID NO:201 to 300 (AAC74114 to AAC74213), each is continuous with the base sequence 5'-CATG-3' to AAC74213), each is continuous with the base sequence can be used for the investigation of the role and mechanism of the involvement of dendritic cells in the immune system and for the study and diagnosis of diseases in which dendritic cells play a significant role, e.g. cancers
                                                                             Groups of genes expressed in human dendritic cells at a greater or lesser extent than in monocytes for investigation and diagnosis of autoimmune disease and tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotides, useful for identifying specific cell type, such as cancer cell, comprises transcriptomes expressed in particular cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; transcriptome; gene expression pattern; cancer; drug screening; cancer diagnosis; cell specific gene expression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human ubiquitously expressed transcriptome sequence SEQ ID NO: 834.
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                                                                                                                                                                                                                                                                                                                                         Sequence 10 BP; 1 A; 2 C; 1 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kinzler KW;
           (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                Claim 10; Page 13; 95pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH63994 standard; cDNA; 10 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vogelstein B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-NOV-2000; 2000WO-US031922.
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 90.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYJO ) UNIV JOHNS HOPKINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                  and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                731 AGGAGAAACA 740
                                                                                                                                                                                                                                                                                                                                                                                                                                       10 AGGATAAACA 1
                                                         WPI; 2000-619172/59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200138577-A2
                                  Hashimoto S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotides, useful for identifying specific cell type, such as cancer cell, comprises transcriptomes expressed in particular cell types.
                                                            Human; transcriptome, gene expression pattern; cancer; drug screening; cancer diagnosis; cell specific gene expression; ss.
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Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1363.
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Pred. No. 5.2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10 BP; 1 A; 2 C; 1 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kinzler KW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 13; Page 70; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Velculescu VE, Vogelstein B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.2%;
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Best Local Similarity 90.0%
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                                                                                                                                                                                                                       WO200138577-A2
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                                                                                                                                                             Homo sapiens.
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Claim 13; Page 58; 94pp; English.

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(USSH ) US DEPT HEALTH & HUMAN SERVICES.
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WO200109161-A1
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a method of identifying the type of cell in a sample, involving determining which of the sequences AAH63161-AAH64724 is expressed by the cell. The transcriptomes described in the invention are cell-type specific, cancer specific or ubiquitously expressed in humans. They can also be used to screen for drugs, reduce cancer specific gene expression, standardise expression and restore the function of a diseased cell or tissue. The present sequence is one of the transcriptomes described in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        isolated polynucleotides, useful for identifying specific cell type, as cancer cell, comprises transcriptomes expressed in particular
                                                                                                                                                                                                                                                                                                                                                                                                                transcriptome; gene expression pattern; cancer; drug screening; diagnosis; cell specific gene expression; ss.
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                                                                                                                                                                                                                                                                                                                                                 Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1293.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kinzler KW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 68; 94pp; English.
                                                                                                                                                                     AAH64453 standard; cDNA; 10 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-NOV-2000; 2000WO-US031922.
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Best Local Similarity 90...
Best Social Similarity 70...
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             GATAAACAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200138577-A2.
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                                                                                                                                                                                                                                                                                            20-SEP-2001
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                                                                                                                                                                                                                             AAH64453
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cancer
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AAF74014/C
ID AAF74014/C
XX
AC AAF740
XX
XX
DT 30-APR
XX
XX
DE Human
XX
XX
XX
Sclute
KW Sclute
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Sclute

                                                                                                                                    AAH64453/

XXX AAH6

XXX AAH6

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       serous cystadenocarcinoma; mucinous cystadenocarcinoma; mucinous cystadenocarcinoma; mucinous cystadenoma; borderline mucinous tumour; endometrioid carcinoma; undifferentiated carcinoma; clear cell adenocarcinoma; cystadenofibroma; adenofibroma; Brenner tumour; serial analysis of gene expression; immune response pathway; cell proliferation regulation; protein folding; membrane localised; secreted; therapeutic target; cytostatic;
                                                                                                                                                                                                                                                            New isolated polynucleotide comprising a polymorphic variant for the solute carrier family 6 neurotransmitter transporter, serotonin member 4 gene for identifying drugs for treating disorders related to expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eIF-2-associated p67 ovarian tumour marker gene SAGE tag, SEQ ID NO:102
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                                                                                                                              Stephens JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38.2%; Score 8.4; DB 1; Length 10; larity 90.0%; Pred. No. 5.2e+02; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10 BP; 0 A; 2 C; 2 G; 6 T; 0 U; 0 Other;
                                                                                                                                 Sanchis A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy; vaccine; SAGE tag; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; Page 22; 152pp; English.
                                                                                                                                 Nandabalan
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99US-0146290P
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                                                                                                                                 Duda A,
                                                                (GENA-) GENAISSANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 CCAGAAGAAA
                                                                                                                                                                                                  WPI; 2001-123317/13
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nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                            of the protein.
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29-JUL-1999;
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                                                                                                                                     Denton RR,
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The invention relates to methods for diagnosing and prognosing ovarian tumours in an individual via the detection and measurement of the tumours in an individual via the detection and measurement of the expression of ovarian tumour marker genes (ABA81312-ABA81312, ABA81318), ABA813181 and ABA813183). The methods of the invention are useful for ABA813181 and ABA813183). The methods of the invention are useful for detecting an ovarian tumour in a patient, for identifying an individual at increased risk for developing ovarian cancer, in prognostic tests for assessing the relative seveloping ovarian cancer, in prognostic tests for assessing the relative seveloping ovarian cancer, in tests for monitoring disease status in a patient being treated for ovarian cancer. The methods can additionally be used to identify a particular tumour as being an ovarian tumour (i.e., an epithelial ovarian tumour selected from serous tumour, serous cystadenocarcinoma, orderline meucinous tumour, mucinous cystadenocarcinoma, borderline meucinous tumour, mucinous cystadenocarcinoma, endometrioid carcinoma, undifferentiated carcinoma, clear cell adenocarcinoma, portaenofibroma, adenofibroma and Brenner tumour marker genes of the invention were identified or services of in a broad variately of ovarian pathelial tumour cells crelative to normal ovarian epithelial cells. The marker genes are membraned prognostic markers, the ovarian tumour marker genes or their encoded prognostic markers, the ovarian tumour marker genes or their encoded prognostic markers, the ovarian tumour marker genes or their encoded prognostic markers, the ovarian tumour marker genes or their encoded prognostic markers, the ovarian tumour marker genes or their encoded prognostic markers, the ovarian tumour marker genes or their encoded prognostic markers, the ovarian tumour marker genes or their encoded prognostic markers, the ovarian tumour marker genes or their encoded proversure genes of the invention Detecting and identifying ovarian tumor, identifying increased risk for developing ovarian cancer, and determining effectiveness of ovarian cancer treatment, by measuring expression level of ovarian tumor marker Morin PJ, Sherman-Baust CA, Pizer ES, Hough CD; Claim 25; Page 31; 140pp; English. WPI; 2001-626450/72 gene 

Sequence 10 BP; 5 A; 2 C; 2 G; 1 T; 0 U; 0 Other;

Query Match

38.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 5.2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels

g

AAF35790 standard; DNA; 10 BP. RESULT 670 

AAF35790;

23-MAR-2001 (first entry)

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2529.

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; de.

Saccharomyces cerevisiae

WO200077214-A2

21-DEC-2000

14-JUN-2000; 2000WO-US016223.

99US-00335032 16-JUN-1999;

(UYJO ) UNIV JOHNS HOPKINS.

Kinzler K; Vogelstein B, Jelculescu V,

WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 90; 419pp; English.

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonamontated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (MI) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate cell; and (b) monitoring expression of a NORF gene whose expression of cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (MM) for identifying human genes which are involved in cell cycle progression contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression in a contiguous nucleotides of a NORF gene whose expression is affected by the class of the cell congrising contacting a yeast cell with a candidate drug as a member of a class of drugs expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of the cell cycle, the differentially cexpressed genes may be used to identify candidate drugs which affect the cell cycle and for identify candidate drugs which affect the cell cycle and for identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. The NORF genes may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. ARF33262 to AAF33267 represent linkers and PCR primers used in the exemplification of the present invention.

ARF33262 to AAF33267 represent linkers and PCR primers used in the EAPS CR method, in the exemplification of the present invention. 

Sequence 10 BP; 6 A; 1 C; 3 G; 0 T; 0 U; 0 Other;

o ;

0; Gaps

Gaps .; 0 38.2%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 5.2e+02; ive 0; Mismatches 1; Indels Best Local Similarity 90.0 Matches 9, Conservative Query Match

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RESULT 671

AAF43163 standard; DNA; 10 BP. AAF43163 ID AAF4

AAF43163;

23-MAR-2001 (first entry)

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11302.

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae.

WO200077214-A2

Kinzler K;

Vogelstein B,

99US-00335032

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AAF43935 standard; DNA; 10 BP.
                                                                                                                                  23-MAR-2001 (first entry)
                                                                                                            727 TGCCAGGAGA 736
                                                                                                                1 TGCCAGCAGA 10
                      WPI; 2001-061874/07.
          16-JUN-1999;
                                                                                                                              AAF43935;
                                                                                                    Query Match
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Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
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                                                                                                                                               14-JUN-2000; 2000WO-US016223
                                                                                                                                                                                                                                            (UYJO ) UNIV JOHNS HOPKINS.
Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-061874/07.
                                               WO200077214-A2.
                                                                                                                                                                                                                                                                                                 Velculescu V,
                                                                                                                                                                                                 16-JUN-1999;
                                                                                                  21-DEC-2000
The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonaminotated ORF) genes comprising a SAGB (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate or antifungal drugs comprising: (a) contexting a test substance which sets expression or varies as in M1, where a test substance which modifies the expression of varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression contiguous nucleotides of a NORF gene whose expression in a comprising contexting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression in a diffect day the class of drugs. The NORF gene whose contiguous nucleotides of a NORF gene whose contiguous nucleotides of a NORF gene whose expression is affected by the class of drugs. The NORF gene whose expression is affected by the class of the cell cycle, the differentially contexting a yeast cell with a method way be used to identify candidate drugs which affect the cycle and for identification of antifungal drugs. The NORF genes may be used to identify candidate drugs which affect the cycle and for identification of antifungal drugs. The present invention terpresent SAGB tags used in the exemplification of the present invention.

AAF31326 to AAF33267 represent linkers and PCR primers used in the SAGB company of the present invention of the present invention.
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                                                                                                                                                                                                                                                                                                                         Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                               Kinzler K;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Example; Page 353; 419pp; English
                                                                             14-JUN-2000; 2000WO-US016223
                                                                                                                                                                                                                               Velculescu V, Vogelstein B,
                                                                                                                            99US-00335032
                                                                                                                                                                                 SNING OHIO JOHNS HOPKINS
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Matches 9; Conservative
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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonaminotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at cycle comprising administering a NORF gene whose expression or arises by at the fittingal drugs comprising: (a) a method (M2) for screening candidate antifungal drugs of monitoring expression of a NORF gene whose expression of varies as in M1, where a test substance which modifies the expression of varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression contiguous nucleotides of a NORF gene whose expression of a drugs having a characteristic effect on gene expression in a characteristic effect on gene expression in a class of drugs. The NORF gene whose expression is affected by the class of the cell cycle progression in the yeast cell with a candidate drug as a member of contioning expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of the cell cycle the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle of cycle end for identify candidate drugs which affect the cycle enthods may be used to identify candidate drugs which affect the cell cycle represent SAGE tags used in the exemplification of the present invention of the p
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Best Local Similarity 90.0%; Pred. No. 5.2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10 BP; 1 A; 2 C; 2 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF37363 standard; DNA; 10 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        729 CCAGGAGAA 738
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Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:12074.

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Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
                  Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; SACE; SACE; lanalysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.
                                                                                                                                                                                                                                                                                                                 Velculescu V, Vogelstein B,
                                                                                                                                                                                                             14-JUN-2000; 2000WO-US016223
                                                                                                                                                                                                                                                                               (UYJO) UNIV JOHNS HOPKINS
                                                                                                       Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-061874/07.
                                                                                                                                        WO200077214-A2
                                                                                                                                                                                                                                              16-JUN-1999;
                                                                                                                                                                           21-DEC-2000
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonamnotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate catifurgal drugs comprising: (a) contexting east unbitstance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for che yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression of comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotidaes of a NORF gene whose expression in a contiguous nucleotidaes of a NORF gene whose expression in a contiguous nucleotidaes of a norsk gene whose expression is affected by the class of drugs. The NORF gene whose expression is affected by the class of the cell cycle, the differentially contacting a yeast cell with a candidate drug as a member of contiguous nucleotidae and affect phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle corpused and for identify candidate drugs which affect the cell cycle corpused corpuses may be used as markers of phases of the cell cycle. The cycle and for identify candidate drugs which affect the cell cycle are cycle and for identify candidate drugs which affect the cell cycle are cycle and for identify candidate drugs which affect the cell cycle cycle and for identify candidate drugs which affect the cell cycle methods, in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                               Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
serial analysis of gene expression, antifungal, tag, identification, linker, PCR primer, ds.
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38.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 5.2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10 BP; 5 A; 2 C; 2 G; 1 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                               Kinzler
                                                                                                                                                                                                                                                                                                                                                                                                    Example; Page 146; 419pp; English.
                                                                                                                                                       14-JUN-2000; 2000WO-US016223
                                                                                                                                                                                          99US-00335032
                                                                                                                                                                                                                                                             Vogelstein B,
                                                                                                                                                                                                                        (UYJO ) UNIV JOHNS HOPKINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF40688 standard; DNA; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                 Saccharomyces cerevisiae.
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                                                                                                                                                                                                                                                                                              WPI; 2001-061874/07.
                                                                                 WO200077214-A2
                                                                                                                                                                                        16-JUN-1999;
                                                                                                                                                                                                                                                           Velculescu V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2001
                                                                                                                    21-DEC-2000
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ID AAF4
XX
AC AAF4
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DT 23-M
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Kinzler K;

99US-00335032

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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonamnotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a contiguous nucleotides of a NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to stonic phases of the cell cycle. The contiguous mucleotides as markers of phases of the cell cycle. The contiguous may be used to identify candidate drugs which affect the cell cycle and for identify candidate drugs which affect the cell cycle and for identify candidate drugs which affect the cell cycle and for identify candidate drugs which affect the cell cycle are markers of phases of the cell cycle and for identify candidate drugs which affect the cell cycle and for identify candidate drugs which affect the cell cycle and for identify and the exemplification of antifungal drugs, the differentially represent SAGE tags used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;
Example; Page 265; 419pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP
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-AAF38499
ID AAF3849
XX
AC AAF3845
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Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7427.

Yeast, Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification;

Kinzler K;

Velculescu V, Vogelstein B,

WPI; 2001-061874/07.

UNJO ) UNIV JOHNS HOPKINS

99US-00335032.

16-JUN-1999;

Kinzler K;

14-JUN-2000; 2000WO-US016223

Saccharomyces cerevisiae.

WO200077214-A2.

21-DEC-2000.

linker; PCR primer; ds.

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4132.

23-MAR-2001 (first entry)

AAF37393;

```
Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
                              Yeast, Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.
                Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5238.
                                                                                                                                                                                                                                                         Example; Page 187; 419pp; English.
                                                                                                                                                                                     Velculescu V, Vogelstein B,
                                                                                                                                 14-JUN-2000; 2000WO-US016223.
                                                                                                                                                  99US-00335032
                                                                                                                                                                    (UYJO ) UNIV JOHNS HOPKINS
23-MAR-2001 (first entry)
                                                                             Saccharomyces cerevisiae.
                                                                                                                                                                                                     WPI; 2001-061874/07.
                                                                                               WO200077214-A2.
                                                                                                                                                  16-JUN-1999;
                                                                                                                21-DEC-2000
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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonamnotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log the cast 10% between any two phases of the cell cycle selected from log comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of varies as in M1, where a test substance which modifies the expression of the yeast gene with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of comprising contacting human DNA with a probe which comprises at least 10 comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a continuitor and affect phases of the cell cycle procession is affected by the class of drugs. The NORF gene whose expression is affected by the class of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the class of cycle and for identify candidate drugs which affect the cycle and for identify candidate drugs which affect the cycle and for identify candidate drugs which affect the cycle and for identify candidate drugs which affect the cycle and for identify candidate drugs which affect the cycle and for identify candidate drugs which affect the cycle and for identify candidate drugs which affect the cycle and for identify candidate drugs which affect the cycle and the exemplification of antifungus m
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                                                 Gaps
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Query Match 38.2%; Score 8.4; DB 1; Length 10; Best Local Similarity 90.0%; Pred. No. 5.2e+02; Matches 9; Conservative 0; Mismatches 1; Indels
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AAF37393 standard; DNA; 10 BP.

RESULT 676 AAF37393 ID AAF

g

736 AAACAGAACA 745 AAACAGAGCA 10

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729 CCAGGAGAAA 738
                                                   1 CCAGAAGAAA 10
Best Loca
Matches
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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonaminotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at cycle comprising administering a NORF gene whose expression nearly phase, S. phase and G2/M; (2) a method (M2) for screening candidate on thirdungal drugs comprising: (a) contacting a test substance which a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for contacting human genes which are involved in cell cycle progression of comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression is affected by the class of drugs. The NORF gene whose contiguous nucleotides of a nor gene candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a feet phases of the cell cycle, the differentially contenting expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of the cell cycle, the differentially contents may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. Analysise to AAF4316C cycle and for identification of antifungal drugs. Analysise in the exemplification of the present invention. .; 0 Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle. Gaps .. 0 Similarity 90.0%; Pred. No. 5.2e+02; 9; Conservative 0; Mismatches 1; Indels Sequence 10 BP; 6 A; 2 C; 2 G; 0 T; 0 U; 0 Other; Example; Page 147; 419pp; English Query Match Best Local Similarity

scnurczı-/2/.rng

AAF38223 standard; DNA; 10 BP. (first entry) 23-MAR-2001 AAF38223; RESULT 677

reast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonamotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds. Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4962.

Saccharomyces cerevisiae.

WO200077214-A2

21-DEC-2000.

14-JUN-2000; 2000WO-US016223.

99US-00335032. 16-JUN-1999;

(UYJO ) UNIV JOHNS HOPKINS

Kinzler K; Vogelstein B, Velculescu V,

WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 177; 419pp; English.

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonamontated ORP) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate cell; and (b) monitoring expression of a NORF gene whose expression of varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for cell; and (b) monitoring expression of a NORF gene whose expression of identifying human genes which are involved in cell cycle progression contiguous nucleotides of a NORF gene whose expression varies as in M1, and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a contiguous nucleotides of a NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to stressed genes may be used to dentify candidate drugs which affect the cell cycle in the expession of an expression of a cycle and for identification of an expressed genes may be used to identify candidate drugs which affect the cell cycle and for identification of an expression of the present invention.

AAF31262 to AAF31267 represent linkers and PCR primers used in the exemplification of the present invention. AAF3

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XAC

AAF3

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AAF3

YAF3

Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 U; 0 Other;

0; Gaps Query Match

38.2%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 5.2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels

TGCCAGGAAA 10

g

AAF42636 standard; DNA; 10 BP.

AAF42636;

(first entry) 23-MAR-2001 Teast NORF gene SAGE tag oligonucleotide SEQ ID NO:10775.

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae.

WO200077214-A2

21-DEC-2000

14-JJN-2000; 2000WO-US016223.

99US-00335032 16-JUN-1999;

(UYJO ) UNIV JOHNS HOPKINS.

Kinzler K; Vogelstein B, Jelculescu V,

WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 334; 419pp; English.

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonmoneted OR7) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF gene whose expression varies by at cycle comprising administering a NORF gene whose expression varies by at cast 10% between any two phases of the cell cycle selected from log phase. S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a MORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression of a Mortising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a contiguous nucleotides of a NORF gene whose expression in a class of drugs having a characteristic effect on gene expression in a contoring expression in the yeast cell of work gene whose corresponding and monitoring expression in the yeast cell of cut of the differentially expression is affected by the class of drugs. The NORF gene whose expression in a contoding may be used to identify candidate drugs which affect the cell cycle. The methods may be used to identify candidate drugs. April 2056 to AAF31205 t method, in the exemplification of the present invention 

Sequence 10 BP; 1 A; 1 C; 1 G; 7 T; 0 U; 0 Other;

Gaps .; 0 Score 8.4; DB 1; Length 10; Pred. No. 5.2e+02; 0; Mismatches 1; Indels Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative

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727 TGCCAGGAGA 736

736 AAACAGAACA 745 ò g

10 AAACAGAATA

RESULT 679

AAF42385 standard; DNA; 10 BP.

AAF42385;

(first entry) 23-MAR-2001 Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:9124.

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonamnotated ORF; SAGE; sectal analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae.

WO200077214-A2.

21-DEC-2000

14-JUN-2000; 2000WO-US016223

99US-00335032 16-JUN-1999;

SNINGO ONIV JOHNS HOPKINS

Kinzler K;

Velculescu V, Vogelstein B,

WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 325; 419pp; English

Example; Page 82; 419pp; English

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonamnotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag, Also described are: (1) a method (M1) of using NORF genes to affect the cell comprising administering an NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate of the cell; and (b) monitoring expression of a NORF gene whose expression of antifungal drugs comprising: (a) contacting a test substance which a yeast cell; and (b) monitoring expression of a NORF gene whose expression of varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression controlled and comprises of a NORF gene whose expression varies as in M1, and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a control expression is affected by the class of drugs. The NORF gene whose expression is affected by the class of the cell cycle, the differentially expression is affected by the class of the cell cycle, the differentially expression is affected as markers of phases of the cell cycle, the differentially expression and feet phases of the cell cycle, the differentially expressed genes may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF33261 represent sAGE tags used in the exemplification of the present invention AND SECOND CONTROLL OF THE SECOND CONTROLL OF

Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;

ö Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle. Yeast, Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds. Gaps .. 0 Score 8.4; DB 1; Length 10; Pred. No. 5.2e+02; 0; Mismatches 1; Indels Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2309. Kinzler K; AAF35570 standard; DNA; 10 BP 38.2%; 90.0%; 99US-00335032. Velculescu V, Vogelstein B, 14-JUN-2000; 2000WO-US016223 SNINGO NINU ( OLYU) (first entry) 9; Conservative Saccharomyces cerevisiae. 728 GCCAGGAGAA 737 1 GCCAGGACAA 10 WPI; 2001-061874/07. Best\_Local Similarity Matches 9; Conserv WO200077214-A2. 16-JUN-1999; 23-MAR-2001 21-DEC-2000. AAF35570; Query Match RESULT 680 AAF3557 임 à 

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previoually assigned open reading frame; or nonnoctated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising admissering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, 5 phase and G2/M; (2) a method (M2) for screening candidate attituding a comprising of (a) contacting a test substance which a yeast cell; and (b) monitoring expression of a NORF gene whose expression of varies as in M1, where a test substance which modifies the expression of varies as in M1, where an explained in cell; (3) a method (M3) for identifying a method (M3) for identifying a contiguous nucleotides of a NORF gene whose expression in a method (M4) for identifying a condidate drug as a member of a contiguous nucleotides of a NORF gene whose expression is affected by the class of the cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of the cell cycle, the differentially expression is affected by the class of the cell cycle, the differentially expression is affect by a markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. Antiferentially expression is affected by the class of the cell cycle the present invention. April 222 to AAF13267 represent linkers and per method, in the exemplification of the present invention.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                    Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
                                                                                                                                                                                                                                                                                                                        nor previously assigned open reading frame; nonamotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.
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                                         38.2%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 5.2e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                        Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8426.
               BP; 5 A; 2 C; 2 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kinzler K;
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                                                                                                                                                                                                     AAF41687 standard; DNA; 10
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                                                                                                                                                                                                                                                            (first entry)
                                                                        Conservative
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                                                                                                  735 GAAACAGAAC 744
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                                                       Local Similarity
les 9; Conserv
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                Sequence 10
                                                                                                                                                                                                                                                            23-MAR-2001
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                                                                                                                                                                                                                                 AAF41687;
                                            Query Match
                                                           Best Loca
Matches
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The present invention describes a method for genotyping a human matrix metalloproteinase 3 (MMP3) gene of an individual. MMP3 has vulnerary, cytostatic and antiatreriosclerotic activity, and can be used in gene therapy. The method can be used: for improving the efficacy and reliability of several steps in the discovery and development of drugs for treating diseases associated with MMP3 as a candidate of an coronary atherosclerosis, to validate MMP3 as a candidate associated with MMP3 activity, and in the design of clinical trials of associated with MMP3 activity, and in the design of clinical trials of candidate drugs for treating a specific condition or disease predicted to be associated with MMP3 activity, and in the design of clinical trials of candidate drugs for treating a specific condition or disease predicted to be associated with MMP3 activity. Polymorphic variants of a reference sequence for MMP3 (see ABL01223) are useful in studying the expression and function of MMP3, and in expressing MMP3 protein for use in screening for candidate drugs to treat diseases related to MMP3 activity. ABL01225 to ABL01246 and ABL01227 to ABL01290 represent allele-specific coligonucleotide (ASO) probes and primers used in the detection of polymorphisms in the human MMP3 gene. ABL01291 to ABL0134 represent preferred primers used in the detection of polymorphisms in the human maps.
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represent SAGE tags used in the exemplification of the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, matrix metalloproteinase 3; MMP3; chromosome 11q22.3; SNP; haplotype; polymorphism; polymorphism; probe; primer; detection; genotyping; vulnerary; cytostatic; cancer; antiateriosclerotic; gene therapy; coronary atherosclerosis;
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                                                                                                                                                                                                                        Length 10;
                                                                                                                                                                                                                    Score 8.4; DB 1; Length 10 Pred. No. 5.2e+02; 0; Mismatches 1; Indels
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                                                                                                                                                    Seguence 10 BP; 7 A; 2 C; 1 G; 0 T; 0 U; 0 Other,
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ID ABL01295 standard; DNA; 10 BP.
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Similarity 90.0%;
9; Conservative (
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2000US-0218092P
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               wound healing; ss.
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13-JUL-2000;
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Primer-extension oligonucleotide #11 to detect human SCYA1 polymorphisms.
SQ Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a method for genotyping a human matrix metalloproteinase 3 (MMP3) gene of an individual. MMP3 has vulnerary, cytostatic and antiarteriosclerotic activity, and can be used in gene therapy. The method can be used: for improving the efficacy and craspy. The method can be used: for improving the efficacy and craspy. The method can be used: for improving the efficacy and craspy. The method can be used: for improving the efficacy and craspy. The method can be used: for improving the efficacy and candidate or associated with MMP3 activity, or alignate MMP3 as a candidate agent for treating a specific condition or disease predicted to be associated with MMP3 activity, and in the design of clinical trials of candidate drugs for treating a specific condition or disease predicted to be associated with MMP3 activity. Polymorphic variants of a reference or and function of MMP3, and in expressing MMP3 protein for use in screening for candidate drugs to treat diseases related to MMP3 activity, ABL01225 to ABL01247 to ABL01290 represent allele specific oligonucleotide (ASO) probes and primers used in the detection of polymorphisms in the human MMP3 gene. ABL01291 to ABL0134 represent MMP3 gene

MMP3 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, matrix metalloproteinase 3; MMP3; chromosome 11q22.3; SNP;
haplotype; polymorphism; polymorphic; single nucleotide polymorphism;
probe, primar; detection; genotyping; vulnerary; cytostatic; cancer;
antiarteriosclerotic; gene therapy; coronary atherosclerosis;
wound healing; ss.
                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene polymorphism detection primer SEQ ID NO:89.
                                                                                                   Score 8.4; DB 1; Length 10;
Pred. No. 5.2e+02;
0; Mismatches 1; Indels
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                                                   Sequence 10 BP; 6 A; 2 C; 2 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Choi JY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 17; Page 15; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    ABL01310 standard; DNA; 10 BP.
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13-JUL-2000; 2000US-0218092P.
                                                                                                         38.2%;
90.0%;
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                                                                               Query Match
Best Local Similarity 90.0
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  MMP3 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a human maturation/activation dendritic cell (DC) expression among the group consisting of 100 genes which show the highest expression among the genes expresd in human maturation/ activation DC. Also described are: (1) a protein expressed by the above human maturation/activation DC expression gene; (2) an antibody against the protein, and (3) an antagonist against the expression of each gene belonging to the above gene group. The gene group is useful for the treatment and the diagnosis of various human diseases related to human
                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, maturation/activation dendritic cell expression gene, tag, maturation, activation, dendritic cell, ss.
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Pred. No. 5.2e+02;
0; Mismatches 1; Indels
  Length 10;
                                                  Indels
Score 8.4; DB 1; L
Pred. No. 5.2e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10; Page 13; 41pp; Japanese.
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  Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative
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Similarity 90.0%;
9; Conservative (
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                                                                                                     727 TGCCAGGAGA 736
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Best Local Similarity
Matches 9; Conserv
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AAS14466
ID AAS1446
AC AAS1446
XX
DT 23-APR
XX
DE Primer
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Human chronic hepatitis C tissue expression exasperating gene group comprises 100 high-ranking genes.
              (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                           Claim 19; Page 16; 139pp; Japanese.
                                        WPI; 2002-631294/68.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to novel single nucleotide polymorphisms (SNPs) in the human small inducible cytokine A1-1309 (SCYA1) gene located on chromosome 17, and methods for haplotyping and/or genepotics of the solution make use of allele specific oligonucleotides (ASOs) as probes and primers and/or primer-extension oligonucleotides for detecting the SCYA1 gene polymorphisms. The polymucleotides and screened compounds are useful for the treatment of diseases associated with SCYA1 activity, such as atherosclerosis, human mannodeficiency virus (HIV) infection, and other inflammatory disorders detecting human SCYA1 gene polymorphisms
           Human, single nucleotide polymorphism, SNP, SCYA1; chromosome 17;
small inducible cytokine Al-I-309, haplotyping; genotyping; gene;
atherosclerosis; human immunodeficiency virus; HIV infection; primer; ss.
                                                                                                                                                                                                                                                                                     Genotyping human small inducible cytokine Al-I-309, homologous to mous
Tca-3 gene of individual, involves determining identity of nucleotide
pair at specific polymorphic sites for two copies of the gene.
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                                                                                                                                                                                                                                                                                                                                             Claim 17; Page 13; 58pp; English.
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                                                                                                                                                                                                                                 Koshy B,
                                                                                                                                                                                                     (GENA-) GENAISSANCE PHARM INC
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                                                                                                                                                 16-APR-2001; 2001WO-US012305.
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Matches 9; Conservative
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                                                                                                                                                                                                                                 Choi JY, Kliem SE,
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                                                                  Homo sapiens
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The invention relates to SAGE (serial analysis of gene expression) tags representing groups of genes which are differentially expressed in human chronic hepatitis C (CH) liver cingsue or hepatitis C-induced human human liver consists of the SAGE tags of this invention consist of a sequence of 10 nucleotides located downstream of the 5'-CATG-3' sequence motif lying nearest to the polyA region of cDNAs derived from a variety of genes. These tags serve to uniquely identify each transcript and can thus be used to analyse the pattern of gene expression in particular cell types. The invention also relates to proteins encoded by the genes expressed in chronic hepatitis C inchronic hepatitis C antibodies against these proteins, and inhibitors of the expression of groups of genes that are overexpressed in chronic hepatitis C liver tissue or HCC. Groups of genes differentially expressed the chronic hepatitis C tissue or HCC droups of genes differentially expressed in chronic hepatitis C tissue or HCC droups of genes differentially expressed treatment of these diseases. Such genes, inhibitors of their expression or activity, and antibodies against the gene products may be used in the ABV84391-ABV84490 are SAGE tags representing the 100 most highly expressed in the expressed genes out of those genes which are overexpressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAGE tag; serial analysis of gene expression; human; chronic hepatitis C; CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC; expression pattern; differential expression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hepatocellular carcinoma compared with normal liver tissue
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les 9; Conserv
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Page 312

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The invention relates to SAGE (serial analysis of gene expression) tags representing groups of genes which are differentially expressed in human chronic hepatitis C (CH) liver tissue or hepatitis C induced in human chronic hepatocellular carcinoma (HCC) compared with normal human liver tissue.

The SAGE tags of this invention consist of a sequence of 10 nucleotides looky region of the S'-CATG-3' sequence motif lying nearest to the polyh region of cobns derived from a variety of genes. These tags serve to uniquely identify each transcript and can thus be used to analyse the pattern of gene expression in particular cell types. The invention also relates to proteins encoded by the genes expressed in chronic hepatitis C liver tissue or HCC, antibodies against these proteins, and inhibitors of the expression of groups of genes that are overexpressed in chronic hepatitis C liver tissue or HCC (groups of genes differentially expressed in chronic hepatitis C tissue or HCC (groups of genes differentially expression of these diseases. Such genes, inhibitors of their expression or activity, and antibodies against the gene products may be used in the expression of analyse to treat dironic hepatitis C and/or HCC. Sequences and antibodies against the gene products may be used in the expression are contracted the expression are contracted the expression are contracted to a contracted the expression of these diseases. Such genes inhibitors of their expression are contracted the expression are contracted the expression are contracted to a contracted the expression are contracted the expression are contracted to the expression are contracted to the expression are contracted the expression and the expressi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expressed genes out of those genes which are overexpressed in hepatcocllular carcinoma compared with chronic hepatitis C liver tissue
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Claim 37; Page 22; 139pp; Japanese
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90.0%;
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located downstream of the 5'-CATG-3' sequence motif lying nearest to the polyA region of cDNAs derived from a variety of genes. These tags serve to uniquely identify each transcript and can thus be used to analyse the pattern of gene expression in particular cell types. The invention also relates to proteins encoded by the genes expressed in chronic heparitis of liver tissue or HCC, antibodies against these proteins, and inhibitors of the expression of groups of genes that are overexpressed in chronic hepatitis of lisue or HCC groups of genes differentially expressed in chronic hepatitis of lisue or HCC may be used for the diagnosis and treatment of these diseases. Such genes, inhibitors of their expression or activity, and antibodies against the gene products may be used in the development of drugs to treat chronic hepatitis of and/or HCC. Sequences ABV844201-ABV84430 are SAGE tags representing the 100 least highly expressed genes out of those genes which are underexpressed in chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated androgen-regulated gene (ARG) designated as PMEPA1. The invention is useful for selecting primers and probes for detecting prostate cancer cells in a biological sample by using nucleic acid amplification techniques. The present sequence is human ARG energy metabolism, apoptosis and redox regulator
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te cancer cells in
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                                                                                                                                                                                                                                                                       expressed genes out of those genes which are underexpresse
hepatitis C liver tissue compared with normal liver tissue
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31-JAN-2000; 2000US-0179045P.
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Best Local Similarity 90.0
Matches 9; Conservative
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Score 8.4; DB 1; Length 10; Pred. No. 5.2e+02;

38.2%; 90.0%;

Best Local Similarity

Query Match

The invention relates to SAGE (serial analysis of gene expression) tags representing groups of genes which are differentially expressed in human chronic hepatitis C (CH) liver tissue or hepaticis C-induced hepatocellular carcinoma (HCC) compared with normal human liver tissue. The SAGE tags of this invention consist of a sequence of 10 nucleotides

Claim 10; Page 14; 139pp; Japanese.

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Matches

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The invention relates to identifying (MI) genes in vitro that, in humans or animals, are important for skin ageing and/or skin stress by serial analysis of gene expression between mixtures of transcribed and optionally translated, genetically encoded factors (A) obtained from young and aged skin, to identify that genes that show strong differential expression. (A) comprises protein or mRNAs or their fragments. (MI) is useful for: identifying markers of skin ageing and/or stress; determining skin ageing and/or stress; and identifying or determining the effects of pharmaceutical or cosmetic agents for control of skin ageing. The present sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ86246-ABQ87680) of the invention
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                      Human; skin ageing; skin stress; EST; expressed sequence tag;
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    Indels
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    Mismatches
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                                                                                                                                                                      ABQ86777 standard, cDNA; 11 BP
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ABQ86292 standard; cDNA; 11
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Matches 9; Conservative
9; Conservative
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                                       731 AGGAGAACA 740
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RESULT 691

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WPI; 2002-528865/56
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Matches 9; Conserv
                                                                                                                         WO200253773-A2
                                                                                                                                                    Petersohn D,
                                                                                                                    Homo sapiens
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                                                                                               ABQ86986,
                  Claim
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ABQ86986
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skin ageing and/or stress; and identifying or determining the effects of pharmaceutical or cosmetic agents for control of skin ageing. The present sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ86246-ABQ87680) of the invention
                                                                                                       Seguence 11 BP; 4 A; 2 C; 4 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human skin stress/ageing related EST
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                                                                                                                                               38.2%;
90.0%;
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Local Similarity 90.0%;
les 9; Conservative (
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Matches 9; Conservative
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                                                                                                                                                                                 The invention relates to identifying (M1) genes in vitro that, in humans or animals, are important for skin ageing and/or skin stress by serial analysis of gene expression between mixtures of transcribed and optionally translated, genetically encoded factors (A) obtained from young and aged skin, to identify that genes that show strong differential useful for: identifying markers of skin ageing and/or stress; determining skin ageing and/or stress; and identifying or determining the effects of pharmacoutical or cosmetic agents for control of skin ageing. The present sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ87680) of the invention
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                                                                     Identifying genes involved in skin stress and aging, useful e.g. in screening for cosmetic or therapeutic agents, based on differential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
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                                                                                                                                                     German.
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                                                                                                                                                     8; Page 62; 325pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying genes involved in skin stress and aging, useful e.g. in screening for cosmetic or therapeutic agents, based on differential gene
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Score 8.4; DB 1; Length 11; Pred. No. 5.4e+02; 0; Mismatches 1; Indels
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ABV68185;

RESULT 695

ABV68185,

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sumburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
                                                                                                                                                                                                                                                                                                                                                                          In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis,
psoriasis, dermatitis, skin cancer, EST, expressed sequence tag; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence 11 BP; 3 A; 4 C; 3 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38.2%; Score 8.4; DB 1;
90.0%; Pred. No. 5.4e+02;
tive 0; Mismatches 1;
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ID ABV71340 standard; cDNA; 11
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                                                               WO200253774-A2.
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                       Homo sapiens.
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                                                                                                          11-JUL-2002
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Matches
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                                                                                                                                                                                                           Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGB; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.
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                                 ABV68185 standard; cDNA; 11 BP.
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                                                                                                                                                                     Human skin EST 5971
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Best Local Similarity
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RESULT 696

ABV65377;

ABV65377
ID ABV6
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Length 11; 1; Indels

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Hofmann

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 80; 1345pp; German.
Conradt M,
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-590638/63
                                                                                                                                                                                                                                                                                  Human skin EST 2012
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                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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Petersohn
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so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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                                                                                                                                                              In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermaritis; acne; seborrhea; lupus erythematosus; rosacea, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.
                                                                                                                                                           Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGB; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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                            ABV70263 standard; cDNA; 11
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                                                                                                21-OCT-2002
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                                                              ABV70263;
              RESULT 699
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DB 1; Length 11;

Score 8.4;

38.28;

Query Match

Hofmann K;

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Conradt

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically seconded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
                                                                                        Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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Pred. No. 5.4e+02;
0; Mismatches 1;
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90.08;
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Best Local Similarity
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38.2%; Score 8.4; DB 1; Length 11; 90.0%; Pred. No. 5.4e+02; tive 0; Mismatches 1; Indels
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es 9; Conservative
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ABV62887 standard; cDNA; 11

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Conradt M, .Hofmann K;

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis, to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; contractions is maintain to the contraction of the contraction of
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38.2%; Score 8.4; DB 1; Length 11; 90.0%; Pred. No. 5.4e+02; ive 0; Mismatches 1; Indels

In vitro identification of skin-expressed genes, useful for determining

Hofmann K;

Conradt M,

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression (M1) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; subburn; psoriasis; scleroderma;
                                                                                        The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression (M1) is useful for identifying genes involved in skin homeostasis, to be determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis, subburn, psoriasis, selecterma;
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trive 0; Mismatches 1;
                                                          Disclosure; Page 146; 1345pp; German.
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne, seborrhea; lupus erythematosus; rosaces, melanoma; basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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                                                                                         ABV67553 standard; cDNA; 11
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                                                                                                                                                                                                  Human skin EST 5339
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ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; trosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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38.2%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 5.46+02;
Matches 9; Conservative 0; Mismatches 1; Indels
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                                                                                       Sequence 11 BP; 0 A; 2 C; 3 G; 6 T; 0 U; 0 Other;
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Best Local Similarity 90.00,
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Hofmann K;

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                          Query Match 38.2%; Score 8.4; DB 1; Length 11; Best Local Similarity 90.0%; Pred. No. 5.4e+02; Matches 9; Conservative 0; Mismatches 1; Indels
Sequence 11 BP; 4 A; 1 C; 6 G; 0 T; 0 U; 0 Other;
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736 AAACAGAACA 745

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(M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for tracting skin disorders, specifically neurodermatitis, sumburn; psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; ichthyosis; melanoma; basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic,
immunosuppressive, antiinflammatory, cytostatic; SAGE, neurodermatitis,
psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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ABV68446 standard; CDNA; 11 BP
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AC ABV68446;
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DT 21-OCT-2002 (first entry)
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KW Human skin EST 6232.
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KW immunosuppressive; antiinflamm:
XW psortasis; dermatitis; skin can
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Homo sapiens.
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MO200253774-A2.
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YA-2001; 2001WO-EP015179.
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YA-2001; 2001WO-EP015179.
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Best Local Similarity
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                                                                                   Homo sapiens
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Pred. No. 5.4e+02;
0; Mismatches 1; Indels
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                                           Hofmann K;
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Best Local Similarity 90.0%;
Matches 9; Conservative C
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                                           Conradt M,
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Disclosure; Page 143; 1345pp; German

Sequence 11 BP; 4 A; 2 C; 4 G; 1 T; 0 U; 0 Other;

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(M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis and to test agent (B) that maintains or promotes skin homeostasis and to test agent (B) that maintains or disorders, specifically neurodermatitis; sunburn; psoriasis; soleroderma; ichhyosis; atopic dermaitis; acne; seborrhea; lupus crythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sumburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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Pred. No. 5.4e+02;
0; Mismatches 1; Indels
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Score 8.4; DB 1; Length 11 Pred. No. 5.4e+02; 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 8.4; DB 1;
Pred. No. 5.4e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 24; Page 258; 1345pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hofmann
                                .
                                                                                                                                                                  ABV70308 standard; cDNA; 11 BP.
 38.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                             20-DEC-2001; 2001WO-EP015179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-JAN-2001; 2001DE-01000127.
                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 90.0
Entry 91.0
Conservative
Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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                                                           729 CCAGGAGAAA 738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Petersohn D, Conradt
                                                                                          1 CCAGGAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AACAGAACGC
                                                                                                                                                                                                                                                            Human skin EST 8094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HENK ) HENKEL KGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-590638/63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e.g. skin cancer.
                                                                                                                                                                                                                                                                                                                                                                                 WO200253774-A2.
                                                                                                                                                                                                                                                                                                                                                    sapiens.
                                                                                                                                                                                                                               21-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                              11-JUL-2002.
                                                                                                                                                                                                ABV70308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 712
AAV39563
                                                                                                                                       RESULT 711
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1 3 MES 1 A 32

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A process has been developed for determining the sequence of a target nucleic acid. The process comprises: (i) generating at least two rangements (f) from the target nucleic acid, and (ii) nallysing F by mass spectrometry (WS). The sequences in AAV3483 to AAV3592 are specifically claimed primers for use in the mass spectrometric analysis of the above process. The process is used to detect genetic diseases (e.g. haemophilia, thalassemia, Duchenne muscular dystrophy, Alzheimer's disease, cystic fibrosis and many others) or chromosomal abnormalities (or predisposition); infections and cancers; also for establishing identity and heredity. Particular applications are diagnosis of neuroblascoma, detecting telomerase, determining family relationships and HiA comparibility, and in genetic fingerprinting. Compared with known methods using MS, this process requires fewer specific reagents and is better suited to automation. Extended primers are shorter; primer annealing is more efficient and the process allows detection of many
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing nucleic acid by mass spectrometric analysis - for detecting nucleic acids, telomerase activity, oncogene mutations, or cancerspecific sequences, for diagnosis of disease.
                                                                                                                             Mass spectrometry, diagnosis, detection, biological sample, infection, genetic disease, chromosomal abnormality; identification; heredity; pathogenic organism; telomerase activity; oncogene mutation; cancer-specific sequence; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang K, Fu D, Siegert CW, Little DP, Higgins GS; Damhoffer-Demar B, Jurinke C, Van Den Boom D, Xiang G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 8.4; DB 1; Length 12;
Pred. No. 5.6e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12 BP; 5 A; 3 C; 4 G; 0 T; 0 U; 0 Other;
                                                                                              Mass spectrometric analysis primer SEQ ID NO:86.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 48; Page 266; 478pp; English
ВB
                                                                                                                                                                                                                                                                                                                                                                  960S-0074659
960S-00746036.
970S-0078698.
970S-00787639.
970S-0093792.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38.2%;
                                                                                                                                                                                                                                                                                                                                                       96US-00744481
                                                                                                                                                                                                                                                                                                                     97WO-US020444
AAV39563 standard; cDNA; 12
                                                                  (first entry)
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Best Local Similarity 90..
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences simultaneously
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SEQU-) SEQUENOM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-286975/25.
                                                                                                                                                                                                                                                     WO9820166-A2.
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                                                                  28-SEP-1998
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06-NOV-1996,
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19-SEP-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                           23 - JAN - 1997
                                                                                                                                                                                                                    Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Braun A,
Lough DM:
                              AAV39563
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nucleic acid. The process comprises: (i) generating at least two regaments (F) from the target nucleic acid, analysing F by mass regurences (MS). The sequences in AAV39483 to AAV39592 are specifically claimed primers for use in the mass spectrometric analysis of the above process. The process is used to detect genetic diseases (e.g. process. The process is used to detect genetic diseases (e.g. haemophila, thalassemia, Duchenne muscular dystrophy, Alzheimer's disease, cystic fibrosis and many others) or chromosomal abnormalities (or predisposition); infections and cancers, also for establishing cherrical and heredity. Particular applications are disgnosis of neuroblastoma, detecting telomerase, determining family relationships and HA comparibility, and in genetic fingerprinting. Compared with known methods using MS, this process requires fewer specific reagants and is better suited to automation. Extended primers are shorter; primer anneance of many contains and the process allows detection of many
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing nucleic acid by mass spectrometric analysis - for detecting nucleic acids, telomerase activity, oncogene mutations, or cancer-specific sequences, for diagnosis of disease.
                                                                                                                                              Mass spectrometry; diagnosis; detection; biological sample; infection; genetic disease; chromosomal abnormality; identification; heredity; pathogenic organism; telomerase activity; oncogene mutation; cancer-specific sequence; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Little DP, Higgins GS;
, Van Den Boom D, Xiang G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 12 BP; 5 A; 3 C; 4 G; 0 T; 0 U; 0 Other;
                                                                                                                   Mass spectrometric analysis primer SEQ ID NO:81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tang K, Fu D, Siegert CW, L
Damhoffer-Demar B, Jurinke C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 48; Page 264; 478pp; English.
                AAV39558 standard; cDNA; 12 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                             96US-00746055.
97US-00786988.
97US-00787639.
97US-00933792.
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96US-00746036.
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                                                                                    28-SEP-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequences simultaneously
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SEQU-) SEQUENOM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-286975/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                       WO9820166-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JAN-1997;
19-SEP-1997;
08-OCT-1997;
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06-NOV-1996;
06-NOV-1996;
06-NOV-1996;
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                                                                                                                                                                                                                                        Synthetic.
                                                    AAV39558;
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Lough DM;
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AAV39558
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GCCAGGACAA 11

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Gaps

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737

728 GCCAGGAGAA

GCCAGGACAA 11

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The present invention describes polymer compositions comprising a plurality of covalently bound polymer segments. The segments comprise:

(a) at least one polycation segment. The segments comprise:

conionic polymer segment. The polycation segment is a cationic homo- or copolymer comprising at least three cationic amino acids or at least three eationally lene monomers. The monomers are selected from: (i) at least one tertiary amino monomer of formula (I), or a quaternary salt of this; and (ii) at least one secondary amino monomer of formula (II), or an acid addition or quaternary salt of this. The compositions may be used for delivery of nucleic acids to cells. They may be used for treatment of genetic diseases, neoplastic diseases, cardiovascular diseases, infectious diseases or transplantation related disorders. Administration infectious diseases or transplantation related disorders. Administration by inhalation. The present sequence represents an oligonuclectide used in example from the present invention
                                                                                                                                                                      Cell membrane transfer; polynucleotide; polymer; polycation segment; genetic disease; neoplastic disease; cardiovascular disease; infectious disease; transplantation related disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell membrane transfer; polynucleotide; polymer; polycation segment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polymer compositions which include e.g. polycation segments
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kabanov AV, Alakov VY, Vinogradov SV;
                                                                                                                                       Antisense 12-chain oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 9; Page 56; 94pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 715
AAX19669/c
ID AAX19669 standard; DNA; 12 BP.
                  9666/c
AAX19666 standard; DNA; 12 BP.
                                                                                                                                                                                                                                                                                                                                                                                97US-00912968.
98US-00124943.
                                                                                                                                                                                                                                                                                                                                               98WO-US016012
                                                                                                                                                                                                                                                                                                                                                                                                                                    (SUPR-) SUPRATEK PHARMA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                    (first entry)
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tes 9; Conserv
                                                                                                                                                                                                                                                                             WO9906055-A1
                                                                                                    03-JUN-1999
                                                                                                                                                                                                                                                                                                                                                 31-JUL-1998;
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                                                                                                                                                                                                                                                                                                                11-FEB-1999.
                                                                                                                                                                                                                                            Synthetic.
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                                                                   AAX19666
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RESULT 714
AAX19666/c
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Matches
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The present invention describes polymer compositions comprising a plurality of covalently bound polymer segments. The segments comprise:

(a) at least one polycation segments. The segments comprise:

(a) at least one polycation segment is a cationic homonomic polymer segment. The polycation segment is a cationic homonomer seement. The polycation segment is a cationic homonomer seement monomers. The monomers are selected from:

(i) at least one tertiary amino monomer of formula (I), or a quaternary salt of this, and (ii) at least one secondary amino monomer of formula (II), or an adia addition or quaternary salt of this. The compositions may be used for delivery of nucleic acids to cells. They may be used for treatment of genetic diseases, neoplastic diseases, cardiovascular diseases, infectious diseases or transplantation related disorders. Administration infectious diseases or transplantation related disorders. Administration by inhalation. The present sequence represents an oligonucleotide used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; secreted protein; forensic procedure; gene therapy; chromosome mapping; canneer; autolimune disease; cardiovascular disorder; cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis; brain disorder; skeletal muscle disorder; eye disorder; obesity; mitochondriocyropathy; diabetes; atheroseclerosis; Alzheimer's disease; neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia; septic shock; impotence; promoter; P13H2; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                       New polymer compositions which include e.g. polycation segments.
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genetic disease, neoplastic disease, cardiovascular disease, infectious disease, transplantation related disorder, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 12 BP; 0 A; 4 C; 3 G; 4 T; 1 U; 0 Other;
                                                                                                                                                                                                                                                                                                Vinogradov SV;
                                                                                                                                                                                                                                                                                                                                                                                                              Example 21; Page 68; 94pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                      97US-00912968.
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                                                                                                                                                                                                                                                             (SUPR-) SUPRATEK PHARMA INC.
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Best Local Similarity 90.0.
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                              Alakov VY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           730 CAGGAGAAAC 739
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                                                                                                                                                                                                      01-AUG-1997;
                                                                                                                                                                   31-JUL-1998;
                                                                                                                                                                                                                          30-JUL-1998;
                                                                                          WO9906055-A1
                                                                                                                                                                                                                                                                                                  Kabanov AV,
                                                                                                                               11-FEB-1999
                                                        Synthetic.
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This sequence represents a transcription factor binding site identified in the human P13H2 promoter. The invention relates to sequences AAA87725-A8474 which encode human secreted proteins to sequences AAA87755-A8774 which encode human secreted proteins include signal peptides. The P13H2 promoter is used in the isolation of the cDNAs of the invention. Included in the invention are a host cell containing one of the cDNA sequences, and a purified antibody capable of binding to one of the sequence data on a computer system, and a methods for storing the sequence data on a computer system, and a method for identifying features of the cDNA sequences using a computer programme. The cDNAs are useful for expressing secreted proteins or fragments to obtain antibodies capable of specifically binding to the secreted proteins. The cDNAs may also be useful in diagnostic, forensic, secreted proteins. The cDNAs may also be useful in diagnostic, forensic, secreted proteins and secretion vectors. The proteins of the invention may be used to treat diseases including cancer, autoimmune diseases, cardiovascular disorders, cystic fibrosis, hypothyroidism, immunological disorders, amyloidosis, brain disorders, selectal muscle disorders, eve disorders, selectal muscle disorders, events and secretion and selectal muscle disorders, events and secretion disorders, and disorders, and disorders, and disorders, and dispersed to treat diseases.
                                                                                                                                                                                                                                                                                                                         Polynucleotides and polypeptides encoding proteins with signal peptides, useful in diagnostic, forensic, gene therapy and chromosome mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alzheimer's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neurodegenerative disorders, graft rejection, Alzheim
dementia, hyperlipidaemia, septic shock and impotence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12 BP, 9 A; 2 C; 0 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                          Duclert A;
                                                                                                                                                                                                                                                                                                                                                                                                                          Example 48; Fig 5; 306pp; English.
                                                 99WO-IB002058.
                                                                                                   98US-0113686P
                                                                                                                         99US-0141032P
                                                                                                                                                                                                                          Dumas J,
                                                                                                                                                                                                                                                                         WPI; 2000-442637/38.
                                                                                                                                                                                                                          Bougueleret L,
                                                                                                                                                                           (GEST ) GENSET
                                                                                                                         25-JUN-1999;
                                                 20-DEC-1999;
                                                                                                   22-DEC-1998;
29-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                                        procedures.
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Gaps ö 38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6+02; tive 0; Mismatches 1; Indels Query Match
Best Local Similarity 90.0.
Best Acad 9; Conservative ò

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AAA06954 standard; RNA; 12 BP. 03-JUL-2000 (first entry) AAA06954; RESULT 717 

Human XIAP IRES mutant polypyrimidine tract, SEQ ID NO:18.

X-linked inhibitor of apoptosis protein; XIAP; IRES; internal ribosome entry site; human; cap-independent translation; drug screening; cancer; autoimmune disease; degenerative disease; immunorejection; gene therapy; mutant; polypyrimidine tract; ss.

sapiens. Synthetic

WO200005366-A2

Block copolymer; genetic; neoplastic; cardiovascular; infectious disease; HIV; AIDS; cancer; Herpes Simplex Virus 1; HSV-1; antisense; oligonuclectide; DNA-RNA hybrid; ss.

Human herpesvirus 1.

Oligonucleotide complementary to part of Herpes Simplex Virus 1.

03-FEB-2000

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The invention relates to the identification of modulators of captidependent translation and apoptosis. The method comprises exposing a test compound to an X-linked inhibitor of apoptosis protein (XAAP) compound to an X-linked inhibitor of apoptosis protein (XAAP) compound relative to the translation from the unexposed XIAP IRES reporter cistron exposed to the compound relative to the translation from the unexposed XIAP IRES reporter cistron. A relative increase in translation from the exposed compound relative to the translation from the unexposed XIAP IRES reporter cistron indicates a compound that increases XIAP IRES dependent (app independent) translation. XIAP protein plays a critical cole in the regulation of apoptosis by suppressing activation of downstream caspase-3 and caspase-7. Compounds identified by the method cole in the regulation of apoptosis by suppressing activation of control decrease XIAP IRES-dependent translation (thus leading to reduced expression of XIAP and hence increasing apoptosis) can be used for the dentification of expression of XIAP and there used for the identification of agents that upregulate XIAP translation and hence inhibit apoptosis, which can be used to treat autoimmune diseases, degenerative diseases or immunorejection. Such agents may, for example, be used to inhibit apoptosis of neurons in conditions such as Alzheimer's disease; islet colls in autoimmune diabetes mellitus; photoreceptor cells in retinities pigmentosa and diabetic retinopathy; and cardiomycoytes after myocardial infarction. They can also be used to enhance the survival of cell or organ transplants. XIAP IRES elements can also be used to enhance the survival of cell or organ transplants. Why Pigmentosa and elabetic retinopathy; and cardiomycoytes after myocardial corgan transplants. Why Pigmentos of mutant human XFAP IRES polypyrimidine tract which, along with the wild-type polypyrimidine tract is important for XIAP IRES placed in an exemplification of the present invention to determine to make the intere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                          New isolated X-linked inhibitor of apoptosis internal ribosome entry site, used to develop agents for treating, e.g. cancer.
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                                                                                                                                                          Liston P;
                                                                                                                                                                                                                                                                                                             Example IV; Fig 5A; 87pp; English.
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99WO-IB001415.
                                          98US-00121979.
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Matches 9; Conservative
                                                                                                                                                        Holcik M,
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                                                                                                           UYOT- ) UNIV OFTAWA.
                                                                                                                                                                                                  WPI; 2000-338644/29
                                                                                                                                                        Korneluk RG,
22-JUL-1999;
                                          24-JUL-1998;
14-JUN-1999;
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The present invention relates to compositions of a polynuclectide or its derivatives and at least one polyoxychylene-polyoxypropylene block copolymer. The compositions of the invention form a molecular solution or colloidal dispersion. The invention is used for delivering a polynuclectide to a cell for gene therapy of an animal. Diseases that may be treated by the invention include genetic, neoplastic, cardiovascular and infectious diseases. The use of the block copolymers reduces the number of polynuclectide molecules and the time required to obtain an immune response, so that a booster injection is not required. Additionally, the risk of integration of polynuclectides into the chromosomes of the host organism is reduced and the risk of developing anti-polynuclectide antibodies is reduced. The present sequence is oligonuclectide A complementary to the splice site of the early mRNA of Herpes Simplex Virus I (HSV-1). This antisense oligonuclectide was an included the complementary to the aplice site of the early mRNA of Herpes Simplex Virus I (HSV-1). This antisense oligonuclectide manial man
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Composition for gene therapy comprises polynucleotide and polyoxyethylene polyoxypropylene block copolymer in amounts insufficient for gel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                designed to inhibit Herpes Virus. (Updated on 15-SEP-2003 to standardise
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                                                                                                                                                                                                                                                                                                                                                                                                                   Lemieux PM, Vinogradov SV, Alakhov VY;
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                       /*tag= a
/label= RNA
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misc_RNA
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to compositions of a polynucleotide or its derivatives and at least one polyoxyethylene-polyoxypropylene block copolymer. The compositions of the invention form a molecular solution or colloidal dispersion. The invention is used for delivering a polynucleotide to a cell for gene therapy of an animal. Diseases that may be treated by the invention include genetic, neoplastic, cardiovascular and infectious diseases. The use of the block copolymers reduces the number of polynucleotide molecules and the time required to obtain an Additionally, the risk of integration of polynucleotides into the chromosomes of the host organism is reduced and the risk of developing entipolicy multipolice is enduced. The present sequence is an oligonucleotide complementary to the splicing site at 983-994 of the Herpes Simplex Virus I (HSV-1). This antisense oligonucleotide was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Composition for gene therapy comprises polynuclectide and polyoxyethylene polyoxypropylene block copolymer in amounts insufficient for gel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           designed to inhibit Herpes Virus. (Updated on 15-SEP-2003 to standardise
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vinogradov SV, Alakhov VY,
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                       Location/Qualifiers
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AAA91863 standard; DNA; 12 BP.
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(first entry)
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Best Local Similarity 90.00
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05-JAN-2001
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misc_RNA
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AAA91863/c
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABE99989, ABF00010-ABE99989 and ABI00010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                      Set of oligonucleotides, useful for diagnosis and cell typing, addesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 321079; 29pp + Sequence Listing; German.
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                                                                                                       Berlin K;
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06-APR-2001; 2001WO-IB000713
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                                 07-APR-2000; 2000DE-01019173
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nes 9; Conservative
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                                                                    (EPIG-) EPIGENOMICS
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                                                                              This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and merabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                           Claim 1; SEQ ID NO 272577; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12 BP; 0 A; 0 C; 2 G; 10 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                  Oligonucleotide primer SEQ ID NO 314253 for detecting SNP TSC0026236.
                                                                                                                                Gaps
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                                                                                    38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02; ive 0; Mismatches 1; Indels
                                                   Sequence 12 BP; 0 A; 0 C; 5 G; 7 T; 0 U; 0 Other;
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9; Conservative (
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                 Oligonucleotide primer SEQ ID NO 316641 for detecting SNP TSC0027537.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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ABI16668 standard; DNA; 12 BP
XC
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ABI16668;
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ABI16668;
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DT 22-FBB-2002 (first entry)
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Cligomucleotide primer SEQ ID
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SNP; single nucleotide polymo
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SNP; single nucleotide polymo
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Central nervous system; gastr
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Homo sapiens.
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Chis invention describes nov
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABR00010-ABR9989, ABH00010-ABR9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
                                                                                                      Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                          Claim 1; SEQ ID NO 380688; 29pp + Sequence Listing; German.
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                 Olek A, Piepenbrock C,
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central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Series 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               designed to detect
methylation status.
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                                                                                                 WO200177384-A2
                                                   Homo sapiens
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ABI80715
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
Oligonuclectide primer SEQ ID NO 272424 for detecting SNP TSC0002812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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Length 12;

Score 8.4; DB 1; Length 12 Pred. No. 5.6e+02; ); Mismatches 1; Indels

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38.2%;

Query Match
Best Local Similarity 90.0
Matches 9; Conservative

735 GAAACAGAAC 744

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12 GAAACAAAAC

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and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 -ABC99989, ABF0010-ABF99989, ABF0010-ABF99989 and ABI0010-ABF89989 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                            38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                    1; Indels
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Best Local Similarity 90.0
Matches 9; Conservative
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06-APR-2001; 2001WO-IB000713.

WO200177384-A2. Homo sapiens.

18-OCT-2001.

07-APR-2000; 2000DE-01019173.

Olek A, Piepenbrock C,

WPI; 2001-657177/75.

(EPIG-) EPIGENOMICS AG

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonucleotide primer SEQ ID NO 304044 for detecting SNP TSC0020762.

(first entry)

22-FEB-2002

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ABI04071 standard; DNA; 12 BP.

RESULT 729 ABI04071

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                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE9989, ABF00010-ABE9989, ABH00010-ABH99989 and ABI00010-ABI32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Pred. No. 5.6e+02;
0; Mismatches 1; Indels
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90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
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ABIS9560
ID ABIS956
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Sequence 12 BP; 1 A; 1 C; 2 G; 8 T; 0 U; 0 Other;

ftp.wipo.int/pub/published\_pct\_sequences

bet of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

18-OCT-2001

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                            SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                             Oligonucleotide primer SEQ ID NO 359533 for detecting SNP TSC0051639
                                                                                                                                                                                                                                                                                                                                                                                                                                   set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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 ABI59560;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI83073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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datches 9; Conservative
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                                                                                                                                       Piepenbrock C,
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABF00010-ABF9989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at fixe wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligonucleotide primer SEQ ID NO 351275 for detecting SNP TSC0047201.
Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                         Claim 1; SEQ ID NO 344412; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99889 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                       Length 12;
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                                                                                                    Sequence 12 BP; 0 A; 4 C; 0 G; 8 T; 0 U; 0 Other;
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                                                                                                                                       Score 8.4; DB 1;
Pred. No. 5.6e+02;
                                                                                                                                                                      0; Mismatches
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Best Local Similarity 90.0%
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metholic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 care the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but fip.wipo.int/pub/published_pct_sequences
                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                         Oligonucleotide primer SEQ ID NO 381996 for detecting SNP TSC0064673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                  ABI82023 standard; DNA; 12
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

06-APR-2001; 2001WO-IB000713.

WO200177384-A2

18-OCT-2001

Oligonuclectide primer SEQ ID NO 274637 for detecting SNP TSC0003624.

(first entry)

22-FEB-2002

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Gaps

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ABH74652;

ABH74652 standard; DNA; 12 BP.

RESULT 737

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         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                 Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABF8073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ABI04241/c
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Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

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Berlin

Olek A, Piepenbrock C,

WPI; 2001-657177/75.

(EPIG-) EPIGENOMICS AG

07-APR-2000; 2000DE-01019173.

Claim 1; SEQ ID NO 300071; 29pp + Sequence Listing; German.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SND; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                      Gaps
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                                                             38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02; tive 0; Mismatches 1; Indels
Sequence 12 BP; 1 A; 0 C; 5 G; 6 T; 0 U; 0 Other;
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ABI39615 standard; DNA; 12 BP.
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Best Local 9; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABF00010-ABF9989, and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                             Oligonucleotide primer SEQ ID NO 341601 for detecting SNP TSC0008742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                 Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                Claim 1; SEQ ID NO 377760; 29pp + Sequence
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ABH69031
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Berlin K;

Olek A, Piepenbrock C,

(EPIG-) EPIGENOMICS

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range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99889, ABF00010-ABF99889, ABF00010-ABF99889 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                     38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02;
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Best Local Similarity 90.0.
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ABH96984/C

ABH96984/C

ABH96984/C

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                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                               Oligonucleotide primer SEQ ID NO 272355 for detecting SNP TSC0002794.
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 Mismatches
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                                                                                                                                                   ABH72374 standard; DNA; 12 BP.
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ABI28308

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                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                Oligonucleotide primer SEQ ID NO 328281 for detecting SNP TSC0034210.
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38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02; ive 0; Mismatches 1; Indels

Query Match
Best Local Similarity 90.0.

737 AACAGAACAC 746

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Sequence 12 BP; 7 A; 4 C; 0 G; 1 T; 0 U; 0 Other;

ftp.wipo.int/pub/published\_pct\_sequences

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Berlin K;

Piepenbrock C,

Olek A,

WPI; 2001-657177/75

(EPIG-) EPIGENOMICS AG

06-APR-2001; 2001WO-IB000713 07-APR-2000; 2000DE-01019173

(first entry)

22-FEB-2002

Claim 1; SEQ ID NO 279303; 29pp + Sequence Listing; German.

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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methylation status.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABEG09999, ABE00010-ABE99989 and ABE00010-ABE99989 represent the oligomers described in the invention. NOTE: The sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                       Claim 1; SEQ ID NO 284553; 29pp + Sequence Listing; German.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABF09989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                       Gaps
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                                                                                                               38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02; tive 0; Mismatches 1; Indels
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ftp.wipo.int/pub/published_pct_sequences
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cancertal incrous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                Oligonucleotide primer SEQ ID NO 297818 for detecting SNP TSC0017786.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               designed to detect methylation status.
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peptide nucleic acid, cytosine methylation; cardiovascular; primer, ss; central nervous system; gastrointestinal; respiratory; immune; metabolic
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                                                                                                                                     This invention describes novel oligonucleotide primers or peptide nucleic
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically prerreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic discorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at
                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                        Oligonucleotide primer SEQ ID NO 274235 for detecting SNP TSC0003487
                                                                                                                                                                                                                                                                                                                                                                                                                                                  bet of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                        38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred, No. 5.6e+02; ive 0; Mismatches 1; Indels
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989, ABH00010-ABH99999 and ABI00010-ABI82073 trepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                      designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                             Claim 1; SEQ ID NO 305402; 29pp + Sequence Listing; German.
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oligomers are also used for detecting cell type differentiation. ABC00010 -ABC9989, ABF00010-ABF99899, ABF00010-ABF99899, ABF00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fig. wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                          Gaps
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                                                                                                                          38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02; tive 0; Mismatches 1; Indels
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                                                                                                 Sequence 12 BP; 8 A; 4 C; 0 G; 0 T; 0 U; 0 Other;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 307035; 29pp + Sequence Listing; German
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                   07-APR-2000; 2000DE-01019173.
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                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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  Oligonucleotide primer SEQ ID NO 305010 for detecting SNP TSC0021207.
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                                                                                          This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABH82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but they wipo int/pub/published_pct_sequences
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Claim 1; SEQ ID NO 284188; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 5.6e+02;
0; Mismatches 1; Indels
                                                          Length 12;
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Pred. No. 5.68+02;
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Sequence 12 BP; 9 A; 2 C; 0 G; 1 T; 0 U; 0 Other;
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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                          Oligonucleotide primer SEQ ID NO 290367 for detecting SNP TSC0014319.
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                                                               This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99899, ABF00010-ABF99899, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Claim 1; SEQ ID NO 357680; 29pp + Sequence Listing; German.
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                                                                                                                                                                  This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) eligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The eligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The eligoners are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABH99989 and ABI00010-ABH82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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                                                                    oligonucleotides, useful for diagnosis and cell typing, and to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                      Claim 1; SEQ ID NO 330933; 29pp + Sequence Listing; German.
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90.0%; Pred. No. 5.6e+02;
live 0; Mismatches 1;
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 Berlin K;
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 Piepenbrock C,
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oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligoners are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99899 and ABI00010-ABI82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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ftp.wipo.int/pub/published_pct_sequences
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DB 1; Length 12;

38.2%; Score 8.4;

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABC00010-ABE99889, ABC00010-ABE99889, ABC0010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fitte.wipo.int/pub/published_pct_sequence
                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                 Oligonucleotide primer SEQ ID NO 287381 for detecting SNP TSC0013065.
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ABI14255
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   90.0%; Pred. No. 5.6e+02;
iive 0; Mismatches 1; Indels
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Matches 9; Conservative
                    9; Conservative
                                                      733 GAGAACAGA 742
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretracted genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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18-OCT-2001.
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                                                                                        This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but they wiso obtained in electronic format from WIPO at
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                        Claim 1; SEQ ID NO 316995; 29pp + Sequence Listing; German
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                                                                                                                                                                                                                                                                                                                                                                                                        Length 12
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Best Local Similarity 90.0%; Pred. No. 5.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
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represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fitp.wipo.int/pub/published_pct_sequences
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF0010-ABF9989, ABH0010-ABH99989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic from MIPO at
                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                     Oligonucleotide primer SEQ ID NO 295008 for detecting SNP TSC0016398.
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designed to detect single-nucleotide polymorphisms and cytosine
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Pred. No. 5.6e+02;
0; Mismatches 1; Indels
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                                                                                  ABH95015 standard; DNA; 12 BP.
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Matches 9. Conservative
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3 ACAAAACACC 12
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0; Gaps

38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02; tive 0; Mismatches 1; Indels

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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38.2%; Score 8.4; DB 1; Length 12;

Best Local Similarity 90.0%; Pred. No. 5.6e+02;

Matches 9; Conservative 0; Mismatches 1; Indels
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and merabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                              Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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38.2%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 5.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
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                                        Berlin K;
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                                                                                                                                                                                                                                                                                                                      RESULT 785
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABR00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form at from MIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02; tive 0; Mismatches 1; Indels
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RESULT 786 ABH73493/c

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Berlin K;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, and ABI00010-ABF9073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                               Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                   06-APR-2001; 2001WO-IB000713.
                                                                                                                      07-APR-2000; 2000DE-01019173.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 targresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                    Oligonucleotide primer SEQ ID NO 273478 for detecting SNP TSC0003201.
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ABH73493 standard; DNA; 12 BP
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                                                                                      Query Match 38.2%; Score 8.4; DB 1; Length 12; Best Local Similarity 90.0%; Pred. No. 5.6e+02; Matches 9; Conservative 0; Mismatches 1; Indels
Sequence 12 BP; 10 A; 2 C; 0 G; 0 T; 0 U; 0 Other;
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                              Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                            Claim 1; SEQ ID NO 329002; 29pp + Sequence Listing; German.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF8073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at fire wipo.int/pub/published_pct_sequences
central neivous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 ABC09089, ABF00010-ABC99089, ABF00010-ABC90010 ABF00010-ABC90010 ABC0010 ABC0010
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Query Match
Best Local Similarity 90.0%; Pred. No. 5.6e+02;
Matches 9; Conservative 0; Mismatches 1; Indels

Sequence 12 BP; 3 A; 0 C; 2 G; 7 T; 0 U; 0 Other;

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
              Oligonucleotide primer SEQ ID NO 370262 for detecting SNP TSC0058079.
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                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                       This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cointral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Claim 1; SEQ ID NO 370262; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 8.4, DB 1, Length 12;
Pred. No. 5.6e+02;
0; Mismatches 1; Indels
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ABI70289 standard; DNA; 12 BP

RESULT 792

(first entry)

22-FEB-2002

ABI70289;

ABI70289 ID ABI70 XX AC ABI70 XX DT 22-FI

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE09989, ABF00010-ABE9989, ABH00010-ABE9989 and ABI00010-ABE2073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form mart of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oligonucleotide primer SEQ ID NO 297267 for detecting SNP TSC0017501
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                                                                                                                                                           Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                Claim 1; SEQ ID NO 270944; 29pp + Sequence Listing; German.
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06-APR-2001; 2001WO-IB000713
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABCC0010-ABER9989, ABF00010-ABER9989, ABH0010-ABH99899 and ABI00100-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide primer SEQ ID NO 272598 for detecting SNP TSC0002872.
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            Claim 1; SEQ ID NO 297267; 29pp + Sequence Listing; German.
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ABI52327 standard; DNA; 12
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                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                 Oligonucleotide primer SEQ ID NO 349131 for detecting SNP TSC0045930.
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                                                            38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02; ive 0; Mismatches 1; Indels
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                                     Sequence 12 BP; 9 A; 0 C; 2 G; 1 T; 0 U; 0 Other;
was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                  Query Match
Best Local Similarity 90.0,
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                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                             Oligonucleotide primer SEQ ID NO 352300 for detecting SNP TSC0047801
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22-FEB-2002 (first entry)
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oycosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99889, ABH0010-ABH99889 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                          uer or oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                    Claim 1; SEQ ID NO 357369; 29pp + Sequence Listing; German.
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90.0%; Pred. No. 5.6e+02;
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              Berlin K;
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              Piepenbrock
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             olek A,
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                                                                                                                                                                                                                                                                                                                                                               This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                     Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                        06-APR-2001; 2001WO-IB000713
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                                Homo sapiens.
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Gaps

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Length 12; 1; Indels

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
Oligonucleotide primer SEQ ID NO 292346 for detecting SNP TSC0015179.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE9989, ABF00010-ABE9989, ABH00010-ABH99989 and ABI00010-ABI82073 trepresent the oligomers described in the invention. NOTE: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastroinestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                        38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02; tive 0; Mismatches 1; Indels
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Best Local Similarity 90...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 5.6e+02;
0; Mismatches 1; Indels
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Score 8.4; DB 1; Length 12
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Mismatches 1; Indels
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ID ABH74364

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                                                                                                                                                                                               SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                 Oligonucleotide primer SEQ ID NO 279486 for detecting SNP TSC0007399.
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                                                                                          Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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ID ABH89176 standard; DNA; 12 BP.
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

WO200177384-A2

Homo sapiens

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                                                                                                                                                                                                                                           This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, the ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                    Oligonucleotide primer SEQ ID NO 323270 for detecting SNP TSC0031302
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     was obtained in electronic format from Wl
ftp.wipo.int/pub/published_pct_sequences
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ABI23297 standard; DNA; 12
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Best Local Similarity 90.0
Matches 9; Conservative
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WPI; 2001-657177/75.
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                      uer or oligonucleotides, useful for diagnosis and cell typing, designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                          Berlin K;
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07-APR-2000; 2000DE-01019173
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                                                        Olek A, Piepenbrock C,
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                      Oligonucleotide primer SEQ ID NO 292286 for detecting SNP TSC0015155.
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                     ABH92293 standard; DNA; 12 BP
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ABH92293
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                                                               38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02; ative 0; Mismatches 1; Indels
                     Sequence 12 BP; 1 A; 0 C; 3 G; 8 T; 0 U; 0 Other;
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Matches 9; Conservative
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                                                                                         Local Similarity
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Homo sapiens.

18-OCT-2001

olek A,

22-FEB-2002

ABI14975;

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 345526 for detecting SNP TSC0044075.

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RESULT 814

Query Match

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                     Claim 1; SEQ ID NO 373786; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 12 BP; 1 A; 4 C; 0 G; 7 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire, wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Length 12;

38.2%; Score 8.4; DB 1; Length 12 90.0%; Pred. No. 5.6e+02; ative 0; Mismatches 1; Indels

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a
                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                              Oligonucleotide primer SEQ ID NO 381778 for detecting SNP TSC0000152.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    set or oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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742
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Berlin K;

Piepenbrock C,

olek A,

(EPIG-) EPIGENOMICS AG

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-AB182073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                              Oligonuclectide primer SEQ ID NO 285319 for detecting SNP TSC0012239.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                             Olek A, Piepenbrock C,
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                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                             Oligonucleotide primer SEQ ID NO 315282 for detecting SNP TSC0026831.
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                                                  This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE9989, ABF00010-ABE9989, ABH00010-ABH99989 and ABI00010-ABI82073 tepsesnt the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE09989, ABE00010-ABE99989, ABE00010-ABE99989, ABE00010-ABE99989 and ABI00010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence
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                          Claim 1; SEQ ID NO 342390; 29pp + Sequence Listing; German.
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data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                  ABI73488 standard; DNA; 12 BP.
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                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                             ABI73488;
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                                   RESULT 825
AB173488/C
ID AB1734
XX AB1734
XX AB1734
XX AB1734
XX SNP; S
KW SNP; S
KW SNP; S
KW SNP; S
XX CAPF
CC CAPF

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peptide nucleic acid, cytosine methylation, cardiovascular, primer, ss, central nervous system; gastrointestinal, respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 305009; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Berlin K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               730 CAGGAGAAAC 739
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                   WO200177384-A2
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(EPIG-) EPIGENOMICS

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 targersent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligonucleotide primer SEQ ID NO 359293 for detecting SNP TSC0051542.
                                                                                             oligonucleotides, useful for diagnosis and cell typing, is ed to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Set of oligonuclectides, useful for diagnosis and cell typing, : designed to detect single-nuclectide polymorphisms and cytosine
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                                                                                                                                                                  Claim 1; SEQ ID NO 308129; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12 BP; 6 A; 3 C; 0 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
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                                Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-APR-2001; 2001WO-IB000713
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ABI59320 standard; DNA; 12
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                                Piepenbrock C,
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                                                                 WPI; 2001-657177/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   methylation status.
                                                                                                                 designed to detect methylation status.
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Matches 9; Conser
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                              olek A,
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This invention describes novel oligonucleotide primers or peptide nucleic

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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, expressed sequence tag; EST; ds; promoter P15B4; acute myocardial infarction, acute ischaemic stroke; diabetes; anaemia; growth hormone deficiency; hepatitis; kidney carcinoma; multiple sclerosis; chemotherapy-induced neutropaenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New purified 5' expressed sequence tags useful in diagnostic, forens: gene therapy or chromosome mapping procedures, or for distinguishing human tissues or cells from non-human tissues or cells.
                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                Length 12;
                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                      Sequence 12 BP; 0 A; 0 C; 4 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                           38.2%; Score 8.4; DB 1;
90.0%; Pred. No. 5.6e+02;
tive 0; Mismatches 1;
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polynucleotides comprising the 5' EST sequences, to obtain and express control include full protein coding sequences of the corresponding gene products, to map and clone promoter regions, and open reading frames from a genomic sequence, and clone promoter regions, and open settended conNas encoding portions of the protein. EST-related mucleic diseases resulting from abnormal gene expression, for constructing a high resolution map of human chromosomes, and in gene therapy to control or treat genetic diseases. Proteins expressed from the cDNAs may be used in treating or controlling a variety of human conditions e.g acute treating or controlling a variety of human conditions e.g acute hormone deficiency, hepatitis, kidney carcinoma, multiple sclerosis, chemotherapy-induced neutropaenia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; expressed sequence tag; EST; ds; promoter P13H2; acute myocardial infarction; acute ischaemic stroke; diabetes; anaemia; growth hormone deficiency; hepatitis; kidney carcinoma; multiple sclerosis; chemotherapy-induced neutropaemia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12 BP; 9.A; 2 C; 1 G; 0 T; 0 U; 0 Other;
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Best Local Similarity 90.0.
9, Conservative
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AASO7921
ID AASO7921
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Detween human tissues or cells that do not and do not express polynucleotides comprising the 5' EST sequences, to obtain and express polynucleotides comprising the 5' EST sequences, to obtain and express corresponding gene products, to map and clone promoter regions, and open reading frames from a genomic sequence, and to obtain and express extended cDNAs encoding portions of the protein. EST-related mucleic acids are useful in forensic procedures or in diagnosis of genetic diseases resulting from abnormal gene expression, for constructing a high read genetic diseases. Proteins expressed from the CDNAs may be used in treating or controlling a variety of human chonditions e.g acute myocardial infarction, acute ischaemic stroke, diabetes, anaemia, growth hormone deficiency, hearities, kidney carcinoma, multiple sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an activation inducing composition for dendritic cells in animals comprises a polynucleotide, viral vector or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Activation; dendritic cell; immune response; rheumatoid arthritis; cotchn's disease; ulcerative collifs; thalassemia; muscular dystrophy; cystic fibrosis; ostcopetrosis; tumour; cancer; cardiovascular disease; ischaemia; infectious disease; hepatitis; HIV; infection; vaccine; acquired immunodeficiency syndrome; AIDS; transplant rejection; malaria; cytostatic; antiinflammatory; antirheumatic; antiarthritic; anti-HIV; antiarteriosclerotic; ophthalmological; antiarthritic; anti-HIV; antiarteriosclerotic; vacotropical; antiuncer; cardiant; protozoacide; cerebroprotective; vasotropic; virucide; hepatotropic; tuberculostatic; HSV-1; herpes simplex virus; antisense oligonucleotide; ss.
  to distinguish
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inducing activation composition for dendritic cells in huma polynucleotide, viral vector, or polynucleotide derivative polyoxyethylene-polyoxypropylene block copolymer.
                                                                                                                                                                                                                                                                                                                                                 Score 8.4; DB 1; Length 12; Pred. No. 5.6e+02; 0; Mismatches 1; Indels
  cells,
                                                                                                                                                                                                                                                                                                              Sequence 12 BP; 9 A; 2 C; 0 G; 1 T; 0 U; 0 Other;
human tissues or cells from non-human tissues or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guerin N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 9; Page 62; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSV-1 antisense oligonucleotide 1.
                                                                                                                                                                                                                                                    hormone deficiency, hepatitis, kid
chemotherapy-induced neutropaenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
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90.0%;
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01-JAN-2001; 2001US-0260806P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABA05981 standard; DNA; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                        9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                736 AAACAGAACA 745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABA05981;
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ID ABA059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 831
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polymucleotide derivative and polyoxyethylene-polyoxypropylene block copolymer(s). The composition has cytostatic, antinflammatory, antiarthritic, antiarthocacle cortic, ophthalmological, antialcoholism, osteopathic, dermatological, immunosuppressive, antialcoholism, osteopathic, dermatological, immunosuppressive, composition is for inducing activation of dendritic cells in animals, preferably human; increasing the level of production and inflitration for dendritic cells in response to gene expression and increasing the immuno response and generates large amounts of dendritic cells in vivo or in vitro. It is also used in treating genetic diseases including rhe immuno vitro. It is also used in treating genetic diseases including rhe macoid arthritis, psoriasis, Crohn's disease, ulcerative colitis, alphacter thalassemia, benylketonuria, muscular dystrophy such a subchenne Muscular Dystrophy, hypersarcosinaemia, adenomatous intestinal polyposis, arteriosclerosis and hypercholesterolaemia, cystic immunodeficiency, high cholesterol, arthritis, glaucoma or alcoholism. It can be also used to treat neoplastic diseases including cancer, lymphoma condition are such as repeated acquired immunodeficiency syndrome (AlbS) and transplantation related disorders such as repaid as the as head in vaccine therapies and immunisation, including melanoma orallosis. The present sequence is that of a HSV-1 contisence oligonucleotide, useful to the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Activation, dendritic cell; immune response; rheumatoid arthritis; Crohn's disease; ulcerative colitis; thalassemia; muscular dystrophy; cystic fibrosis; osteopetrosis; tumour; cancer; cardiovascular disease; ischaemia; infections disease; hepatitis; HVV; infection; vaccine; acquired immunodeficiency syndrome; AIDS, transplant rejection; malaria; cytostatic; antiinflammatory; antirheumatic; antiarthritic; anti-HIV; antiartological; immunosuppressive; antiulcer; cardiant; protozoacide; cerebroprotective; vasotropic; virucide; hepatotropic; tuberculostatic; HSV-1; herpes simplex virus; antisense oligonucleotide; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38.2%; Score 8.4; DB 1; Length 12; ilarity 90.0%; Pred. No. 5.6e+02; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12 BP; 0 A; 5 C; 2 G; 4 T; 1 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSV-1 antisense oligonucleotide 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      730 CAGGAGAAAC 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 CAGGAGGAAC 2
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tes 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABA05984;
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The invention relates to an activation inducing composition for dendritic cells in animals comprises a polynuclectide, viral vector or cells in animals comprises a polynuclectide, viral vector or polynuclectide derivative and polyoxyethylene-polyoxypropylene block copolymer(s). The composition has evicated; antiinflammatory, antiinflammatory, antiinflammatory, antiinflammatory, cerebropathic, dermatological, immunosuppressive, antiuloer, cardiant, cerebroprotective, vasotropic, virucide, hepatotropic, anti-HIV, protozoacide and tuberculostatic activity. The composition is for inducing activation of dendritic cells in animals, preferably human, increasing the level of production and infiltration for dendritic, cells in response to gene expression and increasing the immune ceptoms and generates large amounts of dendritic cells in vivo or in vitro. It is also used in tracting genetic diseases including rheumatoid arthritis, bsoriasis, Crohn's disease, ulcerative colitis, alpha-transforms beca-thalassemia, phenylkeconuris, muscular dystrophy such as Duchenne Muscular Dystrophy, hyepersarcosinaemia, adenomatous intestinal polyposis arteriosclerosis and hypertholesterolesmia, cystic fibrosis, osteoperosis, increased sponteneous tumuurs, T and B cell immunodeficiency, high cholesterol, arthritis, glaucoma or alcoholism. It can be also used to treat neoplastic diseases including stroke, myocardial ischaemia, infectious diseases such as hepatikis, HIV infections and acquired immunodeficiency syndrome (AIDS) and transplantation related acquired immuniaation, including melanoma vaccines, HIV vaccines, the present sequence is that of a HSV-Icrops, malaria or tuberculosis, The present sequence is that of a HSV-Icrops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Promoter DNA; diagnostic; forensic; gene therapy; chromosome mapping; expression vector; secretion vector; P15B4; transcription binding site;
                                           contains
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                                        Inducing activation composition for dendritic cells in human, opolynuclectide, viral vector, or polynuclectide derivative and polyoxyethylene-polyoxypropylene block copolymer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38.2%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 5.6e+02; cive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antisense oligonucleotide, useful to the invention
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                                                                                                                            Example 21; Page 72; 126pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAK99268 standard; DNA; 12 BP.
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WPI; 2002-097495/13.
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Best Local Similarity
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                                                                                                                                          selected from any of more than 50000 sequences not defined in the specification. The polymocleotide sequences are useful in making oDNA, polypeptides and promoter DNA, and in diagnostic, forensic, gene therapy or chromosome mapping procedures. The mucleic acid sequences are also useful for designing expression vectors and secretion vectors. This polymucleotide sequence represents a P15B4 promoter transcription binding site of the invention
                                                                                                                                 The invention relates to purified nucleic acids, which comprise sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to purified nucleic acids, which comprise sequences selected from any of more than 50000 sequences not defined in the specification. The polynucleotide sequences are useful in making DNA, polypeptides and promoter DNA, and in diagnostic, forensic, gene therapy or chromosome mapping procedures. The nucleic acid sequences are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Promoter DNA, diagnostic, forensic, gene therapy, chromosome mapping, expression vector, secretion vector, P13H2; transcription binding site,
 Bejanin S;
                                              New nucleic acid sequences comprising human expressed sequence tags (ESTs), useful in diagnostic, forensic, gene therapy or chromosome mapping procedures, or for designing expression vectors and secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bejanin S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid sequences comprising human expressed sequence tags (ESTs), useful in diagnostic, forensic, gene therapy or chromosome mapping procedures, or for designing expression vectors and secretion
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 Tanaka H,
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                                                                                                                                                                                                                                                                   Length 12;
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 Giordano J,
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 Jobert S,
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                                                                                                          Disclosure; Fig 5; 163pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                   BP.
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                                                                                                                                                                                                                                                                                                                                                                                                   AAK99265 standard; DNA; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 90.0
The properties of Conservative
 Dumas Milne Edwards JB,
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                                                                                                                                                                                                                                                                                                                 736 AAACAGAACA 745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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useful for designing expression vectors and secretion vectors. This polynucleotide sequence represents a P13H2 promoter transcription binding site of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention provides primers (AAX29501-X29679) for identifying sequences encoding structurally or functionally related proteins such as nuclear or G-protein coupled receptors, apoptosis-related or DNA repair/replication proteins. The identified sequences are broadly useful in plant biology, agriculture, human or veterinary medicine, reproduction, microbiology or environmental science, e.g. to study expression of nuclear receptors at different stages of fissue development or after treatment with particular drugs. It is also used for DNA indeprinting (to generate products useful for differential hybridisation), or, where a "anchor primer is used, to isolate the 3'-ends of mRNA sequences. Sequences AAX29630-X29679 represent claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid amplification, nuclear receptor; G-protein coupled receptor; appleosis; DNA replainstation; plant biology; agriculture; human; veterinary medicine; reproduction; microbiology; hybridisation; environmental science; DNA fingerprinting; PCR primer; ss.
                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                 38.2%; Score 8.4; DB 1; Length 12;
.larity 90.0%; Pred. No. 5.6e+02;
Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primer for human DNA repair and replication genes.
                                                                                                              G; 1 T; 0 U; 0 Other;
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100.0%; Pred. No. 4.7
:ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 29; Page 78; 92pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX29674 standard; DNA; 8 BP
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                                                                                                              BP; 9 A; 2 C; 0
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Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
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                                                                                                                 Sequence 12
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(EE)

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The invention relates to an isolated nucleic acid (NI) comprising at least 20 but not more than 1500 consecutive nucleotides of the optineurin promoter propagating as ADE1390. Also included are the optineurin promoter operably linked to a heterologous nucleic acid, a nucleic acid capable of promoter, a host cell comprising the promoter operably linked to a heterologous sequence, diagnosing the promoter operably linked to a heterologous sequence, diagnosing the promoter operably linked to a heterologous sequence, diagnosing to promoter operably linked to a heterologous sequence, diagnosing of promoter operably linked to a promoter region of the optineurin gene, associated with a glaucoma phenotype), detecting a SNP sequence variation in a sample containing DNA, detecting the presence of an optineurin promoter sequence variation in a sample containing DNA, determining the presence or increased succeptibility to glaucoma or to a progressive ocular hypertensive disorder resulting in loss of visual field in a patient (or the severity or progression of glaucoma in a patient, comprising providing an uncleic acid region containing the variation within the optineurin containing a sample containing the variation within the optineurin containing a sample containing the variation within the optineurin capable of detecting a SNP located within an optineurin promoter, and progness glaucoma and also to treat glaucoma related disporders. The present sequence is an optineurin promoter motif, repeat element or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid sequences of the optineurin gene are useful to detect polymorphisms particularly single nucleotide polymorphisms in the optineurin promoter to diagnose, prognose and treat glaucoma and related disorders.
                                                                                                                                                                                                                                                                                                                                                                                  Human, optineurin; ds. ophthalmological; single nucleotide polymorphism; SNP; glaucoma; progressive ocular hypertensive disorder; glaucoma related disorder; motif; repeat element; regulatory region.
                                                                                                                                                                                                                                                                                                          Optineurin promoter motif, repeat element or regulatory region #220.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Si.
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                                                                                   ADE14111 standard; DNA; 9 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MORI/) MORISSETTE J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-864168/80.
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RAYMOND V.
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                                                                                                                                                               ADE14111;
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RESULT 836
ADE14111/c
ADE14111/c
AXC ADE1411
XX
AXC ADE141
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ADE141
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Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more decanucleotides (AAQ991015-Q97166) from the LTR region; the sequence of AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The response in humans, and enable the generation of therapeutic, diagnostic and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                      New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or LTR region - can be used in a vaccine to inhibit/reduce productive infection in an individual by a pathogenic strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                            HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
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100.0%; Pred. No. 6e+02;
tiive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                    Crowe S,
                                                                                                   HIV-1 NL4-3 nef gene nucleotide deletion 479.
                                                                                                                                                                                                                                                                                                             (MACF-) MACFARLANE BURNET CENT MEDICAL. (AURE-) AUSTRALIAN RED CROSS SOC.
                                                                                                                                                                                                                                                                                                                                                    Deacon NJ, Learmont JC, Mcphee DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 13; Page 194; 301pp; English.
                                                                                                                                                       Human immunodeficiency virus 1.
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            AAQ96884 standard; DNA; 10 BP.
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                                                              (revised)
(first entry)
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(first entry)
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21-FEB-1994;
23-DEC-1994;
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                                                              16-OCT-2003
26-MAR-1996
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                                      AAQ96884;
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Matches
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AAQ9688
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8; Conservative

Matches

Query Match Best Local Similarity

HIV-1 NL4-3 nef gene nucleotide deletion 478.

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Gaps

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0; Indels

36.4%; Score 8; DB 1; Length 9; 100.0%; Pred. No. 4.1e+03; ative 0; Mismatches 0; Indels

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                                                                                                                                                                                                                                                                              New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or LTR region - can be used in a vaccine to inhibit/reduce productive infection in an individual by a pathogenic strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAGE tag; serial analysis of gene expression; antigen-presenting cell; APC; moncoyte-derived dendritic cell; differential gene expression; immunostimulatory cofactor; costimulatory factor; CTL; cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss
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Mo. 6e+02;
0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10 BP; 5.A; 3 C; 2 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                            Crowe S,
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Pred. No.
                                                                                                                                                                                    (MACF-) MACFARLANE BURNET CENT MEDICAL
                                                                                                                                                                                                                            Deacon NJ, Learmont JC, Mcphee DA,
                                                                                                                                                                                                                                                                                                                                    Claim 13; Page 194; 301pp; English.
                                                                                                                                                                                                  AUSTRALIAN RED CROSS SOC
                        Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36.4%; 100.0%;
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98US-0089844P.
98US-0089853P.
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94AU-000000284.
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Best Local Similarity 100.00
Best Local 8; Conservative
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19-JUN-1998;
19-JUN-1998;
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                                                WO9521912-A1
                                                                                                                                                           23-DEC-1994;
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expression) tags used to identify many tare sendeding immunostimilatory cofactor proteins which are preferentially or differentially expressed in monocyte-derived dendititic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTS (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while preferentially or differentially expressed in dendritic cells, while correspond to novel genes. Antigen-presenting cell of the cytotoxic immune response, particularly against tumour antigen presentation via the MHC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone that under antigen presentation via the MHC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone the tumour antigen presentation via the MHC (major histocompatibility complex) and subsequency cofactors also being required for cefficient activation of cytotoxic T-lymphcotyes (CTEs). Nucleic acid sequences identified using the SAGE tags have several potential uses. They may be used in vaccines to induce an immune response, particularly against a tumour antigen; to modulate the genotype of an APC; to screen for agants that modulate expression of diseases related to abnormal expression of these genes, or of their encoded proteins, can be used to identify expressed genes, or of their encoded proteins, can be used in active immunotherapy (or to stimulate production of a population of antigen-specific effector cells) and vectors containing them are used in gene therapy. Co-administration of tumour antigens and APC-associated costimulatory factors ensures adequate antigen presentation of co-stimulatory factors ensures adequate antigen presentation of co-stimulatory signals, migration of chemokines for recruitment of immune effector cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated polynucleotides differentially expressed in antigen-presenting cells, useful in gene vaccines against cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 80; 130pp; English.
              98US-0089991P
98US-0089994P
98US-0089994P
98US-0089999P
98US-0080999P
98US-0090035P
98US-0090040P
98US-0090040P
98US-0090041P
98US-0090044P
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98US-0090045P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENZ ) GENZYME CORP. (ROBE/) ROBERTS B L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SHAN/) SHANKARA S.
                                                                                                                                                                                                                                                                           19-JUN-1998;
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immunotherapy

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that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ86677 represent tags corresponding to distinct transcribts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). Preferentially transcribed in the primary or non-metastatic breast tumour cells or issue (i.e. are downeagulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts are metastatic. Diagnosis is by standard immunoassys or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines. Polypeptides encoded by the transcripts are also useful in antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agentic sequences the polypeptides or as therapeutic and isolate populations of educated, and these used for adoptive expand and isolate populations of educated, and these used for adoptive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  Human, metastatic breast tumour tissue; breast cancer; tag; primer; non-metastatic breast tumour tissue; gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss.
                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                  Metastatic breast tumour cell upregulated transcript tag #91
                      36.4%; Score %; DB 1; Length 10; 100.0%; Pred. No. 6e+02; Niematches 0; Indels
Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;
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98US-0090039P.
98US-0090040P.
98US-0090041P.
                                                                                                                                                                                                                                                    AAZ80857 standard; DNA; 10 BP
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                                                                                                                                                                                                                                                                                                                               07-APR-2000 (first entry)
                      Query Match
Best Local Similarity 100.
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that are preferentially transcribed in the metastatic breast tumour citissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942

to AAZ86677 represent tags corresponding to distinct transcribts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). These tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of captularly an antigen-encoding sequence for use in gene or cell-based vaccines. Polypeptides encoded by the transcripts are also useful in captularly an antigen-encoding sequence for use and so useful in antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic antibodies (Ab). Ab are used to detect the polypeptides can be used to expand
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and isolate populations of educated, antigen-specific immune effecter cells, e.g. cytotoxic T lymphocytes, and these used for adoptive immunotherapy.
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vaccines. Polypeptides encoded by the transcripts are also useful in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter cells, e.g. cytotoxic T lymphocytes, and these used for adoptive immunotherapy
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e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines. Polypeptides encoded by the transcripts are also useful in vaccines; for diagnoshing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic and isolate populations of educated, antigen-specific immune effecter cells, e.g. cytotoxic I lymphocytes, and these used for adoptive
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                                                                                                                                           immunotherapy
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19-JUN-1998;
19-JUN-1998;
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useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences) particularly an antigen-encoding sequence for use in gene or cell-based vaccines. Polypeptides encoded by the transcripts are also useful in antibodies; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic antibodies is the produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter cells e.g. cytotoxic I lymphocytes, and these used for adoptive
                                                                                                                                                                                                                                                                                                              immunotherapy
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Sequence 10 BP; 3 A; 3 C; 4 G; 0 T; 0 U; 0 Other;

Gaps ö 36.4%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 6e+02; ive 0; Mismatches 0; Indels 8; Conservative Query Match Best Local Similarity Matches

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AAZ83594 standard; DNA; 10 BP. RESULT 846 AAZ83594 

AAZ83594;

(first entry) 07-APR-2000 Metastatic breast tumour cell upregulated transcript tag #2828.

Human, metastatic breast tumour tissue; breast cancer; tag; primer; non-metastatic breast tumour tissue, gene therapy; anticancer; antimetastatic; vaccine; diagnosis; ss.

Homo sapiens

WO9965928-A2

23-DEC-1999.

99WO-US013647 18-JUN-1999; 98US-0089853P. 98US-0089997P. 98US-0090039P. 98US-0090040P. 19-JUN-1998; 19-41-WUD-61 ,8961-NUL-6. 19-JUN-1998;

(GENZ ) GENZYME CORP. (ROBE/) ROBERTS B L. (SHAN/) SHANKARA S.

Shankara BĽ, Roberts

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WPI; 2000-106079/09.

Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer.

Claim 1; Page 134; 219pp; English.

AA280767 to AA283941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour calls). AA283942 to AA286677 represent tags corresponding to distinct transcribts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour calls). These transcribts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is

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by standard immunoassays or hybridisation/amplification reactions. Compounds that modulate expression of the transcripts are potentially useful for treatment of metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequence). Passed vaccines. Polypeptides encoded by the transcripts are also useful in antispen-encoding sequence for use in gene or cell-based vaccines. Polypeptides encoded by the transcripts are also useful in antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter immunotherapy.
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Seguence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

Gaps ; DB 1; Length 10; . 6e+02; ches 0; Indels Query Match
36.4%; Score 8; D3 1
Best Local Similarity 100.0%; Pred. No. 6e+
Matches 8; Conservative 0; Mismatches

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ò 셤 RESULT 847

AAZ82358 standard; DNA; 10

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AAZ82358;

(first entry) 07-APR-2000 Metastatic breast tumour cell upregulated transcript tag #1592.

Human, metastatic breast tumour tissue, breast cancer, tag, primer, non-metastatic breast tumour tissue, gene therapy, anticancer, antimetastatic, vaccine, diagnosis, ss.

Homo sapiens.

WO9965928-A2

23-DEC-1999

99WO-US013647. 18-JUN-1999;

19-JUN-1998; 9-JUN-1998;

98US-0089853P. 98US-0089997P. 98US-0090039P. 98US-0090040P. 19-JUN-1998; 8-4T-NUL-61 9-JUN-1998

(GENZ ) GENZYME CORP. (ROBE/) ROBERTS B L.

SHAN/) SHANKARA S.

Shankara S; Roberts BL,

WPI; 2000-106079/09.

Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer. 

Claim 1; Page 101; 219pp; English.

AA280767 to AA283941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AA28342 to AA286677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These

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treatment of breast cancer, particularly where metastaric. Diagnosis is treatment of breast cancer, particularly where metastaric. Diagnosis is Compounds timunoassays or hybridisation/amplification reactions.

Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic agents. Host cells that produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
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Best Local Similarity luv...
8, Conservative
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19-JUN-1998;
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AA280767 to AA281941 represent tags corresponding to distinct transcripts that are preferentially transcribed in the metastatic breast tumour tissue (i.e. are upregulated in metastatic breast tumour cells). AA283942 to AA286677 represent tags corresponding to distinct transcripts that are

Isolated polynucleotides differentially expressed between metastatic and non-metastatic breast cancer cells, useful for diagnosis, prevention and treatment of cancer.

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Roberts BL, Shankara

SHANKARA S.

(SHAN/)

WPI; 2000-106079/09.

Claim 1; Page 141; 219pp; English.

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preferentially transcribed in the primary or non-metastatic breast tumour tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and treatment of breast cancer, particularly where metastatic. Diagnosis is by standard immunoassays or hybridisation/amplification reactions.

Compounds that modulate expression of the transcripts are potentially useful for treatment of (metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of e.g. therapeutic genes (also ribozymes or antisense sequences), particularly an antigen-encoding sequence for use in gene or cell-based vaccines. Polypeptides encoded by the transcripts are also useful in vaccines; for diagnosing breast cancer and for raising specific antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic and isolate populations of educated, antigen-specific immune effecter central and produce the polypeptides can be used to expand and isolate populations of educated, antigen-specific immune effecter central and produce the polypeptides or a doptive
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                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                              Length 10;
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tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942

to AAZ06677 represent tags corresponding to distinct transcripts that are
preferentially transcribed in the primary or non-metastatic breast tumour
tissue (i.e. are downregulated in metastatic breast tumour cells). These
transcripts can be used for diagnosis, prognosis, monitoring and
treatment of breast cancer, particularly where metastatic. Diagnosis is
by standard immunoassays or hybridisation/amplification reactions.
Compounds that modulate expression of the transcripts are potentially
useful for treatment of (metastatic) breast cancer, while promoters from
the transcripts are used to direct expression, in selected cell types, of
e.g. therapoutic genes (also ribozymes or antisense sequences),
particularly an antigen-encoding sequence for use in gene or cell-based
vaccines. Polypeptides encoded by the transcripts are also useful in
antibodies (Ab). Ab are used to detect the polypeptides can be used to expand
and isolate populations of educated, antigen-specific immune effecter
cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
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(ROBE/) ROBERTS B L.
(SHAN/) SHANKARA S.
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(ROBE/)
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that are preferentially transcribed in the metastatic breast tumour clistic transcripts that are preferentially transcribed in the metastatic breast tumour cells). AA283942 to AA286677 represent tags corresponding to distinct transcripts that are preferentially transcribed in the primary or non-metastatic breast tumour cells). These tissue (i.e. are downregulated in metastatic breast tumour cells). These transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, monitoring and transcripts can be used for diagnosis, prognosis, anothering and transcripts can be used for diagnosis, prognosis, are potentially useful for treatment of metastatic) breast cancer, while promoters from the transcripts are used to direct expression, in selected cell types, of particularly an antigen-encoding sequence for use in gene or cell-based vaccines. Polypeptides encoded by the transcripts are also useful in artibodies (Ab). Ab are used to detect the polypeptides or as therapeutic antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic and isolate populations of educated, antigen-specific immune effecter cells, e.g. cytotoxic T lymphocytes, and these used for adoptive immunotherapy
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Best Local Similarity 100.
Matches 8; Conservative
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AAH63186
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Claim 1; Page 40; 94pp; English.
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Best Local Similarity 100.
Matches 8; Conservative
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                AAH63239;
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cancer specific gene expression, standardise expression and restore the function of a diseased cell or tissue. The present sequence is one of the transcriptomes described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, transcriptome, gene expression pattern; cancer; drug screening;
cancer diagnosis; cell specific gene expression; ss.
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such as cancer cell, comprises transcriptomes expressed in particular
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llarity 100.0%; Pred. No. 6e+02;
Conservative 0; Mismatches 0; Indels
                                                                                                      Query Match 36.4%; Score 8; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 6e+02; Matches 8; Conservative 0; Mismatches 0; Indels
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                                                                      Sequence 10 BP; 6 A; 3 C; 1 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                      AAH63245 standard; cDNA; 10 BP.
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Best Local Similarity
8; Conserve
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cell types.
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AAH63239 standard; cDNA; 10 BP.

RESULT 853 AAH63239 ID AAH632

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The present invention describes a method of identifying the type of cell in a sample, involving determining which of the sequences AAH63161-AH64724 is expressed by the cell. The transcriptomes described in the invention are cell-type specific, cancer specific or ubsquitously expressed in humans. They can also be used to screen for drugs, reduce cancer specific gene expression, standardise expression and restore the function of a diseased cell or tissue. The present sequence is one of the transcriptomes described in the exemplification of the invention
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                                                         Human, transcriptome, gene expression pattern, cancer, drug screening;
cancer diagnosis, cell specific gene expression; ss.
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Human colon epithelium specific transcriptome sequence SEQ ID NO: 79.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kinzler KW;
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expressed in humans. They can also be used to screen for drugs, reduce cancer specific gene expression, standardise expression and restore the function of a diseased cell or tissue. The present sequence is one of the transcriptomes described in the exemplification of the invention
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                                                                                                                                                                       New isolated polynucleotides, useful for identifying specific cell type, such as cancer cell, comprises transcriptomes expressed in particular cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; transcriptome; gene expression pattern; cancer; drug screening; cancer diagnosis; cell specific gene expression; ss.
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                                                                                          Kinzler KW;
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                                                                                                                                                                                                                                                                 Claim 13; Page 69; 94pp; English.
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                                                                                        Vogelstein B,
    99US-00448480
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                                         SNINGOH SNHOL VINU ( OLYU)
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                                                                                                                             WPI; 2001-367706/38
                                                                                        Velculescu VE,
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    24-NOV-1999;
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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonamorated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising; (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying a candidate drug as a member of a contiguous nucleorides of a NORF gene whose expression varies as in M1; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a contoxing expression in the yeast cell or comprises may be used expression is affected by the class of drugs. The NORF genes may be used
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                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.
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Query Match 36.4%; Score 8; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 6e+02; Matches 8; Conservative 0; Mismatches 0; Indels
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The present invention describes a method of identifying the type of cell in a sample, involving determining which of the sequences AAH63161-AAH64724 is expressed by the cell! The transcriptomes described in the invention are cell-type specific, cancer specific or ubiquitously

New isolated polynucleotides, useful for identifying specific cell type, such as cancer cell, comprises transcriptomes expressed in particular cell types.

Claim 1; Page 40; 94pp; English.

yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used as markers of phases of the cell cycle. The represent and for identification of antifungal drugs which affect the cell represent SAGE tags used in the exemplification of the present invention. AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention

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Sequence 10 BP; 4 A; 1 C; 5 G; 0 T; 0 U; 0 Other;

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to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention. AAF33261 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                          Score 8; DB 1; Length 10;
; Pred. No. 6e+02;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                 36.4%; S
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     740 AGAACACC 747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF35950;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.
                                                                                                                                                                                                                                                                                                                                                                          Yeast, Saccharomyces cerevisiae, characterisation, cell cycle, NORF, nor previously assigned open reading frame, nonannotated ORF, SAGE, serial analysis of gene expression, antifungal, tag, identification,
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Query Match 36.4%; Score 8; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 6e+02; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                      Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7808.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example; Page 278; 419pp; English.
                                                                                                                                                                                                                        AAF41069 standard; DNA; 10 BP.
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                                                                                                                                                                                                                                                                                                     23-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                            linker; PCR primer; ds
                                                                                   730 CAGGAGAA 737
                                                                                                                      o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-061874/07.
                                                                                                                        2 CAGGAGAA
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The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame, or nonamotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering an NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal drugs comprising; (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a andidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M3; and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

WPI; 2001-061874/07.

Example; Page 96; 419pp; English.

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contiguous nucleotides of a NORF gene whose expression varies as in MI, and (4) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially expressed genes may be used as markers of phases of the cell cycle. The methods may be used as markers of phases of the cell cycle. The methods may be used in the exemplification of antifungal drugs. AAP33268 to AAF44064 represent SAGE tags used in the exemplification of the present invention.

AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention.
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Sequence 10 BP; 0 A; 3 C; 1 G; 6 T; 0 U; 0 Other;

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Gape
                                     ,
0
          36.4%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 6e+02; ive 0; Mismatches 0; Indels
Query Match
Best Local Similarity 100.
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736 AAACAGAA 743 10 AAACAGAA 3 ò

RESULT 859 AAF38498

AAF38498 standard; DNA; 10 BP. AAF38498; 

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:5237. (first entry) 23-MAR-2001

Yeast, Saccharomyces cerevisiae; characterisation; cell cycle, NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds.

Saccharomyces cerevisiae.

WO200077214-A2

21-DEC-2000

14-JUN-2000; 2000WO-US016223.

99US-00335032 16-JUN-1999;

(UYJO ) UNIV JOHNS HOPKINS

Velculescu V, Vogelstein B,

Kinzler K;

WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 187; 419pp; English.

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (MI) of using NORF genes to affect the cell expression and state of the cell of between any two phases of the cell gyole selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antitungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of varies as in MI, where a test substance which modifies the expression of

the yeast gene is a candidate antifungal drug; (3) a method (W3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (4) a method (W4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF gene whose expression is affected by the class of drugs. The NORF genes may be used to study, monitor and affect phases of the cell cycle, the differentially corpressed genes may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF4064 represent SAGE tags used in the exemplification of the present invention.

AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention. 

Sequence 10 BP; 6 A; 2 C; 2 G; 0 T; 0 U; 0 Other;

Gaps ö h Similarity 100.0%; Pred. No. 6e+02; B; Conservative 0; Mismatches 0; Indels Query Match Best Local Similarity Matches 8; Conserv

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RESULT 860 AAF36885

AAF36885 standard; DNA; 10

BP.

AAF36885;

(first entry) 23-MAR-2001 Yeast NORF gene SAGE tag oligonuclectide SEQ ID NO:3624.

Yeast, Saccharomyces cerevisiae, characterisation, cell cycle, NORF, nor previously assigned open reading frame; nonannotated ORF, SAGE, serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds. 

Saccharomyces cerevisiae.

WO200077214-A2.

14-JUN-2000; 2000WO-US016223.

99US-00335032 16-JUN-1999;

(UYJO) UNIV JOHNS HOPKINS

Kinzler K; Velculescu V, Vogelstein B,

WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 129; 419pp; English.

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell expres comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate

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antifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression to varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human bNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; and (A) a method (M4) for identifying a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a yeast cell with a candidate drug and monitoring expression in the yeast cell of least 1 NORF gene whose expression is affected by the class of drugs. The NORF gene may be used to study, monitor and affect phases of the cell cycle. The methods may be used as markers of phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33268 to AAF4064 represent SAGE tags used in the exemplification of the present invention.

AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention.
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Sequence 10 BP; 7 A; 1 C; 2 G; 0 T; 0 U; 0 Other;

0; Indels Length 10; 36.4%; Score 8; DB 1; L 100.0%; Pred. No. 6e+02; tive 0; Mismatches 0 Conservative 736 AAACAGAA 743 σ Local Similarity les 8; Conserv AAACAGAA ~ Query Match Best Loca Matches 8 g

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Gaps

; 0

RESULT 861

AAF33978 standard; DNA; 10 BP AAF33978; 

23-MAR-2001 (first entry)

Yeast, Saccharomyces cerevisiae, characterisation, cell cycle, NORF, nor previously assigned open reading frame, nonannotated ORF, SAGE, serial analysis of gene expression, antifungal, tag, identification, linker; PCR primer; ds.

Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:717.

Saccharomyces cerevisiae

WO200077214-A2.

21-DEC-2000.

14-JUN-2000; 2000WO-US016223

99US-00335032 16-JUN-1999;

SNINGO NIND ( OCKD)

Velculescu V, Vogelstein B, WPI; 2001-061874/07.

Kinzler K;

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SAGE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Claim 1; Page 400; 419pp; English.

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not previously assigned open reading frame; or nonannotated ORF) genes comprising a SAGE (serial analysis of expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell

cycle comprising administering a NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase. S phase and G2/M; (2) a method (M2) for screening candidate attifungal drugs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of the yeast gene is a candidate antifungal drug; (3) a method (M3) for the yeast gene is a candidate antifungal drug; (3) a method (M3) for comprising contacting human DNA with a probe which comprises at least 10 comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1; contiguous nucleotides of a norrecting a candidate drug as a member of a class of drugs having a characteristic effect on gene expression in a cypression is affected by the class of the cell with a candidate drug and monitor and affect phases of the cell cycle, the differentially expression is affected by the class of drugs. The NORF genes may be used to identify candidate drugs which affect the cell cycle. The cypressed genes may be used to identify candidate drugs which affect the cell cycle. The cypresent SAGE to AAPF33267 represent linkers and PCR primers used in the SAGE method, in the exemplification of the present invention. Gaps . 0 36.4%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 6e+02; cive 0; Mismatches 0; Indels Sequence 10 BP; 4 A; 1 C; 5 G; 0 T; 0 U; 0 Other; Local Similarity 100. 730 CAGGAGAA 737 CAGGAGAA 9 ~ Query Match Matches d

AAF35089 standard; DNA; 10 BP. AAF35089; RESULT 862 AAF35089/c

feast NORF gene SAGE tag oligonucleotide SEQ ID NO:1828. 23-MAR-2001 (first entry)

Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF; nor previously assigned open reading frame; nonannotated ORF; SAGE; serial analysis of gene expression; antifungal; tag; identification; linker; PCR primer; ds. 

Saccharomyces cerevisiae.

WO200077214-A2.

21-DEC-2000.

14-JUN-2000; 2000WO-US016223

99US-00335032 16-JUN-1999; SNINGO UNIV ( OLYU)

Kinzler K; Vogelstein B, Velculescu. V,

WPI; 2001-061874/07.

Yeast gene coding sequences comprising NORF genes with serial analysis of gene expression (SACE) tags, useful for studying, monitoring and affecting phases of the cell cycle.

Example; Page 65; 419pp; English.

The present invention describes an isolated DNA molecule comprising a coding sequence of a yeast gene selected from a group of 745 NORF (not

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Comprising a SAGE (serial analysis of gene expression) tag. Also described are: (1) a method (M1) of using NORF genes to affect the cell cycle comprising administering an NORF gene whose expression varies by at least 10% between any two phases of the cell cycle selected from log phase, S phase and G2/M; (2) a method (M2) for screening candidate antifungal dargs comprising: (a) contacting a test substance with a yeast cell; and (b) monitoring expression of a NORF gene whose expression of varies as in M1, where a test substance which modifies the expression of the yeast gene is a candidate antifungal darg; (3) a method (M3) for identifying human genes which are involved in cell cycle progression comprising contacting human DNA with a probe which comprises at least 10 contiguous nucleotides of a NORF gene whose expression varies as in M1, and (4) a method (M4) for identifying a candidate darg as a member of a class of drugs having a characteristic effect on gene expression in a yeast cell comprising contacting a vasat cell with a candidate drug and monitoring expression in the yeast cell of at least 1 NORF genes may be used to sudy, monitor and affect phases of the cell cycle. The methods may be used to identify candidate drugs which affect the cell cycle and for identification of antifungal drugs. AAF33266 to AAF44664 represent SAGE tags used in the exemplification of the present invention. AAF33262 to AAF33267 represent invention of the present invention. AAF33262 to AAF33267 represent invention of the present invention.
      genes
   previously assigned open reading frame; or nonannotated ORF)
84899999999999999999999
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Sequence 10 BP; 1 A; 2 C; 2 G; 5 T; 0 U; 0 Other;

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0; Indels
36.4%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 6e+02; ive 0; Mismatches 0; Indels
                   Local Similarity 100.
nes 8; Conservative
    Query Match
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734 AGAAACAG 741 8 AGAAACAG 1 ò

ABK24254 standard; DNA; 10 BP. 09-APR-2002 ABK24254; RESULT 863 

Retinaldehyde-binding protein 1 ASO primer extension primer #27. (first entry)

Human, retinaldehyde-binding protein 1; ss; RLBP1; haplotype; primer; genotyping; probe; autosomal recessive retinitis pigmentosa; arRP; PCR; chromosome 15q26; transgenic; ASO; allele specific oligonucleotide.

Homo sapiens.

WO200192278-A2

06-DEC-2001.

26-MAY-2000; 2000US-0207618P.

29-MAY-2001; 2001WO-US017252.

(GENA-) GENAISSANCE PHARM INC.

Koshy B; Choi JY, Kazemi A,

WPI; 2002-122053/16.

t C New genetic variants having polymorphisms in the retinaldehyde-binding protein 1 gene, useful for studying the function of and for expressing RLBP1 protein for use in screening drugs for treating diseases related RLBP1 activity.

Claim 18; Page 14; 107pp; English.

The invention relates to an isolated polynuclectide, which comprises genes and haplotypes of the retinaledwide-binding protein in (RLBP1) gene. The polynuclectide comprises polymorphic attes in the RLBP1 gene, which correct in the gene. Also included are methods for haplotyping or located in the gene. Also included are methods for haplotyping or correct in the RLBP1 gene of an individual, a method for predicting a haplotype pair for the RLBP1 gene of an individual, a method for predicting an association between a trait and at least one haplotype or haplotype pair of the RLBP1 gene of an individual, a method for predicting of pertire and properties of a properties of properties of properties at a PS consisting of PSI-PS24, a kit for genotyping the RLBP1 gene of an individual comprising a set of cilgonucleotides designed to genotyping or compisating a set of cilgonucleotides designed to genotype each of PSI-PS24 recombinant non-human organisms transformed or transfected with the isolated polymcleotide, where the organisms transferred or transfected with the isolated polymcleotide, where the organisms expresses a RLBP1 protein encoded by the first nucleotide sequence or expresses an RLBP1 protein an encoded by the polymcophic variant sequence or expresses an RLBP1 protein an encoded by the polymcophic variant sequence or expresses an RLBP1 protein an encoded by the polymcophic or screening for drugs targeting the antibody, a method for screening for screening of solution of RLBP1, and in expressing RLBP1 protein for use instance and function of RLBP1, and in expressing RLBP1 protein for use in screening and function of RLBP1, and in expressing RLBP1 protein for use or stress are useful in improving the efficiency and output of several sequence or are also useful for designing clinical trials of candidate drugs of propouds, and earlies and candidate drugs argeted against made and early phase clinical trials of condition or disease. The engage of the propouds argeted against made or entiting when the rangement of th the primer extension method 

Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;

Gaps .. Score 8; DB 1; Length 10; Pred. No. 6e+02; 0; Mismatches 0; Indels 36.4%; S Query Match Best Local Similarity 100.0 ادم 8; Conservative

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à d RESULT 864 **ABK68700** 

ABK68700 standard; DNA; 10 BP.

ABK68700;

02-JUL-2002 (first entry)

Human SCYA2 gene allele-specific oligonucleotide PCR primer #8. 

Human, small inducible cytokine A2; SCYA2; primer; ss; haplotype pair; haplotyping; atherosclerosis; antiarteriosclerotic; gene therapy; single nucleotide polymorphism; genotyping; drug screening; PCR; chromosome 17q11.2-q21.1

Homo sapiens.

WO200218413-A2

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New genetic variants having polymorphisms in the small inducible cytokine Al (SCYA2) gene, useful for studying the function of SCYA2, and for treating disorders affected by expression or function of the SCYA2
                                                                                                                                   Claim 19; Page 13; 58pp; English
                                             (GENA-) GENAISSANCE PHARM INC
               28-AUG-2001; 2001WO-US026899.
                               28-AUG-2000; 2000US-0228496P
                                                              Anastasio AE, Finkel K,
                                                                              WPI; 2002-339655/37.
07-MAR-2002
                                                                                                                     isogene.
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The invention relates to single nuclectide polymorphisms in the gene encoding human small inducible cytokine A2 (SCYA2) polypeptide. A method for the amplotyping the SCYA2 gene in an individual comprises identifying the nuclectide at one or more polymorphic sites and determining whether one of the specification or whether both copies are defined by a haplotypes given in the specification or whether both copies are defined by a haplotype pair. This method is useful in genotyping, whereby all possible haplotype pair. This method is useful in genotyping, whereby all possible haplotype can be assigned to specific genotypes. An association between a trait and a haplotype or haplotype pair of the haplotype or haplotype pair in a reference population, where a higher haplotype or rapit type pair in a reference population, where a higher haplotype or haplotype pair in a reference population, where a higher haplotype or haplotype pair. SCYA2 and its corresponding DNA are used for studying the expression and function of SCYA2, and in screening for candidate drugs to treat diseases related to SCYA2 and in screening for candidate drugs to treat diseases related to SCYA2 and ilele-specific coligonucleotide PCR primers used for detecting SCYA2 gene polymorphisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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0; Mismatches 0; Indels
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Matches 8; Conserv
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ABL42788 standard; cDNA; 10 BP (first entry) 12-APR-2002 ABL42788 RESULT 865
ABL4278
XX
AC
ABL4278
DT
12-APRXX
DE
Human |
XX
Human

Human maturation/activation dendritic cell expression gene tag #162.

Human, maturation/activation dendritic cell expression gene, tag, maturation, activation, dendritic cell; ss.

Homo sapiens

JP2001327293-A.

27-NOV-2001

22-MAY-2000; 2000JP-00150562

22-MAY-2000; 2000JP-00150562.

(KAGA-) KAGAKU GLJUTSU SHINKO JIGYODAN.

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The present invention describes a human maturation/activation dendritic cell (IC) expression group consisting of 100 genes which show the highest expression among the genes expressed in human maturation/ activation DC. Also described are: (1) a protein expressed by the above the muman maturation/activation DC expression gene; (2) an antibody against the protein; and (3) an antagonist against the expression of each gene belonging to the above gene group. The gene group is useful for the treatment and the diagnosis of various human diseases related to human DC. ABL4267 to ABL4226 represent specifically claimed human maturation/activation DC expression gene tags from the present invention
                                                            Human maturation/activation dendritic cell expression gene group
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                                                                                                                                                                                                                                                                                                                                                                                                                    Score 8; DB 1; Length 10;
Pred. No. 6e+02;
0; Mismatches 0; Indels
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                                                                                                     Claim 10; Page 13; 41pp; Japanese.
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100.0%; Pred
0; N
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                 WPI; 2002-127070/17
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Lee HH;

Kumar AM,

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Koshy

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Gaps

Human; colony stimulating factor 3(granulccyte); CSF3; SNP; isogene; chromosome 17q11-12; single nucleotide polymorphism; immunostimulant; neutropenia; promyelocytic leukaemia; haematological disorder; gene therapy; PCR; primer extension oligonucleotide; ss. Human CSF3 gene allele specific primer extension oligo SEQ ID NO: 52 (first entry) 27-SEP-2002 AAL48074; 

AAL48074 standard; DNA; 10 BP.

RESULT 866 AAL48074/C

Homo sapiens

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WO200194364-A2

13-DEC-2001.

11-JUN-2001; 2001WO-US018813.

09-JUN-2000; 2000US-0210380P.

(GENA-) GENAISSANCE PHARM INC.

Sausker EA; Messer C, Kazemi A, Duda A,

WPI; 2002-566435/60.

for New variants of colony stimulating factor 3 (CSF3) isogenes, useful fimproving efficiency and reliability in the development of drugs for treating diseases associated with CSF3 activity e.g. neutropenia.

Claim 19; Page 13; 68pp; English.

The present invention provides the protein, gene and cDNA sequences of human colony stimulating factor 3 (granulocyte) CSF3. Also described are single nucleotide polymorphisms (SNBs) identified within these sequences. The sequences can be used in the treatment of neutropenia, promyelocytic leukaemia and haematological disorders. The present sequence is an allele specific primer extension oligonucleotide used to isolate the coding sequences of the invention

(first entry)

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SAGE tag; serial analysis of gene expression; human; Thi cell; activated T cell; T lymphocyte; immune response; expression pattern; preferential expression; immune disorder; ss.
                                                                                                                                                                                                                                                                                                                                 Human activated Th1 and Th2 cell expression gene group, diagnosis and treatment of Th1 and Th2-related diseases.
                                                                                                                                                                                                                                                                              (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
                                                     Human COP9 SAGE tag, SEQ ID NO:204.
                                                                                                                                                                                                                                                                                                                                                                           Claim 19; Page 11; 60pp; Japanese.
                                                                                                                                                                                                                        19-DEC-2000; 2000JP-00385816.
                                                                                                                                                                                                                                                  19-DEC-2000; 2000JP-00385816.
                                                                                                                                                                                                                                                                                                       WPI; 2002-594261/64.
                                                                                                                                                                 JP2002186482-A.
                                                                                                                                      Homo sapiens
                         29-NOV-2002
ABV78493;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel human 6-phosphofructo-2-kinase/ fructose -2,6-biphosphatase 2 (PFKFB2) isogene. The PFKFB2 of the invention has eyrostatic and antidiabetic activity. The polymoleotides may have a use in gene therapy. The identified candidate agents targeting PFKFB2, are useful for treating cancer and diabetes. The methods of the invention are useful for improving the efficiency and reliability of several steps in the discovery and development of Grugs for treating diseases associated with PFKFB2 activity. The present sequence represents a PCR primer used in the invention to detect PFKFB2 gene polymorphisms by primer extension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
nt of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New 6-phosphofruoto-2-kinase/fructose-2,6-bisphosphatase 2 (PFKFB2) gene variants, for improving efficiency and reliability in the development of drugs for treating diseases associated with PFKFB2 activity e.g. cancer.
                                                                                                                                                                                                                                                                                                   Human; 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2; PFKFB2; cytostatic; antidiabetic; gene therapy; cancer; diabetes; ss; PCR; primer; polymorphism.
                                                                  Gaps
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                                    Query Match

36.4%; Score 8; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 6e+02;

Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.4%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 6e+02; tive 0; Mismatches 0; Indels
           Sequence 10 BP; 1 A; 4 C; 1 G; 4 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10 BP; 5 A; 2 C; 2 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 17; Page 14; 95pp; English.
                                                                                                                                                                                          ABV99817 standard; DNA; 10 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENA-) GENAISSANCE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-2001; 2001WO-US018458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-2000; 2000US-0209935P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Koshy B;
                                                                                                                                                                                                                                                                           Human PFKFB2 PCR primer #19.
                                                                                                                                                                                                                                                 (first entry)
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                             730 CAGGAGAA 737
                                                                                                                      10 CAGGAGAA 3
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                                                                                                                                                                                                                                                                                                                                                                                         WO200194363-A2.
                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                               24-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                   13-DEC-2001.
                                                                                                                                                                                                                      ABV99817;
                                                                                                                                                                 RESULT 867
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The invention relates to SAGE (serial analysis of gene expression) tage representing groups of genes which are expressed in activated human Th1 and/or Th2 cells. The SAGE tags of this invention consist of a sequence of 10 nucleotides located downstream of the 5'-CATG-3' sequence motif lying nearest to the polya region of cDNAs derived from a variety of genes. These tags serve to uniquely identify each transcript and can thus be used to analyse the pattern of gene expression in particular cell types. The invention also relates to proceins encoded by the genes expressed in Th1 and/or Th2 cells, antibodies against these proteins, and inhibitors of the expression of groups of genes that are expressed in either or both the two cell types. Groups of genes expressed in Th1 and/or Th2 cell types may be used for the diagnosis and treatment of Th1 and/or Th2 cell types may be used for the diagnosis and treatment of Th1 cepresenting 171 genes which are more highly expressed in Th1 cells compared with Th2 cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.4%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 6e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10 BP; 4 A; 2 C; 4 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   729 CCAGGAGA 736
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Best Local Similarity
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ABV78493 standard; cDNA; 10 BP.

ABV78493 ID ABV7 XX

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The present invention relates to a nucleic acid library comprising mycdependent downstream genes or their functional fragments essentially capable of supporting a neoplastic character of cancer such as growth, invasion or spread. These myc target or tag sequences are identified by SAGE (serial analysis of gene expression). The library is useful to new diagnoses and treatments for cancer. The invention is also useful to enhance production of recombinant proteins in a production system with high expression of endogenous or transfected myc oncogenes. ABK23412-ABK23828 represent transcript tag DNA sequences that are activated or repressed by N-myc in human neuroblastoma
                                                                                                                                                                                                                            A new nucleic acid library of myc-dependent downstream genes capable of supporting a neoplastic characteristic of cancer is useful to find new therapies and diagnoses for cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; ss; primer; interleukin-6; ILG; myeloma; arthritis; CAD; Kapos; arrcoma; coronary artery disease; inflammatory cytokine; hypercalcaemia; bone disease; inflammatory disease; HIV; PCR; human immunodeficiency virus infection; stunted growth; isogene; systemic onset juvenile cinonic arthritis; haplotype; genotype; chromosome 7p21-p15; gene therapy; primer extension; SNP; single nucleotide polymorphism.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36.4%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 6e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10 BP; 0 A; 4 C; 4 G; 2 T; 0 U; 0 Other;
                                                                                                                             (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BIJ VAN
                                                                                                                                                                                                                                                                                                Disclosure; Page 50; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABK96609 standard; DNA; 10 BP.
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21-AUG-2001; 2001US-0313963P.
                                               11-MAY-2001; 2001WO-NL000361.
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                                                                             11-MAY-2000; 2000EP-00201698
29-JUN-2000; 2000EP-00202284
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Best Local Similarity 100...
Best as 8; Conservative
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                                                                                                                                                                Caron HN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     728 GCCAGGAG 735
                                                                                                                                                                                                WPI; 2002-066603/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 GCCAGGAG 3
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               15-NOV-2001
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The invention relates to a polynucleotide comprising a first nucleotide sequence (NS1) comprising a IL6 (interleukin-6, an inflammatory cytokine) to sequence (NS1) comprising a IL6 (interleukin-6, an inflammatory cytokine) to sequence comprises the regions of NS1 and is further defined by the corresponding sequence of polymorphisms whose locations and identifies are defined in the specification (PS2-PS6, PS8 and PS10-PS17), or a second nucleotide sequence of NS2) complementary to NS1.

Controlled are methods of haplotyping Squad PS10-PS17), or a second nucleotide sequence comprises a coding sequence for an IL6 predicting the haplotype/genotype) of the IL6 gene of an individual, or isogene. Also included are methods of the Dick gene of an individual, or predicting the haplotype/genotype) of the IL6 gene, a recombinant non-human organism (II) transformed or transfected with the IL6 gene, a recombinant non-human organism (III) crarsformed or transfected with the IL6 gene, a recombinant non-human organism (III) crarsformed or transfected with the IL6 gene, a recombinant non-human organism (III) crarsformed or transfected with the IL6 gene, and containing one of the identified single-nucleotide polymorphisms (SNP), an isolated polymorphic variant of IL6, an isolated monoclonal antibody specific for the IL6 gene, and a genome anthology for the IL6 gene. The IL6 gene, and a genome anthology for the IL6 gene. The IL6 gene, are useful for transfing myebloma, coronary arrery disease (GAD), arthritis, Kaposi sarcoma (associated with human immunodeficiency virus of infection, HIV), hypercalcaemia, bone disease, inflammatory disease, are useful for transfing myebloma, coronary arrery disease (GAD), arthritis, Kaposi sarcoma (associated with human immunodeficiency virus of and development of drugs and in the validation of IL6 as are useful for improving the efficiency and reliability in the discovery and development of drugs and in the validation of IL6 as are useful for improving the efficiency propered to the inservence of
                                                                                                              Genetic variants of interleukin-6 isogenes for improving efficiency and reliability in drug development for treating myeloma, coronary artery disease, arthritis and Kaposi sarcoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; ss; primer; interleukin-6; IL6; myeloma; arthritis; CAD; Kaposi sarcoma; coronary artery disease; inflammatory cytokine; hypercalcaemia; bone disease; inflammatory disease; HIV; PCR; human immunodeficiency virus infection; stunted growth; isogene; systemic onset juvenile chronic arthritis; haplotype; genotype; chromosome 7p21-p15; gene therapy; primer extension; SNP; single nucleotide polymorphism.
Lachowicz M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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Denton RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10 BP; 0 A; 3 C; 4 G; 3 T; 0 U; 0 Other;
  KM, Chew A,
Sausker EA;
                                                                                                                                                                                                              Claim 17; Page 16; 86pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABK96611 standard; DNA; 10 BP.
  Bieglecki
Parks KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-SEP-2002 (first entry)
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                                                                       WPI; 2002-519290/55.
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les 8; Conserv
  Bentivegna SC,
Nandabalan K,
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Primer-extension oligonucleotide #14 to detect human DNAL4 polymorphisms.
                                                                                                                  Human, single nucleotide polymorphism; SNP; DNAL4; chromosome 22q13.1;
dynein axonemal light polypeptide chain 4; haplotyping; genotyping;
neuroprotective; neurological disorder; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genotyping human dynein, axonemal light polypeptide chain 4 gene of individual, useful for determining haplotype of individual, comprises determining identity of nucleotide pair at specific polymorphic sites
                                                                                                                                                                                                                                                                                                                                                                (GENA-) GENAISSANCE PHARM INC.
                                                                                                                                                                                                                                                                                            16-APR-2001; 2001WO-US012304.
                                                                                                                                                                                                                                                                                                                             17-APR-2000; 2000US-0197460P.
                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-075065/10.
                                                                                                                                                                                                                                                                                                                                                                                                 Bentivegna SC,
                                                                                                                                                                                                                         WO200179235-A2
                                                                                                                                                                                          Homo sapiens.
                                                   26-MAR-2002
                                                                                                                                                                                                                                                           25-OCT-2001
                  AAS19962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 873
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                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a polynucleotide comprising a first nucleotide sequence (NSI) comprising a ILG (interleukin-6, an inflammatory cytokine) sequence (NSI) comprising a ILG (interleukin-6, an inflammatory cytokine) there acach isogene comprises the regions of NSI and is further defined by the corresponding sequence of polymorphisms whose locations and indentities are defined in the specification (PS2-PS6, PS9 and PS10-PS17), or a second nucleotide sequence (NS2) complementary to NSI.

Alternatively, the sequence comprises a codaing sequence for an ILG predicting the haplotype/genotype) of the ILG gene of an individual, identifying an association between a trait and at least one haplotype or haplotype pair of the ILG gene, a recombinant non-human organism (II) crament of the ILG gene, a recombinant non-human organism (II) a polymorphism in the ILG gene, a recombinant non-human organism (II) crament of the ILG sene, a recombinant non-human organism (II) a polymorphic variant of ILG, an isolated oligonucleotide of a risolated crament of the ILG sene, a recombinant non-human organism (II) crament organism (II) and polymorphic variant of ILG, an isolated monoclonal antibody specific for ILG gene, and a genome anthology for the ILG gene, The ILG gene, and a genome anthology for the ILG gene, The ILG gene, are useful for treating myeloma, corromary arrey disease (CAD), are useful for treating myeloma, corromary arrey disease (CAD), are useful for treating myeloma, corromary arrey disease (CAD), are useful for improving the efficiency and reliability in the discovery and development of drugs and in the validation of ILG as a drug target.

The ILG isogene is useful in studying the expression and function of ILG and in expressing in prevention of the antibody is useful in diagnostic, prognostic and therapeutic methods are useful for improving the efficiency and reliability in the discovery and development of drugs and in the voltament of an allele specific primer of drugs and in the voltament of an allele specific o
                                                                                                                                                                                                                                                                                                                           Genetic variants of interleukin-6 isogenes for improving efficiency areliability in drug development for treating myeloma, coronary artery
                                                                                                                                                                                                                                           Denton RR, Lachowicz M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10 BP; 0 A; 4 C; 1 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                           Chew A,
                                                                                                                                                                                                                                                                                                                                                            disease, arthritis and Kaposi sarcoma.
                                                                                                                                                                                                                                                          Sausker EA;
                                                                                                                                                                                                                                                                                                                                                                                               Claim 17; Page 16; 86pp; English.
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                                                                                                                                                                                                        (GENA-) GENAISSANCE PHARM INC
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21-AUG-2001; 2001US-0313963P.
                                                                                                                  09-NOV-2001; 2001WO-US047077
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Parks KE,
                                                                                                                                                                                                                                                                                            WPI; 2002-519290/55.
                                                                                                                                                                                                                                         Bentivegna SC,
Nandabalan K,
                                                 WO200238586-A2.
                  Homo sapiens.
                                                                                  16-MAY-2002.
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for

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Choi JY,

Chew A,

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                                                                                                                           The present invention relates to novel single nucleotide polymorphisms (SNPs) in the human dynein, axonemal light polypeptide chain 4 (DNAL4) gene located on chromosome 22q13.1, and methods for haplotyping and/or genotyping the DNAL4 gene. The methods of the invention make use of allele-specific oligonucleotides (ASOs) as probes and primers and/or primer-extension oligonucleotides for detecting the DNAL4 gene polymorphisms. The polymorphisms of diseases and screened compounds are useful for the treatment of diseases ascoidated with DNAL4 activity, such as neurological disorders. AAS19949-AAS19976 represent primer-extension oligonucleotides for detecting human DNAL4 gene polymorphisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, PCR, ss, allele-specific, SNP, single nucleotide polymorphism, cerberus 1 homologue, cysteine knot superfamily, CER1; drug screening; developmental disorder; polymorphic site, CER1 haplotyping, primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.4%; Score 8; DB 1; I 100.0%; Pred. No. 6e+02; ative 0; Mismatches 0
                                                           Claim 18; Page 14; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAL43004 standard; DNA; 10 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
es 8; Conservative
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two copies of gene.
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Matches
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Gaps

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0; Indels

8; Conservative 730 CAGGAGAA 737

Matches

à g

m

10 CAGGAGAA

Local Similarity

AAS19962 standard; DNA; 10 BP.

RESULT 872

AAS19962 ID AAS1

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Claim 18; Page 15; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 17; Page 16; 96pp; English.
                                                                                                                                                                                                                                                                                                               ABN81268 standard; DNA; 10 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENA-) GENAISSANCE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-OCT-2001; 2001WO-US042726.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-OCT-2000; 2000US-0240211P.
                                                                                                                                                                                                                                                                                                                                                           16-AUG-2002 (first entry)
                                                                                                                                                                                               Local Similarity 100.
                                                                                                                                                                                                                                   736 AAACAGAA 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-426265/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Han J, Kliem SE,
                                                                                                                                                                                                                                                        10 AAACAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-APR-2002.
                                                                                                                                                                                                                                                                                                                                     ABN81268;
                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer
                                                                                                                                                                                                                                                                                         RESULT 875
                                                                                                                                                                                                                                                                                                     ABN81268/c
                                                                                                                                                                                                              Matches
The invention relates to the identification of 13 novel polymorphic sites in the human cerberus 1 (Kenopus laevis) homologue (cysteine knot superfamily) (CER1) gene. The invention also comprises the amino acid and coding sequence of CER1. The CER1 protein is useful for screening drugs that target CER1 - for the treatment of developmental disorders. The CER1 for screening and testing of drugs targeted against CER1 isogenes, for screening and testing of thus targeted against CER1 protein, and itsing the efficacy of therapeutic agents for treating developmental useful for haplotyping the CER1 gene of an individual. The present DNA sequence represents a human CER1 gene primer-extension oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; matrix metalloproteinase 13 (collagenase 3); MMP13; cancer;
arthritis; haplotype; single nucleotide polymorphism; SNP; enzyme;
cytostatic; antiarthritic; gene therapy; chromosome 11q22.3; PCR primer;
                                                                                                                                           Novel genetic variants of Cerberus 1 (Xenopus laevis) Homolog (Cysteine Knot Superfamily) (CER1) isogenes, useful for improving efficiency and reliability in drug development for treating developmental disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human MMP13 gene allele specific primer extension oligo SEQ ID NO: 92.
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                     36.4%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 6e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                 Sequence 10 BP; 1 A; 1 C; 3 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tanguay DA;
                                                                                                                                                                                        Claim 16; Page 14; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Messer C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL45804 standard; DNA; 10 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENA-) GENAISSANCE PHARM INC
                                                                             (GENA-) GENAISSANCE PHARM INC
                                 19-OCT-2001; 2001WO-US046100.
                                                       19-OCT-2000; 2000US-0241634P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-JUL-2000; 2000US-0217950P.
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                                                                                                                                                                                                                                                                                                                                                                                             8; Conservative
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                                                                                                                         WPI; 2002-435527/46.
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Best Local Similarity
Matches 8; Conserv
                                                                                                  Shah N;
                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGAACAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                   Kazemi A,
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                                                                                                                                                                                                                                                                                                         The present invention provides the cDNA, protein and gene fragments of the human matrix metalloproteinase 13 (collagenase 3) (MMP13). Also provided are single nucleotide polymorphisms (SNPs) identified within the sequences. The sequences can be used to haplotype an individual and in the treatment of cancer and arthritis, including metastatic cancers. The present sequence is a primer extension oligonucleotide for the MMP13 gene, which is found on chromosome 11q22.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New genetic variants of cytochrome P450, subfamily I dioxin-inducible, polypeptide 1, glaucoma 3, primary infantile gene, CYPIB1 for treatment and expressing CYPIB1 protein for use in identifying drugs to breast
Novel genetic variants of matrix metalloproteinase 13 (collagenase 3) gene useful in studying expression and function of the protein, and for screening drugs to treat diseases e.g. cancer and arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide primer #19 for detecting CYP1B1 gene polymorphisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytochrome P450; dioxin-inducible, glaucoma 3; CYP1B1; cytostatic; ophthalmological; gene therapy; polymorphism; breast cancer; PCR; primary congenital glaucoma; primer extension; primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10 BP; 2 A; 1 C; 1 G; 6 T; 0 U; 0 Other;
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BP.

(first entry)

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Making small interfering RNA useful for treating Huntington's chorea by incorporating nucleotides into siRNA such that the siRNA has a sequence substantially identical to at least a portion of selected target gene.
                                                                                                                                                                       Small interfering RNA; siRNA; RNA interference application; anti-viral; transplant rejection; autosomal dominant genetic disease; anti-tumour; inherited disorder; Huntington's chorea; therapy; ds.
                                                                                                                                           Leader DNA #2 used in the synthesis of siRNA of increased potency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 38; Fig 3; 85pp; English.
                                                                                                                                                                                                                                                                                                                                 31-JAN-2003; 2003WO-US003023.
                                                                                                                                                                                                                                                                                                                                                              01-FEB-2002; 2002US-0353332P.
                                                 AAD58112 standard; DNA; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-689529/65.
                                                                                                                                                                                                                                                                                                                                                                                           (AMBI-) AMBION INC.
                                                                                                                                                                                                                                                                    WO2003064621-A2
                                                                                                                                                                                                                                     Unidentified.
                                                                                                             20-NOV-2003
                                                                                                                                                                                                                                                                                                 07-AUG-2003
                                                                                AAD58112;
                                                                                                                                                                                                                                                                                                                                                                                                                           Brown D,
                     RESULT 877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a reporter construct comprising: (a) an estrogen response segment having 5 or more estrogen response elements (ERE); (b) a promoter segment having at least one promoter nucleic acid sequence; and (c) a nucleotide sequence that encodes a reporter polypeptide, where the nucleotide sequence is operably linked to the promoter segment and the estrogen response segment. The reporter construct and vector are useful in identifying and isolating estrogen-responsive cells. The methods are useful in inhibiting the proliferation or survival of estrogen-responsive breast cancer cells or in enhancing the proliferation or survival of estrogen-receptor non-expressing, estrogen-non-responsive cells. Sequences ACCT8140-75 represent SAGE tags for transcripts specifically or most abundantly expressed in normal estrogen responsive cells
screening for such drugs and reducing bias in clinical trials of such drugs. The sequence represents an oligonucleotide primer, used in the invention to detect polymorphisms in the CYPIB1 gene by primer extension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New reporter construct for identifying and isolating estrogen-responsive cells comprises an estrogen response segment, a promoter segment and a nucleotide sequence that encodes a reporter polypeptide.
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                        ERE; reporter construct, estrogen response element; cytostatic; rat; gene therapy; breast cancer; SAGE; ds.
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                                                                                           36.4%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 6e+02;
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                                                                                                                                                                                                                                                                                                                                                           Normal estrogen responsive cells derived SAGE tag.
                                                              Sequence 10 BP; 0 A; 4 C; 0 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10 BP; 1 A; 4 C; 2 G; 3 T; 0 U; 0 Other;
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100.0%; Pred. No. 6e+02;
                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; Page 32; 51pp; English.
                                                                                                                                                                                                                                                                 ACC78771 standard; DNA; 10 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-NOV-2001; 2001US-0338136P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-NOV-2002; 2002WO-US035901
                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                            8; Conservative
                                                                                                                                                        731 AGGAGAAA 738
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Best Local Similarity
Matches 8; Conserval
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                                                                                                                                                                                    10 AGGAGAAA 3
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                                                                                                       Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                                                                                                                              ACC78771;
                                                                                              Query Match
                                                                                                                                                                                                                                   RESULT 876
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Pasloske

Pallotta V,

Jarvis R,

Ford LP,

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The invention relates to a method for making small interfering RNA (siRNA) of increased potency. The method involves obtaining nuclectides and incorporating the nucleotides into siRNA as that RNA duplex of 15-30 contiguous nucleotides is formed, where the siRNA has a sequence substantially identical to at least a portion of a selected target gene. The method is also useful for attenuating the expression of a target gene in a cell. The siRNA is useful in RNA interference applications which materials and applications. Medical applications include a wide range of research, industrial and medical processes, materials and applications and therapies; and compositions and therapies for inherited disorders. siRNA is also useful in therapies for treating autosomal dominant genetic disease such as Huntington's chorea and management of transplant rejection. The present sequence is a leader DNA used in the synthesis of siRNA of increased potency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10 BP; 4 A; 2 C; 4 G; 0 T; 0 U; 0 Other;
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ID ADD714
XX ADD714
XX DT 15-JAN
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Conservative

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Example; Page 12; 32pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8, Conservative
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         *tag=
                                                                        *tag=
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                                                                                                                                                                                                                                                                                                                                     WPI; 2001-265835/27
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Best Local Similarity
Matches 8, Conser
                                                                                                                                                                                                                                                                                         (GARN/) GARNER P P.
                                                                                                                                                                                                        WO200114398-A1
                                                                                                                                                                                                                                                                       25-AUG-1999;
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                                                               Misc binding
Misc_binding
                                                                                                                             Misc_binding
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                                                                                                                                                                                                                                                                                                                Garner PP;
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ABA01034/
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                                                                                                                                                                                                                                                                               The invention relates to a stimulus-responsive DNA organization undergoing formation/dissociation of a supercoil or rotation in response to an external stimulus and comprises a number of plasmid DNAs ligated in it. The DNA organization is applicable in various materials and body parts or medical micromachines e.g. artificial muscles. This sequence represents an oligonucleotide used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /bound_moiety= "Alpha-helical peptide nucleic acid
(alphaPNA) shown in AAB74017"
/note= "this nucleotide hybridises to the thymine at
position 15 of AB74017 to form an alphaPNA.DNA complex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AlphaFNA; alpha-helical peptide nucleic acid; alphaFNA.DNA complex; solid-phase peptide synthesis; molecular switching; diagnosis; therapy; backbone 2; b2; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/bound molety= "Alpha-helical peptide nucleic acid
(alphaPNA) shown in AB574017"
(alphaPNA) shown in AB574017"
(note= "this nucleotide hybridises to the thymine at
position 19 of AB74017 to form an alphaPNA.DNA complex"
                                                                                                                                                                                                        Stimulus-responsive DNA organization of highly compatible functional material undergoing reversible formation/dissociation of supercoil or rotation in response to external stimulus, useful as e.g. artificial
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      ö
  ss; stimulus-responsive DNA organization; supercoil; rotation; external stimulus; medical micromachines; artificial muscle.
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                                                                                                                                                                                                                                                                                                                                                                                 Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA sequence that forms complex with alphaPNA CTCCT(b2)
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100.0%; Pred. No. 6e+
tive 0; Mismatches
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                                                                                                                                         (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                 28-AUG-2002; 2002WO-JP008656
                                                                                                                      27-FEB-2002; 2002JP-00051927
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/bound
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les 8; Conserv
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                                                      WO2003072772-A1
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                                                                             34-SEP-2003
                                  Synthetic
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Matches
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/bound_molety= "Alpha-helical peptide nucleic acid
(alphaPhA) shown in ABB74017"
/note= "this nucleotide hybridises to the thymine at
position il of AB74017 to form an alphaPNA.DNA complex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptide-based nucleic acid surrogate (PNAs) for use in therapeutic, diagnostic and molecular switching applications e.g. alpha-PNA chips.
                                                                                                                                                                                                                                                                      /bound_moiety= "Alpha-helical peptide nucleic acid (alphaPhA) shown in AAB74017" hoote= "this nucleotide hybridises to the thymine at footies "this nucleotide hybridises to the chymine at position" of AB74017 to form an alphaPNA.DNA complex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= e
/bound_moiety= "Alpha-helical peptide nucleic acid
(alphaPNA) shown in AAB74017"
/note= "this nucleotide hybridises to the thymine at
position 3 of AB74017 to form an alphaPNA.DNA complex"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36.4%; Score 8; DB 1; Length 11; 100.0%; Pred. No. 6.2e+02; rive 0; Mismatches 0; Indels
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The sequence is the polypyrimidine rich region of the capture reverse phase triplex forming oligonucleotide, RP-TFO used to analyse the CSFIPO locus using the method of the invention. The invention relates to analysing target nucleic acid sequences comprising restricting isolated adding at least one triplex forming oligonucleotide (TFO), adding at least one triplex forming oligonucleotide (TFO), adding at least one triplex forming oligonucleotide (TFO), RPAS) tail structure, hybridising the captured structure with a single nucleotide polymorphisms (SNP) identification probe and determining the SNP score. The methods can be used for analysing target nucleic acid sequences, especially genomic DAA sequences, to determine if they contain SNPs or short tandem repeats (STRs). The methods can be used to detect shows to use in population genetics, drug development, forensics, cancer, genetic disease research, genomic analysis, diagnostics and therapeutics in humans, plants and animals
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Analyzing target nucleic acid sequences, useful for population genetics, drug development and diagnosing cancer, comprises hybridizing triple forming oligonuclectide and probe to target sequence.
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                                                                                                                                                  Example 4; Page 69; 141pp; English
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03-NOV-1999; 99US-0163416P.
21-DEC-1999; 99US-0171348P.
07-JUL-2000; 2000US-0216579P.
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Best Local Similarity 100...
Best as 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200132929-A1
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AAS05726/c
C X X X B A X B B B B B B B X X S X X X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a method for detecting mutations in the base sequences of nucleic acids. The method comprises using ion pair chromatography involving a reversed phase column as a separation column, and setting the separation column at temperature that causes differences in stability between hetero- and homoduplaxes. The present sequence is an exon from a mutated DNA sequence that can be analysed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       reverse phase triplex forming oligonucleotide; RP-TFO; protected nucleic acid sequence; PNAS; single nucleotide polymorphism; SNP; short tandem repeat; cancer; CSF1PO; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting mutations in the base sequences of nucleic acids comprises using ion pair chromatography and reversed phase separation columns.
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                                                                                                                                                                                                                                                           19-APR-2000; 2000JP-00118587.
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21-DEC-1999; 99US-0171348P.
07-JUL-2000; 2000US-0216579P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the method of the invention
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                            US2001034029-A1.
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                                                                                                     25-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                              Fujiwake H;
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ABQ87632 standard; cDNA; 11 BP.

RESULT 884

ABQ87632

4 AGGAGAAA 11

10-SEP-2002 (first entry)

ABQ87632;

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forming oligonucleotide, RP-TFO, used to analyse the CSF1PO locus using the method of the invention. The invention relates to analysing target nucleic acid sequences comprising restricting isolated DNA, hybridising at least one triplex forming oligonucleotide (TFO), adding a 3' to 5' exonuclease to form a protected nucleic acid sequence (PNAS) tail structure, hybridising the captured structure with a single nucleotide polymorphisms (SNP) identification probe and determining the SNP score. The methods can be used for analysing target nucleic acid sequences, especially genomic DNA sequences, to determine if they contain SNPs or short tandem repeats (SYRS). The methods can be used to detect SNPs for use in population genetics, drug development, forensics, cancer, genetic disease research, genomic analysis, diagnostics and therapeutics in humans, plants and animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to the coding sequence of human Creaml, which is a protein containing a repetitive 86 amino acid motif. The protein is a transcriptional control factor, and is a conjugate of retinoblastoma protein (Rb). The present sequence is the an intron-exon junction in the coding sequence of the invention
                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                              Query Match 36.4%; Score 8; DB 1; Length 11; Best Local Similarity 100.0%; Pred. No. 6.2e+02; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                              Seguence 11 BP; 0 A; 5 C; 0 G; 6 T; 0 U; 0 Other;
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Best Local Similarity 100.
Matches 8; Conservative
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The invention relates to identifying (M1) genes in vitro that, in humans or animals, are important for skin ageing and/or skin stress by scrial analysis of gene expression between mixtures of transcribed and optionally translated, genetically encoded factors (A) obtained from young and aged skin, to identify that genes that show strong differential useful for. (A) comprises protain or mRNAs or their fragments. (M1) is useful for: identifying markers of skin ageing and/or stress; determining skin ageing and/or stress; and identifying or determining the effects of beharmaceutical or cosmetic agents for conrol of skin ageing. The present sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ866246-ABQ87680) of the invention
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                                                                                                                          Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
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                                                                                           Human skin stress/ageing related EST SEQ ID NO 1387.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 8; Page 96; 325pp; German.
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Matches 8; Conservative
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                                                                                                                                                               Homo sapiens.
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Homo sapiens

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The invention relates to identifying (M1) genes in vitro that, in humans or animals, are important for skin ageing and/or skin stress by serial analysis of gene expression between mixtures of transcribed and optionally translated, genetically encoded factors (A) obtained from young and aged skin, to identify that genes that show strong differential useful for: identifying markers of skin ageing and/or stress; determining skin ageing and/or stress; and identifying or determining the effects of planamedutical or commettic agents for control of skin ageing. The present sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ87680) of the invention
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(M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
screening for cosmetic or therapeutic agents, based on differential gene
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                                                                                                                                                                                                                                                                                                                                        Sequence 11 BP; 1 A; 1 C; 2 G; 7 T; 0 U; 0 Other;
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                                                         Claim 8; Page 55; 325pp; German
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                     expression.
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                                                                                                                                                                                                                                                                                                Identifying genes involved in skin stress and aging, useful e.g. in screening for cosmetic or therapeutic agents, based on differential gene
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                                                                                             20-DEC-2001; 2001WO-EP015178
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Best Local Similarity love.
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ABV71675 standard; cDNA; 11
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                                                                                                                                    Human skin EST 9461
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                         RESULT 889
ABV71675/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to in vitro identification (MI) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (8AGE) so as to identify skin-expressed genes and quantify their expression. (MI) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintenes or promotes skin homeostasis or that can be used for treating skin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
                                                                                                                                                                                                                                                                                                                                           Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
rosacea, melanoma, basal cell carcinoma, and carcinoma or sarcoma of skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
                                                                                                          Gaps
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                                                                                                          0; Indels
                                                                             Query Match

36.4%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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                                                      Sequence 11 BP; 4 A; 4 C; 1 G; 2 T; 0 U; 0 Other;
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                              CAGAACAC 10
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The invention relates to in vitro identification (MI) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression (MI) is useful for identifying genes involved in skin homeostasis, to determine skin homeostasis and to test agent (A) that maintains or promoces skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis, sumburn, psoriasis, scieroderma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ichthyosis; atopic dermatitis, acne, seborrhea, lupus erythematosus; rosscea; melanoma; basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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llarity 100.0%; Pred. No. 6.2e+02;
Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hofmann K;
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(M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriatis scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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                                                                                           20-DEC-2001; 2001WO-EP015179.
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8; Conservative
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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Hofmann K;
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Best Local Similarity 100.
Petersohn D, Conradt M,
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(MI) is useful for identifying genes involved in skin homeostasis, to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis, sunburn, psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; scoacea, melanoma; basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (\$AGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; inchthyosis; atopic dermatitis, anner, seborrhea; lupus erythematosus; rosaces, melanoma; basal call carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGB, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss. In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against 36.4%; Score 8; DB 1; Length 11; 100.0%; Pred. No. 6.2e+02; Live 0; Mismatches 0; Indels Sequence 11 BP; 7 A; 1 C; 2 G; 1 T; 0 U; 0 Other; Disclosure; Page 94; 1345pp; German. Hofmann BP. 20-DEC-2001; 2001WO-EP015179. 03-JAN-2001; 2001DE-01000127. ABV64703 standard; cDNA; 11 21-OCT-2002 (first entry) Query Match
Best Local Similarity luv...
8; Conservative Conradt M, 736 AAACAGAA 743 AAACAGAA 10 Human skin EST 2489. (HENK ) HENKEL KGAA WPI; 2002-590638/63 e.g. skin cancer. WO200253774-A2. Petersohn D, Homo sapiens 11-JUL-2002 m ABV64703; ABSULT 893
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Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 8; Conservative 0; Mismatches 0;
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ABV62451/c ID ABV62451 standard; cDNA; 11 BP.

RESULT 895

Sequence 11 BP; 3 A; 5 C; 2 G; 1 T; 0 U; 0 Other;

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically scroded from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression (AAGE) (M1) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis, sunburn, psoriasis; scleroderma; inchthyosis, atopy dermatitis, acne, sebornhea; lupus expthematosus; rosaces, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis,
psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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WO200253774-A2
                                                                                                                                                                                                                 Petersohn D,
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(M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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                                                                                                                                                 Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis; dermatitis, skin cancer, EST, expressed sequence tag, ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 32; 1345pp; German.
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                                                              (first entry)
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Query Match

Best Loc Matches

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ABV64507

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression ($AGE$) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriais; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea, melanoma; basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
                      In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
                                                                                                                             Disclosure; Page 41; 1345pp; German.
                                                                           e.g. skin cancer.
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Sequence 11 BP; 1 A; 4 C; 2 G; 4 T; 0 U; 0 Other;

Gaps ö 36.4%; Score 8; DB 1; Length 11; 100.0%; Pred. No. 6.2e+02; tive 0; Mismatches 0; Indels 8; Conservative Query Match Best Local Similarity Matches

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729 CCAGGAGA 736 8 CCAGGAGA 1 ð

ABV65528 standard; cDNA; 11 ABV65528; RESULT 898 ABV65528/c 

21-OCT-2002 (first entry)

Human skin EST 3314.

Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

Homo sapiens

WO200253774-A2.

11-JUL-2002

20-DEC-2001; 2001WO-EP015179

03-JAN-2001; 2001DE-01000127

(HENK ) HENKEL KGAA.

M, Hofmann K; Conradt Petersohn D,

WPI; 2002-590638/63.

In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.

Disclosure; Page 117; 1345pp; German.

The invention relates to in vitro identification (M1) of genes.expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or

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Query Match 36.4%; Score 8; DB 1; Length 11; Best Local Similarity 100.0%; Pred. No. 6.2e+02; Matches 8; Conservative 0; Mismatches 0; Indels

Sequence 11 BP; 1 A; 3 C; 2 G; 5 T; 0 U; 0 Other;

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promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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(M1) is useful for identifying genes involved in skin homeostasis, to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea, melanoma; basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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Human skin EST 4031.
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                                                                     ABV69872 standard; cDNA; 11 BP.
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                                                                                                                                  Human skin EST 7658.
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Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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immunosuppressive, antiinflammatory; cytostatic, SAGE, neurodermatitis,
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In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically scooded factors from skin, to serial analysis of gene expression ($AGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to the stagent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; inchthyosis; atopic dermatitis; acne, sebornhea; lupus erythematosus; rosacca; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
                                       The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sumburn; psoriasis; scleroderma;
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Pred. No. 6.2e+02;
0; Mismatches 0; Indels
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Claim 24; Page 237; 1345pp; German.
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100.0%; Pre
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Best Local Similarity 100...
Acconservative
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                                                                                                                     Hofmann K;
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                       03-JAN-2001; 2001DE-01000127
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In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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                          ABV62306 standard; cDNA; 11
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RESULT 906
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immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis,
psoriasis, dermatitis, skin cancer, EST; expressed sequence tag, ss.
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100.0%; Pred. No. 6.2
tive 0; Mismatches
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Matches 8: Conserv
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosace, melanoma; basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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Best Local Similarity 100.
Matches 8; Conservative
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Conradt M, Hofmann K;
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                                 WPI; 2002-590638/63
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                                                                                                        e.g. skin cancer.
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 Petersohn D,
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Gaps

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Indels

6.2e+02;

Mismatches Pred. No.

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8; Conservative

Best Local Similarity Matches 8; Conserv

736 AAACAGAA 743

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11 AAACAGAA 4

100.08;

ABV64213 standard; cDNA; 11 BP.

RESULT 911 ABV64213, 21-OCT-2002 (first entry)

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ABV64213;

Human skin EST 1999

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so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin identhyosis; specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acnes; sebornea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGB, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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                                                                                                                                                                             Length 11;
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                                                                                                                                              Sequence 11 BP; 0 A; 4 C; 4 G; 3 T; 0 U; 0 Other;
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36.4%; Score 8; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 8; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                     ABV71634 standard; cDNA; 11 BP
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                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                     skin. The present seque (EST) of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                           Human skin EST 9420.
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Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory; cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.

In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against

Disclosure; Page 80; 1345pp; German.

e.g. skin cancer.

Α,

Hofmann

Petersohn D, Conradt M,

WPI; 2002-590638/63

(HENK ) HENKEL KGAA

20-DEC-2001; 2001WO-EP015179. 03-JAN-2001; 2001DE-01000127.

WO200253774-A2. Homo sapiens.

11-JUL-2002.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression. (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriaais, scleroderma; ichthyosis; atopic dermatitis; acne, seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11 BP; 1 A; 1 C; 2 G; 7 T; 0 U; 0 Other;
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Best Local Similarity 100.
Matches 8; Conservative
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ABV64254/c
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; cosceea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag

Claim 24; Page 304; 1345pp; German.

DB 1; Length 11;

36.4%; Score 8;

Query Match

Sequence 11 BP; 1 A; 1 C; 2 G; 7 T; 0 U; 0 Other;

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Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic,
immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis,
psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            20-DEC-2001; 2001WO-EP015179.
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                         21-OCT-2002 (first entry)
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Best Local Similarity luv.
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                                                                                 Human skin EST 2040.
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                                                                                                                                                                                                                                                               Homo sapiens
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ID ABV65655
XX ABV656
XX AC ABV636

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically senced from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for trating skin disorders, specifically neurodermatitis; sumburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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                                                                                                                                                                                                                                                                          In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.4%; Score 8; DB 1; Length 11; 100.0%; Pred. No. 6.2e+02; Itive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 120; 1345pp; German.
                                                                                                                                                                                    Conradt M, Hofmann K;
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ABL91967 standard; cDNA; 11 BP.
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                                              20-DEC-2001; 2001WO-EP015179.
                                                                                        03-JAN-2001; 2001DE-01000127
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Matches 8; Conservative
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                                                                                                                                       (HENK ) HENKEL KGAA
                                                                                                                                                                                                                                                                                                                              e.g. skin cancer.
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                                                                                                                                                                                      Petersohn D,
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                                                                                                                 Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hofmann K;
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St Croix B, Kinzler KW, Vogelstein B;

(UYJO ) UNIV JOHNS HOPKINS.

02-AUG-2000; 2000US-0222599P. 11-AUG-2000; 2000US-0224360P. 11-APR-2001; 2001US-0282850P.

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WPI; 2002-291856/33
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An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TBM) protein, useful for inhibiting tumor growth.

Example 4; Page 326; 331pp; English.

The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumour endothelial marker (TEM) protein selected from ABB90732, ABB90749, ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumour growth, neoangiogensis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid archritis and psoriasis Human, mouse and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and ABB90712-ABB90789) are disclosed, as are marker oligonucleotide sequences: tumour endothelial markers (TEM) ABL91904-ABL92014 and ABL921191; normal endothelial markers useful to the invention

Sequence 11 BP; 1 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

36.4%; Score 8; DB 1; Length 11; 100.0%; Pred. No. 6.2e+02; ive 0; Mismatches 0; Indels Query Match
Best Local Similarity luv...
8; Conservative 728 GCCAGGAG 735 11 GCCAGGAG 4 дq ઠે

RESULT 915

ABQ81877 standard; DNA; 11 BP.

Kaposi's Sarcoma SAGE library Tag No.7 SEQ ID NO:27. 19-NOV-2002 (first entry) ABQ81877; 

Human; Kaposi's sarcoma; tumour; angiogenesis; tag; ss

EP1225233-A2. Homo sapiens

24-JUL-2002.

23-JAN-2002; 2002EP-00075264.

23-JAN-2001; 2001EP-00200228. 28-SEP-2001; 2001EP-00203703. 28-SEP-2001; 2001US-0325722P.

(AMST-) AMSTERDAM SUPPORT DIAGNOSTICS

BV.

Cornelissen M; Kuyl AC, Van Der

WPI; 2002-668396/72.

18 Determining presence of a tumor cell or angiogenesis, and the effectiveness of treatment, by detecting the presence of marker genes useful to detect and monitor treatment of Karposi's Sarcoma.

Page 8; 38pp; English. Claim 12;

The present invention describes a method for determining if an individual has a tumour cell or site of angiogenesis, or if a treatment is effective

in changing angiogenesis or changing a status of a set of target cells, comprising determining if a sample of the subject has an expression product of at least one marker gene. Also described is a compound capable of altering the expression or activity of Keratin 14, TIE 1, Salicadhesin or Siglec in a cell. Peripheral blood mononuclear cell (PBMC) expressed Keratin 14, TIE 1, Salicadhesin or Siglec, and kits containing them from the present invention can be used in a diagnostic method, particularly as an indicator of anglogenesis or to determine presence of a tumour cell. The method of the invention is sultable to determine within a few days if a certain treatment against Kaposi's Sarcoma is successful. ABQ818161 to ABQ82006 represent nucleotide sequence used in the exemplification of the present invention

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Sequence 11 BP; 5 A; 3 C; 3 G; 0 T; 0 U; 0 Other;

Gaps ; h Similarity 100.0%; Pred. No. 6.2e+02; 8; Conservative 0; Mismatches 0; Indels Query Match Best Local Similarity Matches

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730 CAGGAGAA 737 4 CAGGAGAA 11 원 ð

ABX71892 standard; DNA; 11 RESULT 916 ABX71892/c

BP.

ABX71892;

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Gaps

; 0

(first entry) 12-MAR-2003

DNA tag used to identify human gene encoding PEM 65.

Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM; Tumour endothelial marker; normal endothelial marker; PEM; pan-endothelial marker; polycystic kidney disease; psoriasis; diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis; necanglogenesis; immune response; cytostatic; antidiabetic; ophthalmological; antirheumatic; antiarthritic; antipsoriatic; ds.

Homo sapiens.

WO200283874-A2.

24-OCT-2002,

10-APR-2002; 2002WO-US008253.

11-APR-2001; 2001US-0282850P. 06-FEB-2002; 2002US-0354262P.

(UYJO ) UNIV JOHNS HOPKINS.

Kinzler KW, St Croix B, Carson-Walter E,

Vogelstein

WPI; 2003-093016/08.

New purified human transmembrane protein, designated as tumor endothelial marker (TEM) 3, useful for detecting, diagnosing or treating tumors, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or psoriasis. ALD STANKE STANK

Disclosure; Page 97; 374pp; English.

The present invention relates to a novel method for the isolation of endothelial cells (ECB), and the identification of genes expressed in normal and tumour ECS. Thmour endothelial marker (TEM), normal endothelial marker (TEM), normal identified in human ECs. The human EC marker proteins and the polynucleotide sequences encoding them are useful for detecting diagnosing or treating tumours as well as polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also

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RESULT 919
  RESULT 918
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            AAX34986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents an antisense oligonucleotide directed against the human protein kinase A-KI-alpha gene. The antisense oligonucleotides is useful as a cardinostatic agent, e.g. for treating leukaemia, large intestinal cancer, rectal cancer, colon cancer, cancer of the lung or stomach, hepatic cancer, malignant lymphoma, cancer of the tongue, oesophagus, breast, uterus or pharynx, brain tumour, melanoma, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligo:nucleotide contg. human protein kinase A gene sequence - useful as cardinostatic agent.
useful for inhibiting necangiogenesis or tumour angiogenesis, for inducing an immune response to tumour endothelial cells in a patient, or for identifying candidate drugs for treating tumours. ABX71828-ABX71999 represent DNA tags for human PEM, TEM or NEM genes
                                                                                                           Gaps
                                                                                                                                                                                                                                                                                         Antisense oligonucleotide targeted to protein kinase A-RI-alpha gene.
                                                                                                                                                                                                                                                                                                              Human protein kinase A-RI-alpha gene; antisense oligonucleotide; carcinostatic; leukemia; large intestinal cancer; rectal cancer; colon cancer; lung cancer; nomach cancer; hepatic cancer; melanoma; malignant lymphoma; tongue cancer; oesophagus cancer; breast cancer; uterus cancer; pharynx cancer; brain tumour; malignant myoma; ss.
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                                                                                    36.4%; Score 8; DB 1; Length 11; 100.0%; Pred. No. 6.2e+02; tive 0; Mismatches 0; Indels
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                                                            Sequence 11 BP; 1 A; 4 C; 4 G; 2 T; 0 U; 0 Other;
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AAX34991 standard; DNA; 12 BP.
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                                                                                                            Conservative
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                                                                                                                                     GCCAGGAG 735
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                                                                                                                                                           11 GCCAGGAG 4
                                                                                             Local Similarity
les 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
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                                                                                                                                                                                                                                              AAX34991;
                                                                                      Query Match
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The present sequence represents an antisense oligonucleotide directed against the human protein kinase A-RI-alpha gene. The antisense oligonucleotides is useful as a carcinostatic agent, e.g. for treating leukaemia, large intestinal cancer, rectal cancer, colon cancer, cancer of the lung or stomach, hepatic cancer, malignant lymphoma, cancer of the tongue, oesophagus, breast, uterus or pharynx, brain tumour, melanoma, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Triplex formation; DNA detection; triple helix; identification; bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligo:nucleotide contg. human protein kinase A gene sequence - useful as
                                                                                                                          Antisense oligonucleotide targeted to protein kinase A-RI-alpha gene.
                                                                                                                                                                     Human protein kinase A-RI-alpha gene; antisense oligonucleotide; carcinostatic; leukemia; large intestinal cancer; rectal cancer; colon cancer; lung cancer; stomach cancer; hepatic cancer; melanoma; malignant lymphoma; tongue cancer; oesophagus cancer; breast cancer; uterus cancer; pharynx cancer; brain tumoux; malignant myoma; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.4%; Score 8; DB 1; Length 12;
llarity 100.0%; Pred. No. 6.4e+02;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12 BP; 6 A; 0 C; 5 G; 1 T; 0 U; 0 Other;
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  ВР
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AAX34986 standard; DNA; 12
                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Geiser TG;
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Homo sapiens.
                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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Query Match Best Local Si Matches 8

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and merabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC0010 ABC0010-ABC0010 and ABC0010-ABC0010 and ABC0010-ABC0010 and for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                         oligonucleotides, useful for diagnosis and cell typing, ied to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                    Claim 1; SEQ ID NO 274736; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                 36.4%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 6.4e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                      Sequence 12 BP; 2 A; 4 C; 0 G; 6 T; 0 U; 0 Other;
                Berlin K;
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Best Local Similarity 100.0
              Olek A, Piepenbrock C,
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                                          WPI; 2001-657177/75.
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                                                                                                        methylation status.
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                                                                                         designed to
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                                                                         Set of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a polynuclectide that is able to form a triple helix with a double stranded sequence. Cytosine bases in the present can be replaced with 5-methylcytosine for increased triplex stability. The present sequence is used in the assay of the invantion, where it can be part of the anchor DNA or reporter DNA sequence. The assay comprises adding a sample containing double-stranded DNA test sequences to an aqueous medium containing at least one complex of anchor DNA, attached to a solid support, and reporter DNA, where either a part of the anchor DNA or reporter DNA, where either a part of the anchor DNA or reporter DNA, where either a part of the anchor DNA or reporter DNA high sesigned to form a triple-strand structure with part of the test sequence. Triplex formation results in displacement of the reporter DNA which is detected as an indication of the presence of the DNA test sequence. The method is used to detect DNA sequences, particularly for identification of bacteria (by detecting genes for ribosomal RNA) in clinical samples, but also detection of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                              Assay of genetic sequences based on triplex formation from double stranded analyte - and hybrid of anchor and reporter sequences, with reporter released if triplex formation occurs, used e.g. to identify bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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                                                                                                                                                                                                                                                                                         Disclosure; Col 13-14; 168pp; English.
                                                                                                                     (PROF-) PROFILE DIAGNOSTIC SCI INC.
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                                                                                                                                                   Wang C;
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                                                                                      29-OCT-1992;
                                                                                                                                                    Hepburn AG,
US5861244-A.
                           19-JAN-1999
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Gaps
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and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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Matches 8; Conservative
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AB145370
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ANC AB1453
AX AB145370
AX AB145370
DT 22-FEF
XX SNP;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE9989, ABF00010-ABE9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

Sequence 12 BP; 7 A; 0 C; 3 G; 2 T; 0 U; 0 Other;

ftp.wipo.int/pub/published\_pct\_sequences

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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36.4%; Score 8; DB 1; Length 12;
100.0%; Pred. No. 6.4e+02;
ative 0; Mismatches 0; Indels
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC09989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                      Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 373725; 29pp + Sequence Listing; German.
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100.0%; Pred. No. 6.4
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                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                 Oligonucleotide primer SEQ ID NO 355769 for detecting SNP TSC0049804.
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tive 0; Mismatches
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but they was obtained in electronic format from WIPO at
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oligonucleotides, useful for diagnosis and cell typing, is to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                Claim 1; SEQ ID NO 379637; 29pp + Sequence Listing; German.
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                                                                          methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
              represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
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731 AGGAGAAA 738

Matches

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WO200177384-A2
                                                                         WO200177384-A2
                                                      Homo sapiens.
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                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide primer SEQ ID NO 319093 for detecting SNP TSC0029068.
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                                                                                                                               Oligonucleotide primer SEQ ID NO 285914 for detecting SNP TSC0012507
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                                                               ABH85921 standard; DNA; 12
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Best Local Similarity 100...
8; Conservative
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AGGAGAAA 10
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                  Set of oligonuclectides, useful for diagnosis and cell typing, is designed to detect single-nuclectide polymorphisms and cytosine methylation status.
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                                                                    Berlin K;
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07-APR-2000; 2000DE-01019173
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                                  (EPIG-) EPIGENOMICS AG
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           This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                   Sequence 12 BP; 5 A; 0 C; 5 G; 2 T; 0 U; 0 Other;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disonders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF3073 for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at
                                                                                                                                       SND; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                    Oligonucleotide primer SEQ ID NO 281108 for detecting SNP TSC0009446.
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ABH81115 standard; DNA; 12
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                                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                         Oligonucleotide primer SEQ ID NO 300224 for detecting SNP TSC0018914.
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                                                                  0; Indels
                              Query Match 36.4%; Score 8; DB 1; Length 12; Best Local Similarity 100.0%; Pred. No. 6.4e+02; Matches 8; Conservative 0; Mismatches 0; Indels
Sequence 12 BP; 5 A; 0 C; 6 G; 1 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                  ABI00251 standard; DNA; 12 BP.
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peptide nucleic and
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Berlin K;

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                                   Gaps
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36.4%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 6.4e+02; ative 0; Mismatches 0; Indels
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                                    8; Conservative
                                                                    731 AGGAGAAA 738
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RESULT 935

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oycosine methylation status in chemically pretreated genemic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989, ABF00010-ABE99989, ABF00010-ABE99989, and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but typ.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonuclectide primer SEQ ID NO 305008 for detecting SNP TSC0021207.
                                                                  Set of oligonuclectides, useful for diagnosis and cell typing, idesigned to detect single-nuclectide polymorphisms and cytosine methylation status.
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                                                                                                                                                                    Claim 1; SEQ ID NO 356916; 29pp + Sequence Listing; German.
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               WPI; 2001-657177/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from wipo at the printed specification, but fire wipo.int/pub/published_pct_sequences
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1es 8; Conservative
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  Homo sapiens.
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range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cartiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99889, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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36.4%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 6.4e+02;

Query Match Best Local Similarity

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06-APR-2001; 2001WO-IB000713
                                  07-APR-2000; 2000DE-01019173
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                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                      Oligonucleotide primer SEQ ID NO 334468 for detecting SNP TSC0038169
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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    Piepenbrock C,
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                                                  This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretracted genomic DNA. The cligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABM0010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
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                           Claim 1; SEQ ID NO 371100; 29pp + Sequence Listing; German.
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data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 the represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                     ABI04086 standard; DNA; 12 BP
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peptide nucleic acid, cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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36.4%; Score 8; DB 1; Length 12;
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ABI01362 standard; DNA; 12
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                                                                                                                                                       Claim 1; SEQ ID NO 349805; 29pp + Sequence Listing; German.
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                              Olek A, Piepenbrock C,
(EPIG-) EPIGENOMICS AG
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and range of diseases including immune system, gastrointestinal, respiratory central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0016-ABC99989, ABC0010-ABP9989 ABH0010-ABH99989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
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New human alanine transaminase polypeptide (ALT2) and gene, useful for detecting injury, damage or disease involving a tissue that contains the ALT2 in an animal, or in diagnosing conditions associated with altered
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                                                                                                                            Human; alanine transaminase; ALT2; diagnosis; injury; ds.
                                                                                       Human ALT2 gene intron11/exon12 junction DNA.
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                                                      Gaps
                                                                                                                                                                                                                                                                                                                               Oligonucleotide primer SEQ ID NO 280828 for detecting SNP TSC0009139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                 DB 1; Length 12; . 6.4e+02; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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                 Score 8; DB 1, Pred. No. 6.46
                 Query Match
Best Local Similarity 100.0%; Pr
Matches 8; Conservative 0;
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                                                                                                                                                                                                                       ABH80835 standard; DNA; 12 BP
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                                                                                                                                                                                                                                                                                             (first entry)
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Best Local Similarity luv...
8, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (EPIG-) EPIGENOMICS AG
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                                                                                           731 AGGAGAAA 738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200177384-A2.
                                                                                                                                                                                                                                                                                             22-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                    Query Match 36.4%; Score 8; DB 1; Length 12; Best Local Similarity 100.0%; Pred. No. 6.4e+02; Matches 8; Conservative 0; Mismatches 0; Indels
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Seguence 12 BP; 3 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human ALT2 gene intron9/exon10 junction DNA.
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RESULT 952 AAD52664 ID AAD526

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17-JAN-2001; 2001US-00765061.
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26-AUG-1998;
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                                                                                                             amaurosis.
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                  (SOHO/) (DAIG/)
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AAZ18763/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, ss; aryl-hydrocarbon receptor interacting protein-like 1, AIPL1, teber congenital amaurosis 4, LCA4, chromosome 17p13, retinopathy, retinal disease, Leber congenital amaurosis, dominant cone-rod dystrophy; juvenile retinitis pigmentosa; ophthalmological.
                                                                                                                                                                                                                            New human alanine transaminase polypeptide (ALT2) and gene, useful for detecting injury, damage or disease involving a tissue that contains the ALT2 in an animal, or in diagnosing conditions associated with altered levels of ALT2.
                                                                                                                                                                                                                                                                                           The invention relates to human alanine transaminase polypeptide (ALT2) and gene. The invention is useful for diagnosing or detecting injury, damage or disease involving a tissue that contains the ALT2 polypeptide in an animal, in diagnosing conditions associated with altered levels of ALT2 and/or ALT1 in bodily fluids. The present sequence is human ALT2 gene intron/exon junction DNA
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36.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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        Location/Qualifiers
                                                                                                                                                                                                                                                                          Disclosure; Page 15; 57pp; English.
                                                                                                                                                                         (UYMA-) UNIV MARYLAND BALTIMORE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                           Yang R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human AIPL1 cDNA fragment #22.
                                                                                                                                                      14-MAY-2001; 2001US-0290829P.
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11. .12
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ACD40404 standard; cDNA; 12
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                                                                                                                  21-NOV-2002
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intron
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The invention relates to a composition comprising an aryl-hydrocarbon receptor interacting protein-like 1 (AIPL1) sequence within the leber congenital amaurosis 4 (LCA4) region of chromosome 17p13, which is a wild type or a mutant AIPL1 sequence. The aryl-hydrocarbon receptor interacting protein-like 1 (AIPL1) polynucleotides and polypeptides are useful for diagnosing or treating retinal diseases associated with AIPL1 mutations, for example, leber congenital amaurosis, juvenile retinitis pigmentosa, dominant cone-rod dystrophy or other inherited or acquired retinopathies. The AIPL1 polynucleotides and polypeptides are also useful cas a retinal disease or has a propensity to pass a retinal disease to component to pass a retinal disease to the mutated polypeptides, which can be used to treat resistant diseases that are associated with the mutations. Sequences Copensially bind to the mutated polypeptides, which can be used to treat resistant diseases that are associated with the mutations. Sequences ACD40383-ACD40433 represent human AIPL1 CDNA fragments of the invention
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                                                                                                                                                                                                                                                                                               New aryl-hydrocarbon receptor interacting protein-like 1 (AIPL1) polynucleotides and proteins, useful for diagnosing or treating retinal diseases associated with AIPL1 mutations, e.g. Leber congenital
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36.4%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 37; 65pp; English.
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98US-0097937P.
98US-0102051P.
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                                                                                                                               Sohocki MM, Daiger SP;
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SOHOCKI M M.
DAIGER S P.
                                                                                                                                                                                                                      WPI; 2003-416983/39
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WPI; 1999-229400/19
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                                                                                                                                                           This invention describes a novel non-MRL healer mouse (M) having at least one quantitative trait locus selected from those given in the specification, exhibiting an enhanced healing response to a wound compared to mice (m) without the locus. The invention describes a novel method of identifying a gene involved in enhanced wound healing by identifying DNA microsatellite markers which can distinguish healer mice from non-healer mice and identifying microsatellite markers which segregate with enhanced wound healing in progeny of the mice, where a chromosomal locus containing at least one enhanced wound healing gene is identified. A method of treating a wound in a mammal is also disclosed. The new methods are useful for treating wounds, especially central and peripheral nerve wound. The methods of the invention are useful for restoring function after nerve injury in a mammal. (M) is useful as a mammalian model of enhanced wound healing, useful for identifying genes and those for wound healing. AAZISG1-Z19036 represent murine SAGE cags from the methods for wound healing, are used to illustrate the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                               New mammalian model for enhanced wound healing - useful for identifying enhanced wound healing genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antisense oligonucleotide; multiple target; antisense treatment; impaired respiration; inflammation; lung disease; pulmorary vasoconstriction; inflammation; allergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; pulmonary hypertension; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinome; colon cancer; breast cancer; lung cancer; pancreatic cancer; hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.5%; Score 7.8; DB 1; Length 11; 81.8%; Pred. No. 6.6e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11 BP; 0 A; 3 C; 3 G; 5 T; 0 U; 0 Other;
                                                                                                                        Claim 13; Page 56; 136pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAX54601 standard; DNA; 11 BP
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       WPI; 1999-494533/41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention
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ID AAX54601/C
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The specification describes antisense oligonucleotides (AAX52869-X55271)

directed against at least 2 mRNAs selected from target genes, coding and
non-coding regions of RNAs corresponding to target genes, genes, interior
codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'
end and the juxta-section between coding and non-coding regions and all
segments of RNAs encoding proteins associated with one or more diseases,
conditions or mixtures. The antisense oligonucleotides may be derived
from sequences AAX5572-74. These multiple target oligonucleotides
conditions or mixtures. The period for the antisense treatment of
diseases and conditions. Typical diseases and conditions are those
associated with impaired respiration and inflammation, including lung
diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
diseases, plank, allergies, asthma, impeded respiration, respiratory
distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
colon cancer, breast cancer, lung cancer, pancreatic cancer,
negatocellular carcinoma, Widney cancer, melanoma, hepatic metastasized
to the lungs, including breast and prostate cancer
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New antisense oligonucleotides used in treatment of, e.g. pulmonary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11 BP; 0 A; 4 C; 1 G; 6 T; 0 U; 0 Other;
                                                                                                                              Disclosure; Page 46; 120pp; English.
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                                                      vasoconstriction
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                                   The present sequence represents a potential triple-helix forming region. It can be used to demonstrate the assay of the invention. The assay comprises adding a sample containing double-stranded DNA test sequences, e.g. containing the present sequence, to an aqueous medium containing at least one complex of anchor DNA, attached to a solid support, and reporter DNA, where either a part of the anchor DNA or reporter DNA is designed to form a triple-strand structure with part of the test sequence. Triplex formation results in displacement of the reporter DNA which is detected as an indication of the presence of the DNA test sequence. The method is used to detect DNA sequences, particularly for identification of bacteria (DN detecting genes for ribosomal RNA) in clinical samples, but also detection of oncogenes and Hepatitis B virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phosphorothioate; impaired respiration; inflammation; allergy; allergy; allergy; antiathergic disease; bronchoconstriction; inhibitor; antiinflammatory; antiallergic; antiasthmatic; cytostatio; analgesic; ingaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; adenosine receptor; low adenosine antisense oligonucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstruction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human adenosine receptor related polynucleotide SEQ ID NO:1737.
                                                                                                                                                                                                                                                                                                                                                              35.5%; Score 7.8; DB 1; Length 11; 81.8%; Pred. No. 6.6e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
                                                                                                                                                                                                                                                                                                                     Sequence 11 BP; 6 A; 0 C; 5 G; 0 T; 0 U; 0 Other;
Disclosure; Col 17-18; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 481; 1343pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA34048 standard; DNA; 11 BP.
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Best Local Similarity 81.0.
Local Similarity 81.0.
Local Similarity 10.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 731 AGGAGAAACAG 741
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useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects affiliat the lungs of a subject. They can be used for treating effects affiliat the lungs of a subject. They can be used for treating in schemic conditions, pulmonary vasoconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibroals, pulmonary hypertension, emphysema, chronic obstructive variouss, and cancers which may metastasise to the lungs, including breater cancer. The reduction of the adenosine content of the owns reduces side effects. The A-containing ONs break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA32313 to AAA3312 represent the invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:1 to 185, but the sequences differ throm the breviously named sequences. SEQ ID NO:1 to 2815, and then the last Sequences given in the disclosure of the present invention. N.B. Sequences given in the disclosure of the present invention on match in the first corresponding SEQ ID NO: sequences given in the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Low adenosine (A) content antisense oligonuclectides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Low adenosine antisense oligonucleotide, phosphorothioate; allergy; human, airway disorder; bronchoconstriction, lung inflammation; surfactant depletion; respiratory, bronchodilator; antinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis, allergic rhinitis; pulmonary hypertension; emplysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human eosinophil derived neurotoxin polynucleotide fragment #1737.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 7.8; DB 1; Length 11;
Pred. No. 6.6e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11 BP; 0 A; 4 C; 1 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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81.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 81.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF20170;
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The present invention describes low adenosine (A) content antisense oligonuclectides and compositions (I) comprising them. In the antisense oligonuclectides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, memunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and [I] can be used to down-regulate the expression and or activity of traget polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activity of traget polypeptides associated with lung/respiratory disorders and transmitters, transcription factors, immunoglobulins and antibodies, and though receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system petide receptors, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antibiding respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CP), allergies, minimity (APS), pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, pulmonary transplantation rejection, pulmonary infections, emphysema,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alpha-amylase; promoter; rice; transgenic plant; angiosperm; monocot; cereal; brewing; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 81.8%; Pred. No. 6.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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                  Claim 14; Page 142; 1592pp; English.
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The present sequence is that of a fragment of HS501, a DNA probe located at the 5' end of the promoter region of a rice alpha-amylase gene. OSAmy-b. It covers nucleotides -108 to -118 of the gene and has a sequence is milar to that of the animal core enhancer. Rice aleurone was found to contain proteins that interacted with this HS501 DNA fragment. The invention relates to the use of an alpha-amylase gene promoter and signal invention relates to the use of an alpha-amylase gene promoter and signal sequence (see ANI70536-39) in the production of recombinant proteins in transgenic plants and transgenic plant seeds. A transgenic monocot is obtained by: transforming an immature embryo with DNA comprising a plant alpha-amylase promoter that is induced under a sugar-depleted or sugar-free condition, a signal peptide sequence, and an exogenous sequence condition, a signal peptide sequence, and an exogenous sequence condition plant, which expresses the gene product under sugar-depleted or sugar-free conditions. The transgenic plants and their products are useful in brewing and to produce glucose from starch
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                                                   Producing a transgenic monocot plant comprising a transgene under control of an alpha amylase promoter and signal peptide sequences, provides transgenic plants particularly cereals for the brewing industry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying genes involved in skin stress and aging, useful e.g. in screening for cosmetic or therapeutic agents, based on differential gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to identifying (M1) genes in vitro that, in humans or animals, are important for skin ageing and/or skin stress by serial analysis of gene expression between mixtures of transcribed and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; skin ageing; skin stress; BST; expressed sequence tag; ss.
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Best Local Similarity 81.8%; Pred. No. 6.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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                                                                                                                                        Example 1; Col 20; 44pp; English.
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                 WPI; 2001-647191/74.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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ABQ87289/4
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optionally translated, genetically encoded factors (A) obtained from Young and aged Stin, to identify that genes that show strong differential expression. (A) comprises protein or mRNAs or their fragments. (MI) is useful for: identifying markers of skin ageing and/or stress; determining skin ageing and/or stress; and identifying or determining the effects of pharmaceutical or cosmetic agents for control of skin ageing. The present sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ86246-ABQ87680) of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to identifying (MI) genes in vitro that, in humans or animals, are important for skin ageing and/or skin stress by serial analysis of gene expression between mixtures of transcribed and optionally translated, genetically encoded factors (A) obtained from young and aged skin, to identify that genes that show strong differential expression. (A) comprises protein or mRNAs or their fragments. (MI) is useful for: identifying markers of skin ageing and/or stress; determining skin ageing and/or stress; and identifying or determining the effects of pharmaceutical or cosmetic agents for control of skin ageing. The present sequence is one of a group of human skin ageing/stress related expressed sequence tags (ABQ86246-ABQ87680) of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying genes involved in skin stress and aging, useful e.g. in screening for cosmetic or therapeutic agents, based on differential gene
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
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                                                                                                                                                                                                               35.5%; Score 7.8; DB 1; Length 11; 81.8%; Pred. No. 6.6e+02; 1ve 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human skin stress/ageing related EST SEQ ID NO 297
                                                                                                                                                                          Sequence 11 BP; 1 A; 5 C; 1 G; 4 T; 0 U; 0 Other;
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Best Local Similarity 81.8-
Best Local Similarity 81.8-
Pest Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
                                                                                                                                     Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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                BP.
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81.8%;
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Best Local Similarity 81.8
Matches 9; Conservative
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                                             ABV63070;
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis, sunburn, psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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          Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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Best Local Similarity 81.8
Matches 9; Conservative
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacaa, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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03-JAN-2001; 2001DE-01000127.
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les 9; Conser
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Disclosure; Page 182; 1345pp; German

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             The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression. (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disordders, specifically neurodermatitis; sunburn, psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematcsus; rosacea; melanoma; basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag.
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(MI) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; coscea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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35.5%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 6.6e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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ABV70917 standard; cDNA; 11 BP.
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                                             Length 11;
                                             35.5%; Score 7.8; DB 1; Length 11
81.8%; Pred. No. 6.6e+02;
iive 0; Mismatches 2; Indels
              Sequence 11 BP; 0 A; 2 C; 1 G; 8 T; 0 U; 0 Other;
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Matches 9; Conservative
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les 9; Conservative
                                                                                                                734 AGAAACAGAAC 744
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                                               Query Match
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RESULT 969

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to skrial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; ichthyosis; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
                                                                                                                                                                                                                                                                In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.
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                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 124; 1345pp; German.
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                                                                                                        20-DEC-2001; 2001WO-EP015179.
                                                                                                                                         03-JAN-2001; 2001DE-01000127.
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nes 9; Conserv
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                                      WO200253774-A2
     Homo sapiens.
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(M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sumburn, psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea, melanoma; basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
                                                                                                                                                         Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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ABV65783 standard; cDNA; 11 BP
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RESULT 970

Matches

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Gaps ·.

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In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.
                                                     Disclosure; Page 226; 1345pp; German.
      WPI; 2002-590638/63.
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from Skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis, or promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; scoacea, melanoma, basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag

Sequence 11 BP; 1 A; 3 C; 2 G; 5 T; 0 U; 0 Other;

35.5%; Score 7.8; DB 1; Length 11; 81.8%; Pred. No. 6.6e+02; tive 0; Mismatches 2; Indels 9; Conservative 733 GAGAACAGAA 743 Local Similarity Query Match Best Loc Matches 8

GTGACACAGAA 1 11

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ABV63496 standard; cDNA; 11 

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(first entry) 21-OCT-2002 ABV63496;

Human skin EST 1282,

Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.

Homo sapiens

WO200253774-A2.

11-JUL-2002.

20-DEC-2001; 2001WO-EP015179

03-JAN-2001; 2001DE-01000127

(HENK ) HENKEL KGAA

× Hofmann Σ Petersohn D, Conradt

WPI; 2002-590638/63.

In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.

Disclosure; Page 60; 1345pp; German.

The invention relates to in vitro identification (MI) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to earial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

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(MI) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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Pred. No. 6.6e+02;
0; Mismatches 2; Indels
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81.8%;
                                                                                                                                                           (EST) of the invention
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Best Local Similarity
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9; Conservative

734 AGAAACAGAAC 744

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11 AAAAAGAGAAC 1

RESULT 97 ABV69104

ABV69104 standard; cDNA; 11 BP.

ABV69104;

(first entry) 21-OCT-2002

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Gaps .. 0 Human skin EST 6890

Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag; ss.

Homo sapiens.

WO200253774-A2

11-JUL-2002

20-DEC-2001; 2001WO-EP015179.

03-JAN-2001; 2001DE-01000127.

(HENK ) HENKEL KGAA

Α, Hofmann Σ Conradt Petersohn D,

WPI; 2002-590638/63.

In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.

Disclosure; Page 216; 1345pp; German.

The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sumburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell.carcinoma; and carcinoma or sarcoma of Skin. The present sequence is that of a human expressed sequence tag (SRI) of the invention

Sequence 11 BP; 3 A; 2 C; 5 G; 1 T; 0 U; 0 Other;

35.5%; Score 7.8; DB 1; 81.8%; Pred. No. 6.6e+02; Query Match Best Local Similarity

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21-OCT-2002 (first entry)
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                                              Human skin EST 2284
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EXECUTED CONTRACTOR SERVICES SERVICES CONTRACTOR SERVICES CONTRACT
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  Gaps
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Pred. No. 6.6e+02;
0; Mismatches 2; Indels
  Indels
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  Mismatches
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81.8%;
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Best Local Similarity
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     Matches
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis, to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis, sunburn, psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea, melanoma, basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (ESI) of the invention
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Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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Pred. No. 6.6e+02;
0; Mismatches 2; Indels
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Best Local Similarity 81.8%;
Matches 9; Conservative C
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ABV70542/c
ID ABV70542 standard; cDNA; 11
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ABV64498 standard; cDNA; 11 BP.

ABV64498, RESULT 975
ABV64498
ID ABV6449
XX
AC ABV6449

733 GAGAAACAGAA 743

GAGCAACAAA

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(M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriaeis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; roscea, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
                                                                                                                                                                         In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.
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Pred. No. 6.6e+02;
0; Mismatches 2; Indels
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                                                                                                            Hofmann K;
                                                                                                                                                                                                                                          Claim 24; Page 266; 1345pp; German.
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                20-DEC-2001; 2001WO-EP015179
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81.8%;
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                                            03-JAN-2001; 2001DE-01000127
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                                                                                                              Petersohn D, Conradt M,
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                                                                              (HENK ) HENKEL KGAA
                                                                                                                                           WPI; 2002-590638/63
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                                                                     The invention relates to in vitro identification (MI) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression (GMI) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; inchthyosis, atopic dermatitis, acne, seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sumburn, psoriaais, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
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Pred. No. 6.6e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                      Sequence 11 BP; 6 A; 0 C; 5 G; 0 T; 0 U; 0 Other;
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                                     Disclosure; Page 64; 1345pp; German.
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81.8%;
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Best Local Similarity 81.0-
Best Local 9; Conservative
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e.g. skin cancer.
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Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.

20-DEC-2001; 2001WO-EP015179.

WO200253774-A2.

11-JUL-2002.

Homo sapiens.

ABV72009 standard; cDNA; 11 BP.

21-OCT-2002 (first entry)

ABV72009

Human skin EST 9795.

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rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                           35.5%; Score 7.8; DB 1; Length 11; 81.8%; Pred. No. 6.6e+02; ative 0; Mismatches 2; Indels
                                                                                                                                                            Sequence 11 BP; 0 A; 1 C; 3 G; 7 T; 0 U; 0 Other;
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ABV68198/CAL
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Pred. No. 6.6e+02;
0; Mismatches 2; Indels
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e.g. skin cancer.
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RESULT 980
AX ABW72009/C
ID ABW7200
AX ABW720
AX ABW720
AX ABW720
AX ABW720
AX LI-OCT
AX Human,
KW MO2002
AX Homeo
AX MO2002
AX Human,
KW Human,
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ABV66736
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Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;

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Gaps

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Ouery Match 35.5%; Score 7.8; DB 1; Length 11; Best Local Similarity 81.8%; Pred. No. 6.6e+02; Matches 9; Conservative 0; Mismatches 2; Indels

734 AGAAACAGAAC 744

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11 ACAAAGAGAAC 1

(HENK ) HENKEL KGAA.

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(M1) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea, melahoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
immunosuppressive, antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
                                                                                                                                                                                                                                                                                              In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
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                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 149; 1345pp; German.
                                                                                                                                                                                                                                   Hofmann K;
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                                                                                                                                        20-DEC-2001; 2001WO-EP015179.
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                                                                                                                                                                      03-JAN-2001; 2001DE-01000127
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                                                                                                                                                                                                    (HENK ) HENKEL KGAA
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                                                                                                                                                                                                                                                                                                                             e.g. skin cancer.
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                                              Homo sapiens.
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                                                                                                                                                                                          In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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Pred. No. 6.6e+02;
0; Mismatches 2; Indels
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                                                           Hofmann K;
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81.8%;
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les 9; Conservative
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                                                           Conradt
                                                                                                                       WPI; 2002-590638/63
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                                                           Petersohn D,
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes and quantify their expression of determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis, sumburn; psoriasis; scleroderma; inchthyosis; atophy dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sumburn; psoriasis; scleroderma;
                                                                                                                                  ichthyosis, atopic dermatitis, acne, seborrhea, lupus erythematosus, rosacea, melanoma, basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
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81.8%;
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(EST) of the invention
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Score 7.8; DB 1; Length 11;
Pred. No. 6.6e+02;
Mismatches 2; Indels
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81.8%;
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h
Similarity 81.8%;
9; Conservative
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Best Local Similarity
Matches 9; Conserv
      Query Match
Best Local Similarity
Matches 9; Conserv
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ABV66108/c
ID ABV6610
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ABW 62644
ABW 62644
ABW 62644
ABW 6264
ABW 721-1
ABW 721-
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ABV66108 standard; cDNA; 11 BP.

Sequence 11 BP; 5 A; 4 C; 2 G; 0 T; 0 U; 0 Other;

of the invention

ABV66108;

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn, psoriaais, scleroderma; ichthyosis; atopic dermatitis; acne, seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag in (EST) of the invention
                                                                                                                                                                                                                                                                                                           In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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Pred. No. 6.6e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 144; 1345pp; German.
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                                                                                                                               03-JAN-2001; 2001DE-01000127
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Best Local Similarity 81.8%;
Matches 9; Conservative
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                                                                                                                                               Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic;
immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
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Best Local Similarity 81.8%;
Matches 9; Conservative (
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ABV66524;

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Gaps ., or that can be used for treating skin

skin homeostasis

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial malysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis, acne; sebonines; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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                                                                                                                         e.g. skin cancer.
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Score 7.8; DB 1; Length 11;
Pred. No. 6.6e+02;
); Mismatches 2; Indels
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  35.5%;
81.8%;
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Best Local Similarity 81.8
Matches 9, Conservative
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ABV68102 standard; cDNA; 11 (first entry) 21-OCT-2002 ABV68102;

BP.

Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory; cytostatic, SAGE, neurodermatitis; psoriasis, dermatitis, skin cancer, EST; expressed sequence tag; ss. Human skin EST 5888

sapiens

WO200253774-A2.

11-JUL-2002

20-DEC-2001; 2001WO-EP015179

03-JAN-2001; 2001DE-01000127

(HENK ) HENKEL KGAA.

In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against Hofmann K; Σ Conradt WPI; 2002-590638/63.

Disclosure; Page 188; 1345pp; German.

e.g. skin cancer.

The invention relates to in vitro identification (MI) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (MI) is useful for identifying genes involved in skin homeostasis, to determine skin homeostasis and to test agent (A) that maintains or

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Query Match 35.5%; Score 7.8; DB 1; Length 11; Best Local Similarity 81.8%; Pred. No. 6.6e+02; Matches 9; Conservative 0; Mismatches 2; Indels

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                      disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag (EST) of the invention
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Pred. No. 6.6e+02;
0; Mismatches 2; Indels
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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression.

(M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis; sunburn; psoriaais, scleroderma; ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus; coscea, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
                                                                                                                                                                                                                                                                                                                                                                       In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
                                 Human, skin, dermatological, vulnerary, antipsoriatic, antiseborrhaeic, immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis, psoriasis, dermatitis, skin cancer, EST; expressed sequence tag, ss.
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                                                                                                                                                                                                                                                                                                         Conradt
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 Human skin EST 251
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AC ABV62465;
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81.8%;
                                                                                                                ABV69886 standard; cDNA; 11
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736 AAACAGAACAC 746
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                              AAACAAATCAC 11
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Best Local Similarity
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                                                                                                                                                                                                                   Human skin EST 7672
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                                                                                                                                                                                                                                                                                                                                                    WO200253774-A2
                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                 ABV69886;
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Hofmann K;

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immunosuppressive, antiinflammatory, cytostatic, SAGE, neurodermatitis,
psoriasis, dermatitis, skin cancer, EST, expressed sequence tag, ss.
                              Gaps
                              .,
Query Match 35.5%; Score 7.8; DB 1; Length 11; Best Local Similarity 81.8%; Pred. No. 6.6e+02; Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                           BP.
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                                                                                                                                                         ABV65390 standard; cDNA; 11
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                                                         727 TGCCAGGAGAA 737
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In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against e.g. skin cancer.
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                                                                                                                                                                                                                                                                                                  ABV70491 standard; cDNA; 11 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JAN-2001; 2001DE-01000127
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                                                                                                                                                                                                                                                                                                                                            Human skin EST 8277
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11 AGAACCAGAGC 1

(first entry)

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The invention relates to in vitro identification (M1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically encoded factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression (M1) is useful for identifying genes involved in skin homeostasis, to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis, sunburn, psoriasis, sclaroderma; ichthyosis, atopic dermatitis, acne, seborrhea; lupus erythematosus; rosacea; melanoma; basal call carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h Similarity 81.8%; Score 7.8; DB 1; Length 11; Similarity 81.8%; Pred. No. 6.6e+02; 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11 BP; 7 A; 1 C; 3 G; 0 T; 0 U; 0 Other;
Claim 24; Page 265; 1345pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            735 GAAACAGAACA 745
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                                                                                                                                                                                                                                                                                                                                                                                                   the invention
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(M1) is useful for identifying genes involved in skin homeostasis; to determine skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin promotes skin homeostasis or that can be used for treating skin to promote skin homeostasis or that can be used for treating skin contributions; actopic dermatitis; acnowing seboriasis; scleroderma; ichthyosis; atopic dermatitis, acne; seborinea; lupus erythematosus; rosacea, melanoma; basal cell carcinoma; and carcinoma or sarcoma of the sexin. The present sequence is that of a human expressed sequence tag
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                                                                                                                                                                                                                                                                            In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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Pred. No. 6.6e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 113; 1345pp; German.
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81.8%;
                                         03-JAN-2001; 2001DE-01000127
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ses 9; Conservative
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(EST) of the invention
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                                                                                                (HENK ) HENKEL KGAA
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The invention relates to in vitro identification (W1) of genes expressed in the skin of humans or animals by subjecting a mixture of genetically senced factors from skin, to serial analysis of gene expression (SAGE) so as to identify skin-expressed genes and quantify their expression. (M1) is useful for identifying genes involved in skin homeostasis; to promotes skin homeostasis and to test agent (A) that maintains or promotes skin homeostasis or that can be used for treating skin disorders, specifically neurodermatitis, sumburn, portasis; scleroderma; inchthyosis; atopic dermatitis; acnow, seborrhea; lupus erythematosus; robacca; melanoma; basal cell carcinoma, and carcinoma or sarcoma of the skin. The present sequence is that of a human expressed sequence tag
                                                                                                                                     Human; skin; dermatological; vulnerary; antipsoriatic; antiseborrhaeic; immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis; psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   In vitro identification of skin-expressed genes, useful for determining homeostasis and identifying cosmetic or pharmaceutical agents against
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BP.
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 ABV71042 standard; cDNA; 11
                                                                      (first entry)
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                                                                                                          Human skin EST 8828
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Hofmann K;

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                                                                                                                                                                                                                                                                  Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic; normal endothelial marker; pan-endothelial marker; immunostimulant; antiangiogenic; tumour; neoangiogenesis; vascularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis; psoriasis; ss.
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.
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                                              Length 11;
                                                                   2; Indels
                       Sequence 11 BP; 6 A; 0 C; 5 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
                                            Score 7.8; DB 1;
Pred. No. 6.6e+02;
0; Mismatches 2.
                                                                                                                                                                                                                                             Human Pan-Endothelial Marker SEQ ID NO 49.
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                                                                                                                                                                        ABL91951 standard; cDNA; 11 BP.
                                             35.5%;
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11-AUG-2000; 2000US-0224360P.
11-APR-2001; 2001US-0282850P.
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                                 Query Match
Best Local Similarity 81.87
                                                                                         733 GAGAAACAGAA 743
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(EST) of the invention
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                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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first active agent comprising an oligonucleotide antisense to the instractive agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genemic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an entilnflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing or depleting levels of, or reducing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject, stissue, or treating bronchoconstriction, lung surfactant in a subject stissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, antisense, lung dysfunction, nasal airway dysfunction, antinflammatory steroid, ubiquinone, antinflammatory, antiallergic, antiasthmatic; hypotensive; immunosuppressive, cytostatic; gene therapy, antisense gene therapy, respiratory; lung; adenosine sensitivity; adenosine receptor, bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human eosinophil derived neurotoxin antisense fragment no.1724.
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81.8%; Pred. No. 6.6e+02;
iive 0; Mismatches 2
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L, Shahabuddin
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Tang L,
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Best Local Similarity
Matches 9; Conserva
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Miller S,
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Query Match 35.5%; Score 7.8; DB 1; Length 11; Best Local Similarity 81.8%; Pred. No. 6.6e+02; Matches 9; Conservative 0; Mismatches 2; Indels

Promoter; Bacillus genus microbe; protein production; ds.

Modified promoter associated DNA #6.

(first entry

23-JUL-2003

ACA61506;

ACA61506 standard; DNA; 11

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New purified human transmembrane protein, designated as tumor endothelial marker (TEM) 3, useful for detecting, diagnosing or treating tumors, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a novel method for the isolation of endothelial cells (ECs), and the identification of genes expressed in normal and tumour ECs. Tumour endothelial marker (TEM), normal endothelial marker (TEM), normal endothelial marker (TEM), normal polynucleotide sequences encoding them are useful for detecting, diagnosing or treating tumours as well as polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also useful for inhibiting neoangiogenesis or tumour angiogenesis, for inducing an immune response to tumour andiogenesis, for for identifying candidate drugs for treating tumours. ABX71828-ABX71999 represent DNA tags for human PEM, TEM or NEM genes
                                                                                                                                                                                                                                                                          Tumour endothelial marker; normal endothelial marker; PEM; pan-endothelial marker; polycystic kidney disease; psoriasis; diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis; necessary immune response; cytostatic; antidiabetic; ophthalmological; antirheumatic; antiarthritic; antipsoriatic; ds.
                                                                                                                                                                                                                                                             Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 7.8; DB 1; Length 11; Pred. No. 6.6e+02; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kinzler KW, Vogelstein B;
                                                                                                                                                                                                                           DNA tag used to identify human gene encoding PEM 49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Page 95; 374pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carson-Walter E, St Croix B,
                                                                                                                       BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.5%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-APR-2002; 2002WO-US008253.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-APR-2001; 2001US-0282850P.
06-FEB-2002; 2002US-0354262P.
                                                                                                                       ABX71876 standard; DNA; 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYJO ) UNIV JOHNS HOPKINS
                                                                                                                                                                                          12-MAR-2003 (first entry)
731 AGGAGAACAG 741
                               AGCAGAAAGAG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-093016/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                       WO200283874-A2
                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-OCT-2002
                                 디
                                                                                                                                                          ABX71876;
                                                                                 RESULT 998
ABX71876
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The invention describes a promoter which can function in a Bacillus genus microbe in which the ratio of adenine to cytosine in the sequence near the 3'-end of said promoter is 0.5 to 2 and the activity of the promoter is higher than that of a natural promoter. The promoter is useful in the preparation of a protein. This sequence represents a modified promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                A modified promoter, an expression cassette, an expression vector, a recombinant microbe, preparation of a protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                 , Match 35.5%; Score 7.8; DB 1; Length 11; Local Similarity 81.8%; Pred. No. 6.6e+02; nes 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Promoter; Bacillus genus microbe; protein production; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11 BP; 4 A; 1 C; 6 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified promoter associated DNA #1.
                                                                                                                                                                                                                                                                                                                      Example 5; Page 8; 15pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACA61501 standard; DNA; 11 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IS-MAR-2001; 2001JP-00074780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .5-MAR-2001; 2001JP-00074780.
                                                                                                                                                                                       15-MAR-2001; 2001JP-00074780.
                                                                                                                                                                                                             15-MAR-2001; 2001JP-00074780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-JUL-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   731 AGGAGAAACAG 741
                                                                                                                                                                                                                                     (SHOS ) SHOWA SANGYO CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11
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                                                                                                                                         JP2002272466-A.
                                                                                                                                                                                                                                                                                                                                                                                                        associated DNA
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                                                                                                                                                                 24-SEP-2002.
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                                                                                                                  Synthetic.
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ACA61501
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Gaps

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Conservative 727 TGCCAGGAGAA 737

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TGCCAGGTGCA

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Length 12;

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Query Match
Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                      AAQ88668;
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Matches
                                                                                                                  AAQ88668,
                                                                                                        RESULT
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                                                       The invention describes a promoter which can function in a Bacillus genus microbe in which the ratio of adenine to cytosine in the sequence near the 3'-end of said promoter is 0.5 to 2 and the activity of the promoter is higher than that of a natural promoter. The promoter is useful in the preparation of a protein. This sequence represents a modified promoter associated DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The inventors claim synthetic porcine preprorelaxin and prorelaxin and synthetic A, B and C peptide chains of prolaxin, and their sub-
expression of porcine preprorelaxin or prorelaxin, and their sub- units (see AAN30186). They also claim a double-stranded DNA fragment for the expression of the signal peptide chain of porcine preprorelaxin comprising a coding strand and a complementary strand corresp. to a defined mRNA sequence (see AAN30187-N30194) which corresp. to the most homologous regions between the pig and rat cDNA sequences. A probe (AAN30195) is also claimed. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genes and DNA transfer vectors for prorelaxin expression - useful in prodn. of porcine relaxin for veterinary and human use.
A modified promoter, an expression cassette, an expression vector, recombinant microbe, preparation of a protein.
                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                           Sequence of probe/primer which corresp. to bps 579-590 porcine
                                                                                                                                                             Query Match 35.5%; Score 7.8; DB 1; Length 11; Best Local Similarity 81.8%; Pred. No. 6.6e+02; Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                      Sequence 11 BP; 4 A; 2 C; 4 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12 BP; 6 A; 1 C; 4 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shine J;
                                 Example 5; Page 8; 15pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Niall HD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12; Page 5; 50pp; English.
                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83AU-00011834.
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                                                                                                                                                                                                                                                                                           AAN30191 standard; DNA; 12
                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                           731 AGGAGAAACAG 741
                                                                                                                                                                                                                                 1 AGGAGTACCAG 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hudson PJ, Haley JD,
                                                                                                                                                                                                                                                                                                                                        (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa domestica.
                                                                                                                                                                                                                                                                                                                                                                                                            Relaxin; hormone; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1983-748587/35.
                                                                                                                                                                                                                                                                                                                                                                                      preprorelaxin cDNA.
                                                                                                                                                                                                                                                                                                                                      25-MAR-2003
25-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-FEB-1983;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A DNA chip was prepared for analysing sequences contained in a 1.3kb fragment of human mitochondrial DNA from the D-loop region, the most polymorphic region of human mitochondrial DNA. The chip comprised a set of 268 overlapping oligonucleotide probes (see AAQ88421-Q88684) of varying length (9-14 mucleotides) with varying overlaps arranged in a lom varying length (9-14 mucleotides) with varying overlaps arranged in a lom probe (usually 2 or more). DNA was amplified from six human donors and then transcribed to give the 1.3kb RNA transcripts which were hybridised and hybridised to the chip. For each individual, a unique hybridisation fingerprint was produced on the chip, all differences could be correlated with differences in the cloned genomic DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tiling strategy, immobilised nucleic acid probe array, mitochondrial DNA, D-loop region; biological chip; hybridisation fingerprint; interrogation position; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/note= "3'-end of probe is covalently attached to chip
surface"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chee M, Cronin MT, Fodor SP, Gingeras TR, Huang XC, Hubbell EA;
Lipshutz RJ, Lobban PE, Miyada CG, Morris MS, Shah N, Sheldon EL;
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New arrays of oligo:nucleotide probes - used for comparing known sequences with variants for detection of mutation(s) and sequencing.
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                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human mitochondrial D-loop region DNA probe 12-15.
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Score 7.8; DB 1;
Pred. No. 6.8e+02;
0; Mismatches 2;
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Pred. No. 6.8e+02;
0; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                              ВЪ.
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94US-00284064.
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35.5%;
ilarity 81.8%;
Conservative
                                                                                                                                                                                                                                                                                                           AAQ88668 standard; DNA; 12
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                                                                                                             735 GAAACAGAACA 745
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                                                                                                                                                                   GAAGCAGAAGA 12
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Best Local Similarity
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modified_base
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02-AUG-1994;
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Homo sapiens.
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Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                        APTI1906-41 are antisense oligonucleotides that are selectively hybridisable with a gene or the transcription products for sub-units of isoprenyl protein transferases, pref. farnesyl protein transferase or a gerany geranyl protein transferase. Oligonucleotides contg. these antisense sequences or their derive, are useful in human or veterinary medicine for treatment of abnormal and/or uncontrolled cell proliferation, e.g. in cases of cardiovascular disease, cancer, viral infections or dermatology. Inhibiting prenylation prevents proteins from binding to active sites on cell membranes, so prevents transduction of extracellular cell signals and thus cell proliferation
                                                                                                                      isoprenyl protein transferase; farnesyl; geranyl geranyl; prenylation; inhibition; abnormal; uncontrolled; cell proliferation; cancer; cardiovascular disease; treatment; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Translation rate; heterologous protein; hydrophobicity; human; 1150RF; transmembrane domain; insertion; vaccine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                            Anti-sense oligo-nucleotide(s) hybridising to isoprenyl protein transferase genes - or their transcripts, for treating abnormal or uncontrolled cell proliferation e.g. cancer.
                                                                                                    Antisense DNA to inhibit isoprenyl protein transferase expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12 BP; 5 A; 1 C; 5 G; 1 T; 0 U; 0 Other;
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Pred. No. 6.8e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Translation rate controlling sequence AN.EKEK.
                                                                                                                                                                                                                                                                    (SCRC ) SCRAS SOC CONSEILS RECH APPL SCI.
                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 12; 27pp; English
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81.8%;
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                                          AAT11908 standard; DNA; 12
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                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                         Colote S, Pirotzky E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGAGTAGCAG
                                                                                                                                                                                                                                                                                                           WPI; 1996-042231/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 9; Conserv
                                                                                                                                                                                                                             29-JUN-1995;
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                                                                                  13-JUL-1996
                                                                                                                                                                                     GB2290791-A.
                                                                                                                                                                 Synthetic
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                                                              AAT11908;
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                                 AAT11908
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This oligonuclectide comprises a sequence that is used to control the rate of translation of a protein in a heterologous organism. The sequence is based on regions of amino acid hydrophobicity in the amino acid sequence of the human 115RP protein and is adapted for controlling the rate of protein translation in Aspergillus nidulans. The rate control sequences are found downstream of regions encoding transmembrana domains (TMD) and at a distance of 50-85 codons from these regions. The control region increases production and assembly yield of the heterologous protein and improves correct insertion into the membrane. The translation delay imposed by the sequence favours formation of the protein with its native 3-dimensional structure. The control sequence can be used to generate can be used to control control sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid encoding protein with hydrophobic or trans-membrane domain includes downstream of this domain a region that slows down translation, improves product and assembly yield and correct incorporation into the membrane, e.g. for use in vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INF-alpha mRNA series 1 (5' untranslated cap region) oligonucleotide 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12 BP; 10 A; 0 C; 2 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                          (COMS ) COMMISSARIAT ENERGIE ATOMIQUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 5; 73pp; French.
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                                                                                                                                                         97WO-FR000523
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Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                                                                                                                                   96FR-00003731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAAAAAGAAA 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-489636/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for use in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-SEP-1996;
                                                                                                                                                                                                                                       26-MAR-1996;
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                                                                                                                                                         25-MAR-1997;
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WO9735972-A1
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                                                                                                                                                                                                                                                                                                                                                                                        Kepes F;
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AAT63016/c
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95GB-00018864.

98US-00019387

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Oligo:nucleotide probes and primers and methods for HLA typing particularly for tissue typing for bone marrow transplants.
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 05-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gorski JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAV16650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                Meyer RB,
                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1007
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                                                                                                                                     oligonucleotides of series 1,AAT63014-21, have specific anti-mRNA sequences to the 5' untranslated cap region of tumour necrosis factor (TNF)-alpha mRNA. These Oligonucleotides are an example of a new chimeric oligonucleotide library, used to identify an antisense binding site in a target mRNA (in this case TNF-alpha). The library comprises a set of distinct chimeric oligonucleotides capable of hybridising to mRNA to form a duplex, the nucleotide sequences of which each have a common length of 7-20 bases. All of the nucleotides of the common length which are present as subsequences in the target mRNA are present in the library. Each as subsequences on the target mRNA are present in the library. Each chapteride sequence comprises a recognition region recognisable by a duplex-cutting RNAse, and a flanking region of chemically modified nucleotides which binds to the mRNA sufficiently tightly to stabilise the duplex for the RNAse. Each oligonucleotide is protected against chaptes attack. The libraries compounds against specific mRNA targets. The effective antisense compounds against specific mRNA targets. The antisense compounds against the respectic against and as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCR-5 gene, CRR-5; chemokine receptor; triple-stranded complex; therapy; co-receptor prevention; human immunodeficiency virus resistance; HIV; macrophage entry inhibition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/note= "ClAmb-NH-(CH2)6-0-pG nucleotide, where ClAmb is
                                                                              Chimeric oligo:nucleotide library - for use in identifying anti-sense binding sites in target messenger RNA.
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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/note= "Gp-O-(CH2)6-OH modified nucleotide"
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12 BP; 0 A; 4 C; 2 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCR-5 gene targeting sequence TFO1.
                                                                                                                   Example 2; Page 27; 44pp; English.
                                                                                                                                                                                                                                                                                                                                      drug target validation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV55018 standard; DNA; 12 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
           (BRAX-) BRAX GENOMICS LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                 734 AGAAACAGAAC 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 AGGAAGAGAAC 2
                                                         WPI; 1997-202228/18
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Matches 9; Conserv
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modified_base
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                                  Schmidt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1006
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This sequence represents an oligonucleotide of the invention, that forms a triple-stranded complex with part of the gene for CRE-5. CR-5 is a chemokine receptor, also known as CRR-5. The oligonucleotide, when modified by attachment of alkylating (cross-linking) agents, modify the CRE-5 gene, preventing its product from acting as a co-receptor for human immunodeficiency virus (HIV), and rendering cells resistant to this virus. They can be used to prevent entry of HIV into macrophages or therapeutically to prevent viral spread in infected subjects. The oligonucleotides can be introduced into cells by any method of mucleic acid delivery, e.g. transfection, co-precipitation, liposome-mediated transfer etc. The sequences have a longer lasting effect than antisense
                                                                                                                                                                                                 Oligo:nucleotide(s) that form triplex(es) with part of chemokine receptor CCR-5 gene - are modified with crosslinking agents to alter gene so that cells are rendered resistant to human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequences directed to mRNA, and may produce heritable modifications in the gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 7.8; DB 1; Le
Pred. No. 6.8e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12 BP; 6 A; 0 C; 6 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe H30 used to identify HLA-DR sequences.
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                                                                                                                                                                                                                                                                                                                                            Claim 7; Page 23; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.5%;
81.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV16650 standard; DNA; 12
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(EPOC-) EPOCH PHARM INC
                                                              Kutyavin IV;
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                                                                                                                               WPI; 1998-447163/38.
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                                                                                                                probes AAV16647-64 are used to identify differences in the DR region of human major histocompatibility complex (HLA-DR). The specification becaribes a method for HLA-Typing, which includes an oligonucleotide probe which undergoes sequence-specific hybridisation with an HLA-DR beta consenus sequence at positions 61-64. The probe contains a labelling substance other than a nucleotide sequence, which facilitates detection of the probe. The HLA sequence of a subject is PCR amplified, and a probe that recognises an allelic polymorphism at a selected HLA locus is contacted with the amplified product. This first probe recognises a HLA-DR became allelic polymorphism. A second (different) probe is brought into contact with a second sample of the amplified DNA in a separate reaction, and hybridisation detected. The probes and primers are used for HLA typing, e.g. for tissue, especially bone marrow, transplants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Antioxidant Response Element (ARE), useful for identifying drugs and transcription factors for increasing transcription of mRNA, useful for treatment of atherosclerosis.
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              Disclosure; Col 29; 20pp; English
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Matches 9; Conservative
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an ARE). UV cross-linking studies using an apoAI-ARE probe isolated two polypeptides of 100 and 115 kDa. These compounds are useful for treatment of a human or animal with atherosclerosis. ARE's can also be used in DNA constructs when operably linked to heterologous protein coding sequences to effect the transcription of those heterologous sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a potential triple-helix forming region. It can be used to demonstrate the assay of the invention. The assay comprises adding a sample containing double-stranded DNA test sequences, e.g. containing the present sequence, to an aqueous medium containing at least one complex of anchor DNA, attached to a solid support, and reporter DNA, where either a part of the anchor DNA or reporter DNA is designed to form a triple-strand structure with part of the test sequence. Triplex formation results in displacement of the reporter DNA which is detected as an indication of the presence of the DNA test sequence. The method is used to detect DNA sequences, particularly for identification of bacteria (by detecting genes for ribosomal RNA) in clinical samples, but also detection of oncogenes and Hepatitis B virus
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                                                                                                                                                             35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; tive 0; Mismatches 2; Indels
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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                                                                                                                         Seguence 12 BP; 5 A; 2 C; 4 G; 1 T; 0 U; 0 Other;
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81.8%;
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nes 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Halococcus morrhuae.
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Best Local Similarity
Matches 9; Conserv
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733 GAGAAACAGAA 743

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Triple-helix forming region; Triplex formation; DNA detection; identification; bacteria; oncogene; virus; ds.
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(first entry)
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                                                                                                                                                                                                                                                    Wang C;
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es 9; Conserv
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                                                               Escherichia coli
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                                                                                                                                                                                                                                                    Hepburn AG,
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20-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                             bacteria.
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                                                                                                                                                                                     Triple helix forming nucleotides1066-1077 of the p53 gene.
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                                                                                           AAX14964 standard; DNA; 12 BP
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1 GAGATAGAGAA 11
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                                                                                                                                                                                                                                                                 Homo sapiens
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The present sequence represents a potential triple-helix forming region. It can be used to demonstrate the assay of the invention. The assay comprises adding a sample containing double-stranded DNA test sequences, e.g. containing the present sequence, to an aqueous medium containing at least one complex of anchor DNA, attached to a solid support, and reporter DNA, where either a part of the anchor DNA or reporter DNA is designed to form a triple-strand structure with part of the test sequence. Triplex formation results in displacement of the reporter DNA which is detected as an indication of the presence of the DNA test sequence. The method is used to detect DNA sequences, particularly for identification of bacteria (By detecting genes for ribosomal RNA) in clinical samples, but also detection of oncogenes and Hepatitis B virus
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Assay of genetic sequences based on triplex formation from double stranded analyte - and hybrid of anchor and reporter sequences, with reporter released if triplex formation occurs, used e.g. to identify
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llarity 81.8%; Pred. No. 6.8e+02;
Conservative 0; Mismatches 2; Indels
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triple stranded binding complex; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biodetector protein, fusion protein, recognition site, cellular targetting sequence, cellular localisation, fluorescent protein, protease activity detection, toxin detection, cellular stress detection, drug discovery, cell based screening, protease recognition site,
                                                                                                                                                                   This sequence represents a probe analyte used to test the method of the invention. The method is for the determination of a nucleic acid A, and comprises formation of a triple stranded binding complex (1) between A and two different nucleic acid binding molecules B and C, the formation of (1) detected by inclusion of B or C. (1) is more thermostable than a complex between A and two Bs or two identical Cs. The nucleic acid binding molecules B and C are useful as probes for specifically determining a nucleic acid, useful in diagnostics. Short Hoogsteen binding oligomer B is stabilised by a longer Watson-Crick molecule C, preventing the need for a long homopurine tract in A, allowing the high discriminative power of short Hoogsteen binding probes without loss of specificity. (Updated on 20-MAR-2003 to correct PA field.)
                                                                                                  Determining nucleic acids by formation of a triple stranded binding complex - using two separate probe molecules which bind to the nucleic acid via Watson-Crick and Hoogsteen base pairing.
                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding caspase-6 substrate recognition sequence, SEQ ID NO:65
                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity, 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                          Sequence 12 BP; 5 A; 3 C; 2 G; 2 T; 0 U; 0 Other;
                                                                                                                                                   Example 1; Page 14; 28pp; English
                      (BOEF ) BOEHRINGER MANNHEIM GMBH. (HOFF ) ROCHE DIAGNOSTICS GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA93383 standard; DNA; 12 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-FEB-2000; 2000WO-US004794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0122152P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0123399P.
99US-00352171.
 22-AUG-1997; 97EP-00114512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                             729 CCAGGAGAAC 739
                                                                                                                                                                                                                                                                                                                                                                                                                   CCAGAAGATAC 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Giuliano KA, Kapur R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CELL-) CELLOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-594086/56.
P-PSDB; AAB22892.
                                                                               WPI; 1999-134650/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cleavage site; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40200050872-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-AUG-2000.
                                                         Naesby M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA93383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1013
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The invention relates to systems, methods and reagents for cell-based screening or detection of compounds which affect particular biological functions. The methods of the invention utilise fluorescent biodetector conclections. The methods of the invention utilise fluorescent biodetector molecules which, when acted on by a compound of interest, cause an alteration in the cellular distribution of at least the fluorescent concerns the concerns of a fluorescent proteins. The collular distribution of at least the fluorescent proteins of a fluorescent proteins are comprise heat shock proteins of protein (GFP), or derivatives thereof). Such biosensors are located in the cytoplasm, but on stress activation translocate to the nucleus. In the cytoplasm, but on stress activation translocate to the nucleus. In the cytoplasm, but on stress activation translocate to the nucleus. In the proteins or mapped at least one collular localisation signal. The latter two proteases and at least one collular localisation signal. The latter two proteases, or may be from the recologous sources. Due to the components of a single protein signal. The latter two call serion of the cell. Once acted on by the protease of interest, the fluorescent protein is cleaved from the localisation sequence, and is cloadlisation of the cell. Once acted on by the protease recognition sequence. The comparament after cleavage of the fluorescent protein adjustion of the fluorescent protein and distribution of the fluorescent protein and distribution of the fluorescent protein and distribution of the fluorescent protein can be used to investigate a wide range of change in distribution of the fluorescent protein can be used to investigate a wide range of camping methods with a high degree of spatial resolution. The methods and become of activities and to screen compounds which may be used for the detection of proteins of comparation, designed to a detected using mapped of data analysis and automating other protease recognition of capables. The procease comparati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; vascular endothelial growth factor; VEGF; phosphorothioate; antisense oligomuclectide; inhibition; cytostatic; angiogenic; gene therapy; abnormal vascular permeability; cell proliferation; cell permeation; angiogenesis; neovascularisation; tumour cell growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Automated cell-based characterization of toxin by contacting cells containing luminescent reporter molecules with test substance and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEGF derived short antisense oligonucleotide SEQ ID NO:21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12 BP; 6 A; 1 C; 3 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                 Example 11; Fig 29B; 336pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA06712 standard; DNA; 12 BP
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Best Local Similarity 81.00.

Best Local Similarity 81.00.
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                                                                                                 analyzing optically.
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Novel oligonucleotides corresponding to a part of a vascular endothelial growth factor, useful for treating e.g. tumor cell growth and/or
                                                                                         Ulhmann E, Peyman A, Bitonti AJ,
                                                                                                                                                 Example 1; Page 16; 73pp; English.
                                                                            (HMRI ) HOECHST MARION ROUSSEL
                                                             98EP-00114853.
                                                 98EP-00114853
                                                                                                        WPI; 2000-258586/23.
Homo sapiens
Synthetic.
                                                              07-AUG-1998;
                                                 37-AUG-1998;
                    EP979869-A1.
                                  16-FEB-2000
                                                                                                                                    metastasis.
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Woessner RD;

DEUT GMBH.

ô The present invention describes oligonucleotides (I) of 10-15 residues corresponding to a part of a vascular endothelial growth factor (VEGF) compribing 1 of 6 sequences given in AAAO6692 to AAAO6697. AAAO6699 to AAAO6693 represent VEGF antisenes oligonucleotides used in the exemplification of the present invention. The antisense oligonucleotides can contain phosphorothioate linkages. Oligonucleotides from the present invention have cytostatic and angiogenic activities, and can be used in gene therapy. The oligonucleotides are useful for inhibiting the expression of VEGF, e.g. for the treatment of diseases associated with angiogenesis, neovascularisation, tumour cell growth and/or metastasis. AAAO6784 represents a human VEGF nucleotide sequence from which the oligonucleotides are derived Gaps . 0 35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; tive 0; Mismatches 2; Indels Sequence 12 BP; 6 A; 2 C; 4 G; 0 T; 0 U; 0 Other;

Query Match
Best Local Similarity 81.0 728 GCCAGGAGAA 738 GACAGCAGAAA 11 g ð

DNA encoding caspase-6 substrate recognition sequence. AAA27583 standard; DNA; 12 BP (first entry) 29-AUG-2000 AAA27583; RESULT 1015 AAA27583 

Protease; biosensor; caspase-6; substrate recognition sequence; cell screening; assay; analysis; drug discovery; ss.

Unidentified

11-MAY-2000

WO200026408-A2.

29-OCT-1999;

98US-0106308P. 99US-0136078P. 30-OCT-1998; 26-MAY-1999;

99WO-US025431.

(CELL-) CELLOMICS INC

The present sequence is that of DNA encoding the substrate recognition sequence (see AAY79594) of caspase-6. The DNA is used in a claimed recombinant mucleic acid encoding a procease biosensor. The mucleic acid (see AAZ25627-43) comprises: (1) a sequence (see AAAZ7568-76) encoding at least 1 detectable signal polypeptide; (2) a sequence (see AAAZ7577-611) sequence; and (3) a sequence (see AAAZ768-76) encoding at that encodes at least 1 protease recognition site, such as the present sequence; and (3) a sequence (see AAAZ7611-26) that encodes at least 1 reactant target sequence. An expression vector, a genetically engineered host cell and a recombinant protease biosensor are also claimed. A call involves contacting a host cell that possesses the recombinant protease biosensor with a test compound, and determining the protease biosensor distribution in the host cell, where changes in the distribution of the protease biosensor are correlated with modification of protease activity by the test compound. Claimed kits for identifying compounds that modify protease activity in a host cell include the recombinant nucleic acid, or the recombinant protease biosensor, or the vector, or the host cell. The protease biosensor is useful in high content screens to detect in vivo activation of enzymatic activity, and to identify specific activity based on cleavage of a known recognition Recombinant nucleic acid encoding a protease biosensor useful for fluorescence based cell and molecular biochemical assays for drug discovery comprising three operably linked nucleic acid sequences Olson K, Burroughs-Tencza S; Claim 6; Fig 29B; 218pp; English Guiliano KA, Bright G, 2000-365644/31. P-PSDB; AAY79594 

35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; ive 0; Mismatches 2; Indels Sequence 12 BP; 6 A; 1 C; 3 G; 2 T; 0 U; 0 Other; Query Match
Best Local Similarity 81.8
Matches 9; Conservative

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Gaps

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> ò g

AAA88229 standard; DNA; 12 BP.

AAA88229,

AAA88229;

Human, pp32, chromosome 15q22.3-q23; cancer; phosphoprotein; APRIL, acidic protein rich in leucine; chromosome 15q25; tumour suppressor; malignant; cytostatic; gene therapy; ss. pp32 upstream consensus sequence for an active steroid receptor #1. (first entry) 15-DEC-2000

Homo sapiens.

10-AUG-2000. 

WO200045852-A1.

03-FEB-2000; 2000WO-US002656.

99US-0118667P. 03-FEB-1999;

(UYJO ) UNIV JOHNS HOPKINS.

Bai J; Pasternack GR,

7 1/2

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The present invention describes a method (M1) for treating malignant cells comprising restoration of pp32 function. Also described are: (1) a method (M2) of screening to determine whether a compound is an inducer of pp32 expression comprising measuring pp32 expression by cells cultured in the presence and absence of the compound, and (2) a method (M3) of screening to determine whether a compound, and inducer of pp32 function comprising measuring protein phosphatase activity in cells cultured in the presence and absence of the compound. The methods are useful for treating cancer and for identifying agents which may be used to treat cancer. Human pp32 is a phosphoprotein which has been mapped to chromosome 1542.3.3423. The present sequence represents a consensus sequence for an active steroid receptor found in the upstream sequence of pp32, which is used in an example from the present invention
                                                  Treatment of cancer comprising restoration of pp32 function in malignant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12 BP; 0 A; 2 C; 0 G; 10 T; 0 U; 0 Other;
                                                                                                                                 Example 3; Page 41; 90pp; English.
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; 0 35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; tive 0; Mismatches 2; Indels Ouery Match
Best Local Similarity 81.8
For Py Conservative 735 GAAACAGAACA 745 à

GAAAAAGAAAA 2 임

AAH20822 standard; DNA; 12 AAH20822; RESULT 1017 

BP

13-AUG-2001 (first entry)

Complex PCR amplification type 2 primer #3.

PCR primer, amplification; microarray; genotyping; mutational analysis; cytosine methylation pattern; ss.

Unidentified

WO200136669-A2.

25-MAY-2001

12-NOV-1999; 99DE-01056203 12-OCT-2000; 2000DE-01051714 12-NOV-1999;

12-NOV-2000; 2000WO-DE003973.

(EPIG-) EPIGENOMICS AG.

Berlin K;

WPI; 2001-343834/36.

Controlling performance of complex polymerase chain reaction amplification, useful e.g. for genotyping, using a set of many specific primers and non-specific counter-strand primers.

Example 2; Page 18; 26pp; German.

This invention describes a novel controllable performance method of complex polymerase chain reaction (PCR) amplifications. Firstly, PCR is carried out with at least 50 different primers (Pl) of one type, complementary to one strand of sample DNA, and with a primer (or library of primers) of a second type (P2) complementary to the other strand of

the DNA, with P2 carrying a marker (M1). Amplicons are hybridized either to an array of oligonucleotides (ON) that hybridize to the primer used for the first step, or to its complement, or to an array of ON complementary to the primers used in PCR, and then the lengths of amplicons bound to the array are determined using a second marker (M2), different from M1, that is correlated with the length of the relevant DNA transments. Signals from M1 and M2 are quantified at relevant positions in the ON array. The method is used in whole genomic amplification for genotyping, mutational analysis or related applications, e.g. determining the cytosine methylation pattern of DNA. The method makes possible determination of the number and length of many different amplicons, something that is almost impossible when using two non-specific primers, as in the conventional method. AAH20756-AAH20823 represent the PCR primers used to illustrate the method of the invention

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Sequence 12 BP; 8 A; 4 C; 0 G; 0 T; 0 U; 0 Other;

Gaps . 0 Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels

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8 g RESULT 1018 AAF61471/

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Gaps

AAF61471 standard; RNA; 12 BP. AAF61471;

(first entry) 18-JUN-2001 Wildtype influenza virus C promoter-UP 3' RNA conserved region.

Major histocompatibility complex restricted antigen; antitumor vaccine; MHC-restricted antigen; T cell-restricted antigen; antigen identification; promoter; ss.

DE19962508-A1

29-MAR-2001.

99DE-01062508 23-DEC-1999; 

99DE-01045171. 99DE-01051543. 21-SEP-1999; 26-OCT-1999;

(GSPU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEI (ARTE-) ARTEMIS PHARM GMBH.

Mautner J, Bornkamm GW, Nimmerjahn F, Hobom G;

WPI; 2001-246290/26.

Identifying major histocompatibility complex-restricted antigens, useful potentially in antitumor vaccines, by forming DNA bank in virus and testing for I cell stimulation.

Disclosure; Col 5; 10pp; German.

This invention describes a novel method for identifying major histocompatibility complex (MHC)-restricted antigens. A gene or CDNA bank is constructed from the cells or organism under test, then incorporated into a retroviral genome or, as additional RNA, into a modified influenza virus that has increased transcription, replication and/or expression rate, relative to the wild type, so as to produce viral particles (VP). VP are used to infect immortalized autologous cells that express MHC class I and/or II molecules on the surface, so that proteins encoded by the gene bank inserts are expressed and their cleavage products exposed

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Gaps

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI32073 data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
on the cell surface. These cells are co-cultured with T cells which are stimulated if the autologous cells express a T cell restricted antigen. Clones that express antigens are isolated and the autigens sequenced. The products of the invention can be used for identifying antigens for possible use in antitutum vaccines, but may also identify autoantigens or microbial antigens. The method does not require knowledge of the restricted MHC molecule, allows unlimited proliferation of target cells and can identify, simultaneously, both Class I and II antigens. The lymphoblastic cells lines used as target cells ensure efficient gene transfer, with high level expression of the inserted gene, providing high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide primer SEQ ID NO 317599 for detecting SNP TSC0028132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 317599; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 7.8; DB 1; Length 12;
Pred. No. 6.8e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12 BP; 0 A; 5 C; 2 G; 0 T; 5 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                      sensitivity and simple detection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.5%;
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Best Local Similarity B1.0.
Best Acas 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Piepenbrock
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ABIIT 626/C
IND XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonuclectide primer SEQ ID NO 294707 for detecting SNP TSC0016233.
                                                                   Gaps
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   Length 12;
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Score 7.8; DB 1; Length 12
Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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81.8%; Pred. No. 6.8e+02;
tive 0; Mismatches 2; Indels
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   35.5%;
81.8%;
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Query Match
Best Local Similarity 81.8
Matches 9; Conservative
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hes 9; Conserv
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ABH69899/c
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ABH69899 standard; DNA; 12 BP.

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Berlin K;

Piepenbrock C,

Page 454

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                Oligonucleotide primer SEQ ID NO 295386 for detecting SNP TSC0016574.
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Best Local Similarity 81.0
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      ABH69899;
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC09989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                 Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 295386; 29pp + Sequence Listing; German
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                                                                                                               06-APR-2001; 2001WO-IB000713
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                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                        Oligonucleotide primer SEQ ID NO 269876 for detecting SNP TSC0001913.
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      35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; rative 0; Mismatches 2; Indels
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Query Match
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Thes 9; Conservative
                                                           737 AACAGAACACC 747
                                                                                 2 AAAATAACACC 12
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ABI22321
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WPI; 2001-657177/75

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but fire wipo.int/pub/published_pct_sequences
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   Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                           Claim 1; SEQ ID NO 322294; 29pp + Sequence Listing; German.
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oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF0010-ABF99889, ABH0010-ABH99989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fip.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                       Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels
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ABH98878 standard; DNA; 12
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ABI00237;

RESULT 1026

Oligonucleotide primer SEQ ID NO 275513 for detecting SNP TSC0003914.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at the printed specification, but the wipo.int/pub/published_pot_sequences
                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                      Oligonucleotide primer SEQ ID NO 300210 for detecting SNP TSC0018905.
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RESULT 1027

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Claim 1; SEQ ID NO 279099; 29pp + Sequence Listing; German.
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35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically prersated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at
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ABI07757 standard; DNA; 12
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RESULT 1032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ABI30078 standard; DNA; 12 BP.
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Matches 9; Conservative
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                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                    Oligonucleotide primer SEQ ID NO 307730 for detecting SNP TSC0022657.
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Best Local Similarity
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             Homo sapiens.
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                                          Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                   Claim 1; SEQ ID NO 284255; 29pp + Sequence Listing; German.
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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81.8%;
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Best Local Similarity 81.8
Matches 9, Conservative
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WPI; 2001-657177/75
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cycosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form mar of the printed specification, but was obtained in electronic format from WIPO at
               range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC09989, ABC001010-ABE9989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at they printed specification, but fire wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
  oligonucleotides are used for diagnosis and/or prognosis of cancer and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide primer SEQ ID NO 346512 for detecting SNP TSC0044618
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hes 9; Conservative
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                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                           Oligonucleotide primer SEQ ID NO 368968 for detecting SNP TSC0057362.
                   Gaps
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designed to detect single-nucleotide polymorphisms and cytosine
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Pred. No. 6.8e+02;
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pred. No. 6.8e+02;
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81.8%;
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                                                  732 GGAGAACAGA 742
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ABI69973;

35.5%; Score 7.8; DB 1; Length 12;

Query Match

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH0010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                     Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 356373; 29pp + Sequence Listing; German.
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ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretracted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                               Oligonucleotide primer SEQ ID NO 369946 for detecting SNP TSC0057901.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12 BP; 6 A; 0 C; 3 G; 3 T; 0 U; 0 Other;
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                   22-FEB-2002 (first entry)
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Set of oligonucleotides, useful for diagnosis and cell typing, is

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABF82073
                                                                                                                                                                                                                                                                          acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABR00010-ABE99898, ABR00010-ABE99898, ABR00110-ABE99898, ABR00110-ABE998989, ABR00110-ABE99889, ABR00110-ABE
                                                                                                                                                                                                                                                 invention describes novel oligonucleotide primers or peptide nucleic
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designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                           Claim 1; SEQ ID NO 357949; 29pp + Sequence Listing;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                Oligonucleotide primer SEQ ID NO 376769 for detecting SNP TSC0010247.
                                                                                                                                                                  Gaps
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                                                                                                                            15.5%; Score 7.8; DB 1; Length 12; llarity 81.8%; Pred. No. 6.8e+02; Conservative 0; Mismatches 2; Indels
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                                                                                              Sequence 12 BP; 0 A; 0 C; 3 G; 9 T; 0 U; 0 Other;
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                                                                                                                                                 Local Similarity
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                            Oligonucleotide primer SEQ ID NO 366962 for detecting SNP ISC0005306.
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Best Local Similarity
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                     set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABC0010-ABF9989, ABH00010-ABH99999 and ABI00010-ABIE2073 trepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide primer SEQ ID NO 294115 for detecting SNP TSC0015962.
                                                                                                         oligonuclectides, useful for diagnosis and cell typing, is at to detect single-nuclectide polymorphisms and cytosine
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                                                                                                                                                                       claim 1; SEQ ID NO 293675; 29pp + Sequence Listing; German.
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Best Local Similarity 81.0.
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                                             Piepenbrock C,
               (EPIG-) EPIGENOMICS AG.
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                                                                            WPI; 2001-657177/75
                                                                                                                          designed to detect methylation status.
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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

WPI; 2001-657177/75.

Claim 1; SEQ ID NO 294115; 29pp + Sequence Listing; German.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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81.8%; Pred. No. 6.8e+02;
ative 0; Mismatches 2; Indels
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Best Local Similarity
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                             Oligonucleotide primer SEQ ID NO 271142 for detecting SNP TSC0002409.
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ABH71165 standard; DNA; 12 BP.
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Matches 9, Conservative
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                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
                                     35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred, No. 6.8e+02; ive 0; Mismatches 2; Indels
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     Sequence 12 BP; 6 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
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                    WPI; 2001-657177/75.
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Berlin K;

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                       ABH96584 standard; DNA; 12 BP.
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736 AAACAGAACAC 746
                                 1 AAACAACACAC 11
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RESULT 1049 ABH71165

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35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; ive 0; Mismatches 2; Indels

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                              Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                     Claim 1; SEQ ID NO 323559; 29pp + Sequence Listing; German
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Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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WPI; 2001-657177/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABH99989 and ABI00010-ABI82073 trepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 296577; 29pp + Sequence Listing; German.
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Best Local Similarity 81.0
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                  736 AAACAGAACAC 746
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ABI02367/
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central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 ABC99989, ABR00010-ABR99989 and ABI00010-ABR182073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at fip.wipo.int/pub/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                     Similarity 81.8%; Score 7.8; DB 1; Length 12; Similarity 81.8%; Pred. No. 6.8e+02; 9; Conservative 0; Mismatches 2; Indels
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ABI02156 standard; DNA; 12 BP.
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ID ABIO2
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AC ABIO3
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AD 22-FI
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DB OligG
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WW SNP;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Best Local Similarity 81.0
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06-APR-2001; 2001WO-IB000713.
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Best Local Similarity 81.0
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                                                                         Olek A, Piepenbrock C,
                                                                                                                                                                                                 ACAAAAAACCG 11
                                                                 (EPIG-) EPIGENOMICS AG
                                                                                WPI; 2001-657177/75
                                                                                             designed to detect
methylation status.
                                  WO200177384-A2
                           Homo sapiens
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but they wipo int/pub/published_pct_sequences
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06-APR-2001; 2001WO-IB000713
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                                                                                                    SND; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                    Oligonucleotide primer SEQ ID NO 335774 for detecting SNP TSC0039007.
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designed to detect single-nucleotide polymorphisms and cytosine
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Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Berlin K;

Piepenbrock C,

olek A,

WPI; 2001-657177/75.

WO200177384-A2 Homo sapiens.

18-OCT-2001

schultz1-727.rng

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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              Claim 1; SEQ ID NO 345717; 29pp + Sequence Listing; German.
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35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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81.8%;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in ejectronic format from WIPO at
central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                    AB160839
              RESULT 1060
AB160839
LD AB16083
XX AB16083
XX AB16083
XX AB16083
XX SNP; S
KW SNP; S
KW SNP; S
KW CENTRA
XX CONTRA
X
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Gaps

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
Oligonucleotide primer SEQ ID NO 269788 for detecting SNP TSC0001884.
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ABI18875/ XX XX AC ABI1: XX DT 22-FI XX XX XX XX XW SNP; KW PEPC.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligonucleotide primer SEQ ID NO 296368 for detecting SNP TSC0017049.
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                                                                                     Set of oligonucleotides, useful for diagnosis and cell typing, : designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                          Claim 1; SEQ ID NO 269788; 29pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12 BP; 6 A; 5 C; 1 G; 0 T; 0 U; 0 Other;
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                   Berlin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 81.5-
Best Local 9; Conservative
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                 Piepenbrock C,
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                                                   WPI; 2001-657177/75
                                                                                                                        methylation status.
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                   olek A,
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and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF0010-ABH9989 and ABI0010-ABR9980 and ABI0010-ABR9980 and addition. ABC0010 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SND; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide primer SEQ ID NO 271555 for detecting SNP TSC0002547.
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                                                                                                                                                                                                                                                                          Length 12,
                                                                                                                                                                                                                                                                      Query Match 35.5%; Score 7.8; DB 1; Length 12
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      was obtained in electronic format from Wiftp.wipo.int/pub/published_pct_sequences
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonuclectide primer SEQ ID NO 275630 for detecting SNP TSC0003950.

22-FEB-2002 (first entry)

ABH75639;

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                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                           Gaps
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designed to detect single-nucleotide polymorphisms and cytosine
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35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
 Score 7.8; DB 1; Length 12;
Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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                                                                                                                                    ABH98926 standard; DNA; 12 BP.
35.5%;
ilarity 81.8%;
Conservative 0
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                                                                        2 AACACAACCCC 12
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                                                 737 AACAGAACACC
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Query Match
Best Local Similarity
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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine

Berlin K;

Piepenbrock C,

olek A,

WPI; 2001-657177/75.

methylation status.

(EPIG-) EPIGENOMICS AG

06-APR-2001; 2001WO-IB000713 07-APR-2000; 2000DE-01019173

WO200177384-A2

18-OCT-2001

Homo sapiens

Claim 1; SEQ ID NO 275630; 29pp + Sequence Listing; German.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABF00010-ABF99989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABF8073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo int/pub/published_pct_sequences
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Matches 9; Conservative
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5639/c ABH75639 standard; DNA; 12 BF.

RESULT 1066

ABH75639/ ID ABH7: XX

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ABH77342;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ABH77101 standard; DNA; 12
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Best Local Similarity
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                    18-OCT-2001.
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                                                                                                                                                                                                                                            This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic discorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99899, ABH00010-ABF99899 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but twipo.int/pub/published_pct_sequences
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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                            Claim 1; SEQ ID NO 277094; 29pp + Sequence Listing; German.
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35.5%; Score 7.8; DB 1;
Best Local Similarity 81.8%; Pred. No., 6.8e+02;
Matches 9; Conservative 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SND; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the Oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                               Gaps
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                                                                                                                                                    35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02;
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Best Local Similarity 81.8
Matches 9; Conservative
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Best Local Similarity
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF99899, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fined specification, but fire wipo.int/pub/published_pct_sequences
                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ABI29767 standard; DNA; 12
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Best Local Similarity 81.0.
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Claim 1; SEQ ID NO 284634; 29pp + Sequence Listing; German.
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                                                                  Piepenbrock C,
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           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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3. Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
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                                                                                                                                   set or oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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        This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cointral nervous system, aradiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE99989, ABF00010-ABF99989, ABH0010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide primer SEQ ID NO 310162 for detecting SNP TSC0023842.
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Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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ABI10189 standard; DNA; 12
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                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide primer SEQ ID NO 311003 for detecting SNP TSC0024262.
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                                 Query Match 35.5%, Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels
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Sequence 12 BP; 0 A; 1 C; 3 G; 8 T; 0 U; 0 Other;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (FNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but fep.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                oet or oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                       06-APR-2001; 2001WO-IB000713
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                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                    Oligonucleotide primer SEQ ID NO 286849 for detecting SNP TSC0012849.
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              ABH86856 standard; DNA; 12 BP
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ABH86856/c
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Pred. No. 6.8e+02;
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Sequence 12 BP; 0 A; 1 C; 4 G; 7 T; 0 U; 0 Other;
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ABH91152 standard; DNA; 12
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  WPI; 2001-657177/75
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                                                                                              ABH91152;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, astdowascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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single-nucleotide polymorphisms and cytosine
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               oligonucleotides,
                                                        designed to detect methylation status.
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Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                      735 GAAACAGAACA 745
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GTAACACAACA 2

Oligonucleotide primer SEQ ID NO 291145 for detecting SNP TSC0014659.

SND; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS

Berlin

Set of oligonucleotides, useful for diagnosis and cell typing, i deaigned to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 291145; 29pp + Sequence Listing; German.

This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a

35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02;

Query Match Best Local Similarity

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99899, ABF00010-ABF99899 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC099889, ABF00010-ABE99889, ABF00010-ABE9989, ABF00010-ABE9989, ABF00010-ABE9989, ABF00010-ABE9989, add and ABI00010-ABE9003 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPD at the printed specification, but the wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                   Match 12; Match 15.5%; Score 7.8; DB 1; Length 12; Local Similarity 81.8%; Pred. No. 6.8e+02; les 9; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                 Sequence 12 BP; 5 A; 0 C; 6 G; 1 T; 0 U; 0 Other;
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) cligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                        Oligonucleotide primer SEQ ID NO 267240 for detecting SNP TSC0000063.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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     22-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
     Gaps
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Best Local Similarity 81.8
Matches 9; Conservative
9; Conservative
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ABI16969/c
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/ Match 35.5%; Score 7.8; DB 1; Length 12; Local Similarity 81.8%; Pred. No. 6.8e+02; les 9; Conservative 0; Mismatches 2; Indels
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ABH67263 standard; DNA; 12

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ABH67263;

ABH67263/CID ABH6 XX ABH6 AC ABH6

736 AAACAGAACAC 746

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                        Olek A, Piepenbrock C,
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                                                                        WPI; 2001-657177/75
                                                                                                  designed to detect methylation status.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABF00010-ABF99989, ABF00010-ABF99989, and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                           claim 1; SEQ ID NO 367431; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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   methylation status.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                         06-APR-2001; 2001WO-IB000713
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This invention describes novel oligomucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic discorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABF09989, ABF00010-ABF99989 ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence
                                                                                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                         Oligonucleotide primer SEQ ID NO 368435 for detecting SNP TSC0057027.
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                                                                                    ABI68462 standard; DNA; 12
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AB168462/
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AXX AB16
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(first entry)

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                            ABI57057 standard; DNA; 12
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                              RESULT 1088
ABI57057
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                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
                                                                                                                                                                                                                                                                                                                                              Oligonucleotide primer SEQ ID NO 368901 for detecting SNP TSC0057306.
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35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                   35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; ive 0; Mismatches 2; Indels
                                                        Sequence 12 BP; 1 A; 0 C; 6 G; 5 T; 0 U; 0 Other;
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                              ftp.wipo.int/pub/published_pct_sequences
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hes 9; Conservative
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81.8%; Pred. No. 6.8e+02;
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Olek A, Piepenbrock C,
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This invention describes novel oligonuclectide primers or peptide nucleic
(EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                       This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE9989, ABH00010-ABH99999 and ABI00010-ABI82073 trepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
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peptide nucleic acid, cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                     Gaps
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   Length 12;
                                                                         2; Indels
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Score 7.8; DB 1;
Pred. No. 6.8e+02;
0; Mismatches 2;
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ID ABH94174 standard; DNA; 12 BP.
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81.8%;
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   Query Match
Best Local Similarity 81.8
Matches 9; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99889, ABF00010-ABF9989, ABF00010-ABF99899 and ABI00010-ABF3073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                        Oligonucleotide primer SEQ ID NO 294167 for detecting SNP TSC0015981.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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.larity 81.8%; Pred. No. 6.8e+02;
Conservative 0; Mismatches 2; Indels
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                                                      (first entry)
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                 ABH94174
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at

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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

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Berlin

Piepenbrock C,

olek A,

WPI; 2001-657177/75

(EPIG-) EPIGENOMICS

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173.

WO200177384-A2

18-OCT-2001

Claim 1; SEQ ID NO 296939; 29pp + Sequence Listing; German.

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                              Oligonucleotide primer SEQ ID NO 299360 for detecting SNP TSC0018537.
                                                                                                                                                                                                                                                                                                                                        Berlin K;
                                                 367/c
ABH99367 standard; DNA; 12 BP.
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                                                                                                      22-FEB-2002 (first entry)
2 AAACACAAAAC 12
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                                                                                                                                                                                                                                                                                                                  (EPIG-) EPIGENOMICS AG.
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                                   RESULT 1096
ABH99367/c
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Gaps

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WPI; 2001-657177/75.

SNP; single nucleotide polymorphism; human; diagnosis; FNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

Oligonucleotide primer SEQ ID NO 296939 for detecting SNP TSC0017352.

ABH96946 standard; DNA; 12 BP

RESULT 1095 **ABH96946** 

733 GAGAAACAGAA 743

GAGAGAAAGAA 1

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22-FEB-2002 (first entry)

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Length 12;

35.5%; Score 7.8; DB 1; Length 12 81.8%; Pred. No. 6.8e+02; wiematches 2; Indels

Local Similarity 81.8 ses 9; Conservative 736 AAACAGAACAC 746

Query Match

Matches

8

Seguence 12 BP; 9 A; 3 C; 0 G; 0 T; 0 U; 0 Other;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligoners are also used for detecting cell type differentiation. ABC0010-ABC99999, ABF00010-ABF9989, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but two, who, int/pub/published_pct_sequences
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                               Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                       Claim 1; SEQ ID NO 299360; 29pp + Sequence Listing; German.
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                                                                                                         methylation status.
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XX ABILS5367/6
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35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; tive 0; Mismatches 2; Indels

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99899 and ABI00010-ABI32073 trepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF0010-ABF99889, ABH0010-ABH99989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at flow but pub/published\_pct\_sequences SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Gaps Gaps Oligonucleotide primer SEQ ID NO 326828 for detecting SNP TSC0033289 set of oligonuclectides, useful for diagnosis and cell typing, is designed to detect single-nuclectide polymorphisms and cytosine methylation status. .; 0 ö Claim 1; SEQ ID NO 326828; 29pp + Sequence Listing; German. 35.5%; Score 7.8; DB 1; Length 12; llarity 81.8%; Pred. No. 6.8e+02; Conservative 0; Mismatches 2; Indels Length 12; Score 7.8; DB 1; Length 12 Pred. No. 6.8e+02; 0; Mismatches 2; Indels Sequence 12 BP; 0 A; 0 C; 3 G; 9 T; 0 U; 0 Other; Sequence 12 BP; 1 A; 1 C; 3 G; 7 T; 0 U; 0 Other; ftp.wipo.int/pub/published\_pct\_sequences Berlin K; ABI26855 standard; DNA; 12 BP. 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173. 35.5%; (first entry) Ouery Match
Best Local Similarity 81.0 734 AGAAACAGAAC 744 Olek A, Piepenbrock C, 11 ACAAACAAAAC 1 (EPIG-) EPIGENOMICS AG WPI; 2001-657177/75. Local Similarity Les 9; Conserv WO200177384-A2 22-FEB-2002 18-OCT-2001 Query Match Best Local S: Matches 9 ABI26855; 8888888888 ઠે . 0

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Oligonucleotide primer SEQ ID NO 303807 for detecting SNP TSC0020650
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                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                           Oligonucleotide primer SEQ ID NO 301735 for detecting SNP TSC0019628.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPD at
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABF00010-ABF99899, ABH00010-ABF99899 and ABI00010-ABF8073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but typ.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                         Claim 1; SEQ ID NO 305863; 29pp + Sequence Listing; German.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, ardiovascular and metabolic disorders. The coingomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from NIPO at
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                                  This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
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Claim 1; SEQ ID NO 305954; 29pp + Sequence Listing; German.
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE09989, ABF00010-ABE99989, ABH0010-ABH99989 and ABI00010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPD at the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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ABI32585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                           Match 35.5%; Score 7.8; DB 1; Length 12; Local Similarity 81.8%; Pred, No. 6.8e+02; les 9; Conservative 0; Mismatches 2; Indels
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                                                Sequence 12 BP; 1 A; 0 C; 3 G; 8 T; 0 U; 0 Other;
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ftp.wipo.int/pub/published_pct_sequences
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RESULT 1104
ABH91845/C
ID ABH8184
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AC ABH8184
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SNP; S:
KW SNP; S:
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KW SNP; S:
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 trepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from NIPO at
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                                                            Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                         Claim 1; SEQ ID NO 283985; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels
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Piepenbrock C,
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Olek A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, aradiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99889, ABF00010-ABH99988 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ABH83992 standard; DNA; 12 BP.
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les 9, Conservative
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                       Homo sapiens.
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ID ABH85351 standard; DNA; 12 BP
AC ABH85351;
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22-FEB-2002 (first entry)
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SNP; single nuclectide polymo peptide nucleic acid; cytosin KW

SNP; single nuclectide polymo central nervous system; gastra
XX

SNP; single nuclectide polymo CS
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Homo sapiens.
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NO200177384-A2.
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NO-APR-2000; 2000DE-01019173.
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NO-APR-2000; 2000DE-01019173.
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O7-APR-2000; 2000DE-01019173.
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CPAR-2001; 2001WO-IB000713.
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NO-APR-2000; 2000DE-01019173.
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CPAR-2001; 2001Genore AG.
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CPAR-2001; 2001Genore G.
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CPAR-2001; 2011-657177/75.
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CTALS invention describes nove
CC acid (PNA) oligomers for dete
CC and cytosine methylation stat
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointéstinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                   Oligonucleotide primer SEQ ID NO 335449 for detecting SNP TSC0038833.
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                  Indels
Pred. No. 6.8e+02;
; Mismatches 2;
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ABH89723 standard; DNA; 12 BP.
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Best Local Similarity 81.8
Matches 9; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically prereated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                   Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 341275; 29pp + Sequence Listing; German.
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                                           06-APR-2001; 2001WO-IB000713.
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                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                              Oligonucleotide primer SEQ ID NO 289716 for detecting SNP TSC0014062.
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Set of oligonucleotides, useful for diagnosis and cell typing, is

Berlin K;

Olek A, Piepenbrock C,

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABI82073
                                                                                                                                                                    This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                          Claim 1; SEQ ID NO 346679; 29pp + Sequence Listing; German
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ABI49128 standard; DNA; 12 BP.
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represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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81.8%; Pred. No. 6.8e+02;
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                             Olek A, Piepenbrock C,
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Best Local Similarity
Matches 9; Conserv
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                                                                                                        Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF9989, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                            Oligonucleotide primer SEQ ID NO 352117 for detecting SNP TSC0047677.
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                                                                                                                      ABI52144 standard; DNA; 12
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11 ATACACACAC
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                                                                     RESULT 1116
ABI52144/C
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ABI52144/C
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ABI52144/C
DT 22-FEB-2
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DE Oligonuc
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SNP; SII
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NOO1017;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide primer SEQ ID NO 355037 for detecting SNP TSC0000340.
Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                     Claim 1; SEQ ID NO 367669; 29pp + Sequence Listing; German.
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SNP; single nuclectide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC09989, ABF00010-ABF99899, ABF00010-ABF99899, ABF00010-ABF99899, and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at the printed specification, but the wipo.int/pub/published_pct_sequences
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Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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                                                                                                                                   Berlin K;
                                                                                                                                   Olek A, Piepenbrock C,
                                                                   (EPIG-) EPIGENOMICS AG.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically prerreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic discorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC09989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at
                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                              Oligonuclectide primer SEQ ID NO 267681 for detecting SNP TSC0000442.
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BP.
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ABH67704 standard; DNA; 12
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                          Oligonucleotide primer SEQ ID NO 268597 for detecting SNP TSC0001243.
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designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
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 ABH68620 standard; DNA; 12 BP
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                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide primer SEQ ID NO 317872 for detecting SNP TSC0028313.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                     Length 12;
                                                                         2; Indels
Sequence 12 BP; 10 A; 2 C; 0 G; 0 T; 0 U; 0 Other;
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                                   35.5%; Score 7.8; DB 1;
81.8%; Pred. No. 6.8e+02;
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                 736 AAACAGAACAC 746
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                                                                                                                                                2 AAAAACAAAAC 12
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Berlin K;

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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734 AGAAACAGAAC 744
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 for this patent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic formant from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytoshe methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                  Set of oligonucleotides, useful for diagnosis and cell typing, : designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                         Claim 1; SEQ ID NO 319191; 29pp + Sequence Listing; German
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                                                                                                                                                                                                                                                                                                                                                                                        acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989 and ABI00010-ABF32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                            This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
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central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF99889, ABF00010-ABF99899 and ABI00100-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format from WIPO at fine bulblished_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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             Oligonucleotide primer SEQ ID NO 298420 for detecting SNP TSC0018084
                                                                                                                                                                                                                                                                                                                                                                                                          oligonucleotides, useful for diagnosis and cell typing, is to detect single-nucleotide polymorphisms and cytosine
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, asriovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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'Match 35.5%; Score 7.8; DB 1; Length 12; Local Similarity 81.8%; Pred. No. 6.8e+02; les 9; Conservative 0; Mismatches 2; Indels

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733 GAGAACAGAA 743

11 GAGGAAGAGAA 1

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Seguence 12 BP; 1 A; 5 C; 0 G; 6 T; 0 U; 0 Other;

was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, aradiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABF8073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardicovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173

WO200177384-A2. Homo sapiens.

18-OCT-2001.

(EPIG-) EPIGENOMICS AG

Oligonucleotide primer SEQ ID NO 303466 for detecting SNP TSC0020490.

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ABI03493 standard; DNA; 12

RESULT 1132

ABI03493,

ABI03493;

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coingomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) acid cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABF09989, ABF00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but

Claim 1; SEQ ID NO 277608; 29pp + Sequence Listing; German

methylation status.

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central nervous system; gastrointestinal; respiratory; immune; metabolic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                        Oligonucleotide primer SEQ ID NO 304355 for detecting SNP TSC0020884
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                                                                                           ABI04382 standard; DNA; 12 BP.
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Lag 9; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretracted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central inervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
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                                                                                                                                                            Claim 1; SEQ ID NO 305113; 29pp + Sequence Listing; German.
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35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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                 Olek A, Piepenbrock C,
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and cytosine methylation status in chemically pretreated genomic DNA. The oligomicleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABCC0010-ABEC99899, ABF00010-ABE9989, ABF00010-ABE9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP, single nucleotide polymorphism, human; diagnosis, PNA, cancer; CNS, peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Best Local Similarity 81.8
Matches 9; Conservative
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                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                           Gaps
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  Length 12;
Query Match 35.5%; Score 7.8; DB 1; Length 12 Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oyosoine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC09989, ABF00010-ABF99989, ABF00010-ABF99989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at the printed specification, but ftp.wipo.int/pub/published_pot_sequences
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                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                     Oligonucleotide primer SEQ ID NO 333223 for detecting SNP TSC0037427.
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22-FEB-2002 (first entry)
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Best Local Similarity 81.8
Matches 9; Conservative
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ABI33250 standard; DNA; 12 BP.

RESULT 1139 ABI33250/ ID ABI3 XX

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nuclectide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                        06-APR-2001; 2001WO-IB000713.
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                                                                                                                                  Olek A, Piepenbrock C,
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                                                                                                    (EPIG-) EPIGENOMICS AG
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                                                                                                                      This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) eligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The eligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, entrain nervous system, cardiovascular and metabolic disorders. The eligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF0010-ABF9989, ABH0010-ABH9989 and ABT00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastroihtestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABCO0010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Set of oligonuclectides, useful for diagnosis and cell typing, i designed to detect single-nuclectide polymorphisms and cytosine methylation status.
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                                                                                        Claim 1; SEQ ID NO 284738; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                      Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989, ABH00010-ABE99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but typ.wipo.int/pub/published_pct_sequences
                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                     Oligonucleotide primer SEQ ID NO 289342 for detecting SNP TSC0013898.
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                ABH89349 standard; DNA; 12 BP.
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Best Local Similarity 81.8
Matches 9; Conservative
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35.5%; Score 7.8; DB 1; Length 12; llarity 81.8%; Pred. No. 6.8e+02; Conservative 0; Mismatches 2; Indels

Query Match Best Local Similarity Matches 9; Conserv

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG

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             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNP, single nucleotide polymorphism; human; diagnosis; PNA, cancer; CNS, peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
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Matches 9; Conservative
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acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNN. The oligomuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABH82073 trepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at invention describes novel oligonucleotide primers or peptide nucleic (PNA) oligomers for detecting simple mucleical Sequence 12 BP; 1 A; 1 C; 4 G; 6 T; 0 U; 0 Other; ftp.wipo.int/pub/published\_pct\_sequences Query Match 35.5 Best Local Similarity 81.8 Matches 9; Conservative %%866666666666668% %%866666666666668%

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739/c ABI68739 standard; DNA; 12

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22-FEB-2002 ABI68739 ABEGULT 114
ABIGB739/C
ABIGB730/C

(first entry)

Oligonucleotide primer SEQ ID NO 368712 for detecting SNP TSC0057176

SND; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2

18-OCT-2001

06-APR-2001; 2001WO-IB000713

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG

Berlin K; Piepenbrock C, olek A,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, addesigned to detect single-nucleotide polymorphisms and cytosine Claim 1; SEQ ID NO 368712; 29pp + Sequence Listing; German. methylation status

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically prereated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC09989, ABF00010-ABF99889 and ABI00010-ABI82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 358096 for detecting SNP TSC0050951. .; 0 35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; tive 0; Mismatches 2; Indels Seguence 12 BP; 3 A; 4 C; 0 G; 5 T; 0 U; 0 Other; ВР. ABI58123 standard; DNA; 12 (first entry) Conservative 732 GGAGAAACAGA 742 12 GGAGAAATTGA 2 Local Similarity nes 9, Conserv 22-FEB-2002 Homo sapiens. ABI58123; Query Match Matches AB158123 8

oet or oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status. WPI; 2001-657177/75

Berlin K;

Piepenbrock C,

olek A,

(EPIG-) EPIGENOMICS AG

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173

WO200177384-A2

Claim 1; SEQ ID NO 358096; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymoxphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989, ABH00010-ABE99989 and ABI00010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

Sequence 12 BP; 0 A; 2 C; 0 G; 10 T; 0 U; 0 Other;

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735 GAAACAGAACA 745 GAAAAAAAAA 12

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                                                                                                      SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                   Oligonucleotide primer SEQ ID NO 372229 for detecting SNP TSC0000966.
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            ABI72256 standard; DNA; 12 BP
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pot_sequences
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ABH94621;
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Best Local Similarity 81.8
Matches 9; Conservative
WPI; 2001-657177/75
                                                                                                                                                          methylation status
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ABH94151 standard; DNA; 12 BP. 732 GGAGAAACAGA 742 2 GGAAAAAGAGA 12

Oligonucleotide primer SEQ ID NO 294144 for detecting SNP TSC0015973. (first entry)

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

(EPIG-) EPIGENOMICS

Berlin Olek A, Piepenbrock C,

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 294144; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PRA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a

Score 7.8; DB 1; Length 12; Pred. No. 6.8e+02;

35.5%;

Best Local Similarity

Query Match

Seguence 12 BP; 0 A; 2 C; 2 G; 8 T; 0 U; 0 Other;

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Best Local Similarity
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                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                              Oligonucleotide primer SEQ ID NO 294752 for detecting SNP TSC0016258.
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9; Conservative
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                     733 GAGAAACAGAA
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                                                   SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonucleotide primer SEQ ID NO 321146 for detecting SNP TSC0030082
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81.8%; Pred, No. 6.8e+02;
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Matches 9; Conservative
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                         Claim 1; SEQ ID NO 322055; 29pp + Sequence Listing; German.
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Matches 9, Conserv
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ABH72736
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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81.8%;
                               06-APR-2001; 2001WO-IB000713
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Gaps

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h Similarity 81.8%; Score 7.8; DB 1; Length 12; Similarity 81.8%; Pred. No. 6.8e+02; 9; Conservative 0; Mismatches 2; Indels

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE09989, ABE00010-ABE99989, ABE00010-ABE99989, ABE00010-ABE99989 and ABE00010-ABE9073 represent the oligomers described in the invention. NOTE: The sequence
                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                            Oligonucleotide primer SEQ ID NO 272721 for detecting SNP TSC0002916.
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ABH72736 standard; DNA; 12 BP.
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                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                      (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        methylation status.
                                                                                                                                                                                                                                                                 WO200177384-A2
                                                                          22-FEB-2002
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                                      ABH72736;
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Berlin K;

BP.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                              Oligonucleotide primer SEQ ID NO 273265 for detecting SNP TSC0003118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine
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ftp.wipo.int/pub/published_pct_sequences
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                                                                      ABH73280 standard; DNA; 12
                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
the printed specification, but
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                                                                                                       35.5%; Score 7.8; DB 1; Length 12; llarity 81.8%; Pred. No. 6.8e+02; Conservative 0; Mismatches 2; Indels
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                                                                      Sequence 12 BP; 7 A; 0 C; 5 G; 0 T; 0 U; 0 Other;
data for this patent did not form part of the pars obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Best Local Similarity 81.8
Matches 9; Conservative
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Berlin K;

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                                                                      Gaps
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                                    Length 12;
                                Query Match 35.5%; Score 7.8; DB 1; Length 12
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
Sequence 12 BP; 1 A; 0 C; 4 G; 7 T; 0 U; 0 Other;
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11 AAAAACAAAAC 1

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99899, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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Matches 9; Conservative C
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                                                        Piepenbrock C,
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(EPIG-) EPIGENOMICS AG
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                                                        olek A,
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peptide nucleic acid, cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 6.8e+02;
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Best Local Similarity
Matches 9; Conserv
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DT 22-FEB-7

DF 22-FEB-7

XX SNP, sin

KW Peptide

KW Central

XX SNP, sin

KW PORT-3

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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides and land and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory. Central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF0010-ABR9989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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81.8%; Pred. No. 6.8e+02;
iive 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Best Local Similarity 81.8%; Pred. No. 6.8e+02;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, aradiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 tapeses this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                              SND; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, azdiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at the printed specification, but typ.wipo.int/pub/published\_pct\_sequences

of oligonucleotides, useful for diagnosis and cell typing, is igned to detect single-nucleotide polymorphisms and cytosine

Berlin K;

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olek A,

WPI; 2001-657177/75.

methylation status.

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06-APR-2001; 2001WO-IB000713.

WO200177384-A2

18-OCT-2001

07-APR-2000; 2000DE-01019173.

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Claim 1; SEQ ID NO 275736; 29pp + Sequence Listing; German.

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

Oligonucleotide primer SEQ ID NO 275736 for detecting SNP TSC0003981.

ABH75743 standard; DNA; 12 BP

RESULT 1168

22-FEB-2002 (first entry)

ABH75743;

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35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; Artive 0; Mismatches 2; Indels

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                                                                                                                               This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC001016-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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oligomers are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99999 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
                                                                                                                                     Sequence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
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Oligonucleotide primer SEQ ID NO 306291 for detecting SNP TSC0021928
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                                                                                                                                                                                                                                                                              methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABE99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but fer wipo int/pub/published_pct_sequences
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                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ABI29661 standard; DNA; 12
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Best Local Similarity 81.8
Matches 9; Conservative
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   736 AAACAGAACAC 746
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                         AAACGTAACAC 11
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA). Oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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Best Local Similarity 81.87
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                   Olek A, Piepenbrock C,
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            (EPIG-) EPIGENOMICS AG.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically prereated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
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Claim 1; SEQ ID NO 282661; 29pp + Sequence Listing; German.
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ABI37377 standard; DNA; 12 BP.
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RESULT 1178
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                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                        Oligonucleotide primer SEQ ID NO 337350 for detecting SNP TSC0039831.
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ID AB113567 standard, DNA, 12 BP.
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AC AB113567;
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C Oligonucleotide primer SEQ ID NO
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KW SNP; single nucleotide polymorph
KW peptide nucleic acid; cytosine m
KW central nervous system; gastroin
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC091999, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF0010-ABF99889, ABH0010-ABH99989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                       uer or oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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Sequence 12 BP; 0 A; 1 C; 1 G; 10 T; 0 U; 0 Other;

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

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oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligoners are also used for detecting cell type differentiation. ABC00010-ABC9989, ABC0010-ABF9989, ABH0010-ABH99989 and ABI0010-ABI82073 represent the oligoners described in the invention. NoTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 315089 for detecting SNP TSC0026713 Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine Claim 1; SEQ ID NO 315089; 29pp + Sequence Listing; German. / Match 12; Score 7.8; DB 1; Length 12; Local Similarity 81.8%; Pred. No. 6.8e+02; les 9; Conservative 0; Mismatches 2; Indels Sequence 12 BP; 2 A; 3 C; 0 G; 7 T; 0 U; 0 Other; ftp.wipo.int/pub/published\_pct\_sequences Berlin K; ABI15116 standard, DNA; 12 BP. 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173 (first entry) 731 AGGAGAAACAG 741 Olek A, Piepenbrock C, Н (EPIG-) EPIGENOMICS AG 11 AAGAGAAATAG WPI; 2001-657177/75 designed to detect methylation status. WO200177384-A2. Homo sapiens 22-FEB-2002 18-OCT-2001 ABI15116; Query Match RESULT 1182 Matches ABIIBII6/
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Best Local Similarity 81.6
Matches 9; Conservative
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                            Best Local Similarity 81.8
Matches 9, Conservative
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073 topseen the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                  Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                         Berlin K;
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                                             06-APR-2001, 2001WO-IB000713.
                                                                                           07-APR-2000; 2000DE-01019173.
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Local Similarity 81.8%;
nes 9; Conservative C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                               Oligonucleotide primer SEQ ID NO 350123 for detecting SNP TSC0046517.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
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designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                           SEQ ID NO 354059; 29pp + Sequence Listing; German
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represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                      SNP, single nucleotide polymorphism, human, diagnosis, PNA, cancer; CNS, peptide nucleic acid; cytosine methylation, cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                          Oligonucleotide primer SEQ ID NO 372475 for detecting SNP TSC0059414.
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ftp.wipo.int/pub/published_pct_sequences
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Best Local Similarity 81.00,
Best Local Similarity 61.00,
                                                        ABI72502 standard; DNA; 12
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SNF; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                      Homo sapiens.
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                                                                                                                                                                                         Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 375427; 29pp + Sequence Listing; German.
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                                                                                           Berlin K;
                                                                                        Piepenbrock C,
                                  (EPIG-) EPIGENOMICS AG
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Gaps
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35.5%; Score 7.8; DB 1; Length 12; ilarity 81.8%; Pred. No. 6.8e+02; Conservative 0; Mismatches 2; Indels
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Matches 9, Conserv
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ABI75528 standard; DNA; 12
                                                                          (first entry)
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SNP, single nucleotide polymorphism, human, diagnosis, PNA, cancer, CNS, peptide nucleic acid, cytosine methylation, cardiovascular, primer; ss, central nervous system; gastrointestinal; respiratory, immune; metabolic. Oligonucleotide primer SEQ ID NO 375501 for detecting SNP TSC0061294

WO200177384-A2

07-APR-2000; 2000DE-01019173

Olek A, Piepenbrock C,

Berlin K;

WPI; 2001-657177/75

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF99899, ABH00010-ABF99899 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published\_pct\_sequences

Set of oligonucleotides, useful for diagnosis and cell typing, addesigned to detect single-nucleotide polymorphisms and cytosine

Berlin K;

Piepenbrock C,

olek A,

WPI; 2001-657177/75

methylation status.

(EPIG-) EPIGENOMICS

Claim 1; SEQ ID NO 362480; 29pp + Sequence Listing; German

oligonucleotides, useful for diagnosis and cell typing, is to detect single-nucleotide polymorphisms and cytosine methylation status. Set of oldesigned

Claim 1; SEQ ID NO 375501; 29pp + Sequence Listing; German.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but two, int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ABI62507 standard; DNA; 12 BP.
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(first entry)

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic discorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABE9989, ABF00010-ABE9989, ABF00010-ABE9989, ABF00010-ABE9989, and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WFPO at
                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                             Oligonucleotide primer SEQ ID NO 365840 for detecting SNP TSC0055386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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ABI65867 standard; DNA; 12 BP
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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 Sequence 12 BP; 0 A; 0 C; 3 G; 9 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                               ABI77328 standard; DNA; 12
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                                                                                                                                                 12 AAAAAAACACC 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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Berlin K;

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                                Gaps
                                                                                                                                                                                                                                                              Oligonucleotide primer SEQ ID NO 366047 for detecting SNP TSC0055502
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35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                       ABI66074 standard; DNA; 12 BP.
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                                                             736 AAACAGAACAC 746
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9; Conservative 737 AACAGAACACC 747

Matches

AACAAACCACC 12

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RESULT 1195 ABI65867/c

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ABH93366 standard; DNA; 12 BP
                        06-APR-2001; 2001WO-IB000713.
                                   37-APR-2000; 2000DE-01019173.
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                                                      Piepenbrock C,
                                                                                                                                                                                                                 ATAAACAAAAC 11
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                                            (EPIG-) EPIGENOMICS AG
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                                                                 WPI; 2001-657177/75
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              18-OCT-2001
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                                                      olek A,
                                                                                                                                                                                                                                 RESULT 1197
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABR00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide primer SEQ ID NO 268661 for detecting SNP TSC0001286.
                          designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                 Claim 1; SEQ ID NO 293359; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12 BP; 1 A; 0 C; 3 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
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Best Local Similarity 81.5-
Best Local 9; Conservative
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WPI; 2001-657177/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABF99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                     set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                   Berlin K;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNN) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory,

Berlin K,

Claim 1; SEQ ID NO 268661; 29pp + Sequence Listing; German

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Gaps

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737 AACAGAACACC 747

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RESULT 1200
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central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABCO0010 -ABC99989, ABF00010.ABF9989, ABF00010.ABF9989, ABF00010.ABF9989, ABF00010.ABF9989, ABF00010.ABF9989, ABF00010.ABF9989, ABF00010.ABF9989, ABF00010.ABF9989, CAPPERSENT THE SEQUENCE AREA for this parent did not form part of the printed specification, but was obtained in electronic format from WIFO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide primer SEQ ID NO 321437 for detecting SNP TSC0030239.
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                                                                                                                                             / Match 35.5%; Score 7.8; DB 1; Length 12; Local Similarity 81.8%; Pred. No. 6.8e+02; les 9; Conservative 0; Mismatches 2; Indels
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                                                                                                                   Seguence 12 BP; 8 A; 4 C; 0 G; 0 T; 0 U; 0 Other;
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Best Local Similarity
Matches 9; Conservat
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                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                    RESULT 1199
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                Oligonucleotide primer SEQ ID NO 322110 for detecting SNP TSC0030668
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ABI22137 standard; DNA; 12
                                                                                                                                   (first entry)
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Best Local Similarity 81.8
Matches 9; Conservative
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                                                                     ABI22137;
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Berlin K;

Piepenbrock C,

olek A,

(EPIG-) EPIGENOMICS

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173.

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
          Oligonucleotide primer SEQ ID NO 323079 for detecting SNP TSC0031211.
                                                                                                                                                                                                                                                  ligonucleotides, useful for diagnosis and cell typing, is to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 323079; 29pp + Sequence Listing; German.
                                                                                                                                        06-APR-2001; 2001WO-IB000713.
                                                                                                                                                               07-APR-2000; 2000DE-01019173
                                                                                                                                                                                                                                                   Set of oligonucleotides,
                                                                                                                                                                                                        Piepenbrock C,
                                                                                                                                                                                    (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                             WPI; 2001-657177/75
                                                                                                                                                                                                                                                                        methylation status.
                                                                                             WO200177384-A2
                                                                            Homo sapiens
                                                                                                                    18-OCT-2001
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 +ABC9989, ABF00010-ABF9989, ABF00010-ABF9989 and ABI00010-ABF8073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published\_pct\_sequences

35.5%; Score 7.8; DB 1; Length 12; Conservative 0: Mismatches Sequence 12 BP; 7 A; 4 C; 1 G; 0 T; 0 U; 0 Other; Query Match Best Local Similarity o,

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ABH98694;

Oligonucleotide primer SEQ ID NO 298687 for detecting SNP TSC0018236.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

18-OCT-2001

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734 AGAAACAGAAC 744 AAAAACCGAAC 12

ABH98694 standard; DNA; 12 BP 22-FEB-2002 (first entry) RESULT 12( ABH98694/c 

ó This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE9989, ABF0010-ABE9989, ABF0010-ABE9989, ABF0010-ABE9989, and ABI0010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but twipo.int/pub/published\_pct\_sequences Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status. . 0 Claim 1; SEQ ID NO 298687; 29pp + Sequence Listing; German. 35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; ative 0; Mismatches 2; Indels Sequence 12 BP; 1 A; 0 C; 3 G; B T; 0 U; 0 Other; Conservative 736 AAACAGAACAC 746 WPI; 2001-657177/75. Local Similarity es 9; Conserv Query Match Matches . 염

11 AAAAACAACAC 1

ABH75214 standard; DNA; 12 BP

22-FEB-2002 (first entry) ABH75214;

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Gaps

Oligonucleotide primer SEQ ID NO 275205 for detecting SNP TSC0003823.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2

18-OCT-2001

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG.

Berlin K; Piepenbrock C, olek A,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

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Gaps

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734 AGAAACAGAAC 744

1 ATAAACAAAAC 11

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Ouery Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels
                               Sequence 12 BP; 8 A; 2 C; 0 G; 2 T; 0 U; 0 Other;
was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                          This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers ealso used for detecting cell type differentiation. ABC0010-ABC99889, ABC0010-ABR99989, ABC0010-ABR99989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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         Claim 1; SEQ ID NO 275205; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                   35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02;
                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                              Sequence 12 BP; 1 A; 0 C; 2 G; 9 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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Best Local Similarity 81.5-
Best Local 9; Conservative
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                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                  Oligonucleotide primer SEQ ID NO 306360 for detecting SNP TSC0021973.
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cytosine
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                                                            ABI06387 standard; DNA; 12
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Best Local Similarity 81.6-
Best Local Similarity
Conservative
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RESULT 1205
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(EPIG-) EPIGENOMICS AG
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                        Homo sapiens.
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                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                         Oligonucleotide primer SEQ ID NO 306536 for detecting SNP TSC0022068.
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                                    ABI06563 standard; DNA; 12
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ABI08091 standard; DNA; 12
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Best Local Similarity 81.8
Matches 9; Conservative
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                                                            ABI06563
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       RESULT 1207
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central nervous system; gastrointestinal; respiratory; immune; metabolic
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretracted genomic DNN. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABH82073 tepseson the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide primer SEQ ID NO 337796 for detecting SNP TSC0040079.
                                                                   designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                         Claim 1; SEQ ID NO 333900; 29pp + Sequence Listing; German.
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35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12 BP; 7 A; 5 C; 0 G; 0 T; 0 U; 0 Other;
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                Berlin K;
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               Piepenbrock C,
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                                             WPI; 2001-657177/75
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and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF0010-ABF9989, ABF0010-ABF99989, ABF0010-ABF99989 and ABI0010-ABF9973 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but two obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABF9989 and ABI00010-ABF82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                    Score 7.8; DB 1; Length 12; Pred. No. 6.8e+02;
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Best Local Similarity 81.8%;
Matches 9; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (FNA) oligomers for detecting single nucleotide polymorphisms (SNP)

Set of oligonuclectides, useful for diagnosis and cell typing, idesigned to detect single-nuclectide polymorphisms and cytosine methylation status.

Berlin K;

Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Claim 1; SEQ ID NO 337796; 29pp + Sequence Listing, German.

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically prefreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF99989, ABH00010-ABF99989, ABH00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at this point/pub/published_pot_sequences
                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                             Oligonucleotide primer SEQ ID NO 340006 for detecting SNP TSC0041301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                set or oligonucleotides, useful for diagnosis and cell typing, i
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
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Local Similarity 91.8-
Local Similarity 1.8-
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                              ABI40033;
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Pred. No. 6.8e+02;
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Query Match
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                         Oligonucleotide primer SEQ ID NO 340992 for detecting SNP TSC0041786.
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                                                                               ABI41019 standard; DNA; 12
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WO200177384-A2.

ABI40033 standard; DNA; 12 BP.

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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomers for detecting single nucleotides of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABF82073 data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but fit wipo.int/pub/published_pct_sequences
                                                                                                                               This invention describes novel oligonucleotide primers or peptide nucleic
      Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                       Claim 1; SEQ ID NO 342017; 29pp + Sequence Listing; German
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                                                            06-APR-2001; 2001WO-IB000713.
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2; Indels

35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABCO0010
                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                         Oligonucleotide primer SEQ ID NO 343331 for detecting SNP TSC0043003.
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Berlin K;

Olek A, Piepenbrock C,

WPI; 2001-657177/75.

(EPIG-) EPIGENOMICS AG

07-APR-2000; 2000DE-01019173. 06-APR-2001; 2001WO-IB000713

WO200177384-A2.

18-OCT-2001.

Oligonucleotide primer SEQ ID NO 342017 for detecting SNP TSC0042333.

(first entry)

22-FEB-2002

ABI42044;

ABI42044 standard; DNA; 12 BP.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, the ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide primer SEQ ID NO 348458 for detecting SNP TSC0045601.
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                                                                                                                                                      35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; vative 0; Mismatches 2; Indels
                                                                                                                  Seguence 12 BP; 7 A; 4 C; 0 G; 1 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                  ABI48485 standard; DNA; 12
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC09989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABI82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                                                 SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                  Oligonucleotide primer SEQ ID NO 348716 for detecting SNP TSC0045718.
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                                  ABI48743 standard; DNA; 12
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Oligonucleotide primer SEQ ID NO 356734 for detecting SNP TSC0050284.

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Gaps

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35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; ative 0; Mismatches 2; Indels

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic formmat from WIPO at
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                                                                                                                                             set or oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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07-APR-2000; 2000DE-01019173.
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             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC09089, ABF00010-ABF99089, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
           This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH0010-ABF99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
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ABI62103 standard; DNA; 12 BP.
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                                                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                             35.5%; Score 7.8; DB 1; Length 12; llarity 81.8%; Pred, No. 6.8e+02; Conservative 0; Mismatches 2; Indels
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Sequence 12 BP; 1 A; 0 C; 4 G; 7 T; 0 U; 0 Other;
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81.8%;
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Matches 9; Conservative
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RESULT 1223

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Homo sapiens.
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                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                         Oligonucleotide primer SEQ ID NO 317789 for detecting SNP TSC0028274.
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ftp.wipo.int/pub/published_pct_sequences
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BP.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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81.8%;
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Matches 9; Conservative
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WO200177384-A2.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a
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range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE09989, ABE00010-ABE99989, ABE00010-ABE99989, ABE00010-ABE99989, ABE00010-ABE99989, ABE00010-ABE99989 and ABI00010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic formm part of the printed specification, but the wipo.int/pub/published_pct_sequences
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                                                                                  oet or oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF9989, ABH00010-ABH99999 and ABI00010-ABI82073 trepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
                                                                                                                                   SNP, single nucleotide polymorphism; human; diagnosis; PNA, cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                Oligonucleotide primer SEQ ID NO 273915 for detecting SNP TSC0003360.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               designed to detect methylation status.
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Score 7.8; DB 1; Length Pred. No. 6.8e+02;

35.5%; 81.8%;

Query Match Best Local Similarity

Sequence 12 BP; 6 A; 4 C; 1 G; 1 T; 0 U; 0 Other;

Matches

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF3073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                               Oligonucleotide primer SEQ ID NO 275099 for detecting SNP TSC0003783
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  22-FEB-2002 (first entry)
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Best Local Similarity 81...
Pest Local 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Olek A, Piepenbrock C,
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                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                      Oligonucleotide primer SEQ ID NO 323965 for detecting SNP TSC0031691.
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Mismatches
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les 9; Conservative
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                                                                                     2 CCACGATAAAC 12
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABC0010-ABF9989, ABH0010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from NIPO at
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                                 06-APR-2001; 2001WO-IB000713.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic discorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE099899, ABF00010-ABE99989, ABR00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence
                                                                This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI22073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                    Claim 1; SEQ ID NO 276855; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                   1 35.5%; Score 7.8; DB 1; Length 12; Similarity 81.8%; Pred. No. 6.8e+02; 9; Conservative 0; Mismatches 2; Indels
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                                                                  Sequence 12 BP; 9 A; 3 C; 0 G; 0 T; 0 U; 0 Other;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI32073 tepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                         Oligonucleotide primer SEQ ID NO 333587 for detecting SNP TSC0037618
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ABI33614 standard; DNA; 12 BP.
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from NIPO at
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                                                                                                               Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                  Claim 1; SEQ ID NO 335839; 29pp + Sequence Listing; German.
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                                     Piepenbrock C,
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  peptide nucleic acid, cytosine methylation, cardiovascular; primer; ss; central nervous system; gastrointestinal, respiratory; immune; metabolic.
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The ABC99989, ABF0010-ABE9999, ABF0010-ABP9999, ABF0010-ABP99999, ABF0010-ABP9999, ABF0010-ABP99999, ABF0010-ABP99999, ABF0010-ABP99999, ABF0010-ABP99999, ABF0010-ABP99999, ABF0010-ABP99999, ABF0010-ABP99999, ABF0010-ABP99999, ABF0010-ABP99999, ABF0010-ABP999999, ABF0010-ABP99999, ABF0010-ABP99999, ABF0010-ABP99999, ABF0010-ABP99999, ABF0010-ABP99999, ABF0010-ABP99999, ABF0010-ABP999999, ABF0010-ABP99999, ABF0010-ABP999999, ABF0010-ABP99999, ABF0010-ABP99999, ABF0010-ABP99999, ABF0010-ABP99999, ABF0010-ABP99999, ABF0010-ABP99999, ABF0010-ABP999999, ABF0010-ABP99999, ABF0010-ABP99999, ABF0010-ABP99999, ABF0010-ABP99999, ABF0010-ABP99999, ABF0010-ABP99999, ABF0010-ABP999999, ABF0010-ABP99999, A
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AC ABI3825
XX ABI3825
XX ABI3825
XX ABI3825
XX ABI3626
XX SNP; S:
KW PEPLIGE
XX HOMO S:
XX CICTOR
XX SEQUEI
XX SEQUEI
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Sequence 12 BP; 2 A; 0 C; 3 G; 7 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                  Gaps
                                                                                                                                                                                                                                                                                        Oligonucleotide primer SEQ ID NO 289917 for detecting SNP TSC0014148
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 Length 12;
                                2; Indels
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Score 7.8; DB 1;
Pred. No. 6.8e+02;
                                0; Mismatches
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35.5%;
81.8%;
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                                                                                                                                                                                                                                                       (first entry)
            Best Local Similarity 81.8 Matches 9; Conservative
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                                                                736 AAACAGAACAC 746
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Berlin K;

Piepenbrock C,

olek A,

WPI; 2001-657177/75

06-APR-2001; 2001WO-IB000713.

WO200177384-A2.

18-OCT-2001

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide primer SEQ ID NO 316470 for detecting SNP TSC0027461.
                                                                                Oligonucleotide primer SEQ ID NO 315650 for detecting SNP TSC0027020.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                     (EPIG-) EPIGENOMICS AG
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Best Local Similarity
9; Conserv?
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peptide nucl
                                                  22-FEB-2002
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              ABI15677;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABF00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
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Best Local Similarity 81.8
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 AACAAAAACC 1
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Gaps

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WPI; 2001-657177/75

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligoners for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligoners are also used for detecting cell type differentiation. ABC0010-ABE99989, ABF00010-ABE99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status. Claim 1; SEQ ID NO 348054; 29pp + Sequence Listing; German ftp.wipo.int/pub/published\_pct\_sequences 

Sequence 12 BP; 6 A; 6 C; 0 G; 0 T; 0 U; 0 Other;

ô 0; Gaps 35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; cive 0; Mismatches 2; Indels Local Similarity 81.8 Query Match

737 AACAGAACACC 747 1 AACACACCACC 11 셤

ABI50311 standard; DNA; 12 RESULT 1243 ABIS 0311
ABIS 0311
ABIS 0311
ABIS 0311
ABIS 04
ABIS 04
ABIS 05
ABIS 0

(first entry) 22-FEB-2002 ABI50311;

Oligonucleotide primer SEQ ID NO 350284 for detecting SNP TSC0046584.

SNP, single nucleotide polymorphism, human, diagnosis, PNA, cancer, CNS, peptide nucleic acid; cytosine methylation, cardiovascular, primer; ss, central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 350284; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The

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oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99889, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Sequence 12 BP; 9 A; 2 C; 1 G; 0 T; 0 U; 0 Other;

Gaps . 0 Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels

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RESULT 1244

ABI51092

ABI51092 standard; DNA; 12 BP.

ABI51092;

22-FEB-2002 (first entry)

Oligonucleotide primer SEQ ID NO 351065 for detecting SNP TSC0047060.

SNP; single mucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens.

WO200177384-A2

18-OCT-2001.

06-APR-2001; 2001WO-IB000713

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 351065; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE09989, ABF00010-ABE99989, ABH00010-ABE99989 and ABI00010-ABE3073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at 

Seguence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other;

Gaps .. 0 35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; cive 0; Mismatches 2; Indels Best Local Similarity 81.8 Matches 9; Conservative Query Match

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Homo sapiens

ABI53202;

RESULT 1245

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99989, ABH00010-ABF99989, and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonucleotide primer SEQ ID NO 357031 for detecting SNP TSC0050442.
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ABI72935 standard; DNA; 12 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE9989, ABF00010-ABE9989, ABF00010-ABE9989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                             Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The coligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99899 and ABT00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from NIPO at
                              This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Claim 1; SEQ ID NO 292395; 29pp + Sequence Listing; German.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE99989, ABF00010-ABE99989, ABH00010-ABE99989, and ABI00010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide primer SEQ ID NO 268523 for detecting SNP TSC0001198.
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                                                                   35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; cive 0; Mismatches 2; Indels
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Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
                                     Sequence 12 BP; 1 A; 1 C; 2 G; 8 T; 0 U; 0 Other;
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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclocides are used for disquosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory. Central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABC0010-ABE9989, ABH0010-ABH99989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes novel oligonuclectide primers or peptide nucleic
                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                       Oligonucleotide primer SEQ ID NO 270546 for detecting SNP TSC0002178.
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ABH70569 standard; DNA; 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 271378; 29pp + Sequence Listing; German.
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                                                                                                                                                                Berlin K;
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Best Local Similarity 81.0
For 9, Conservative
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            Homo sapiens.
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                                                                                 Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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Olek A, Piepenbrock C,
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                          range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting call type differentiation. ABC00010-ABC09989, ABF00010-ABF99889, ABF00010-ABH99989 and ABI0010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from MIPO at the printed specification, but the wipo.int/pub/published_pct_sequences
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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used for diagnosis and/or
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Best Local Similarity 81.8%;
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35.5%; Score 7.8; DB 1; Length 12;

Query Match

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                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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81.8%; Pred. No. 6.8e+02;
tive 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Berlin K;
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                  9; Conservative
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                                                     732 GGAGAAACAGA
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but two, wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                               Jet or oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 275096; 29pp + Sequence Listing; German
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligoners are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABF82073 represent the oligoners described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                       Oligonucleotide primer SEQ ID NO 274505 for detecting SNP TSC0003574.
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ABH75109 standard; DNA; 12
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                     Oligonucleotide primer SEQ ID NO 301070 for detecting SNP TSC0019335.
                                                                                                                                                                                                                                                                                        Set of oligonucleotides, useful for diagnosis and cell typing, is
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methylation status
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                                                                  Homo sapiens
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                                                  ABI01648;
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                                                                                    Olek A,
                                            RESULT 1260
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represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                  This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                              Claim 1; SEQ ID NO 301070; 29pp + Sequence Listing; German
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Local Similarity 81.8%; Pred. No. 6.8e+02;
les 9; Conservative 0; Mismatches 2;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF0010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent din out form part of the printed specification, but was obtained in electronic format from MIPO at
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                                                          Query Match
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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Sequence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
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Matches 9; Conservative
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                                                  Homo sapiens
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                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                     Oligonucleotide primer SEQ ID NO 328638 for detecting SNP TSC0034432.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 328638; 29pp + Sequence Listing; German.
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                                                             ABI28665 standard; DNA; 12
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                                                                                     ABI28665;
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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Best Local Similarity 81.8%;
Matches 9; Conservative (
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06-APR-2001; 2001WO-IB000713
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ABIO7748/C

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, asrdowascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form art of the printed specification, but was obtained in.electronic format from WIPO at
                                                                                                                                      Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 306361; 29pp + Sequence Listing; German.
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                                                                 Berlin K;
                                                              Piepenbrock C,
                       (EPIG-) EPIGENOMICS AG
                                                                                                           WPI; 2001-657177/75
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Score 7.8; DB 1; Length 12;
Pred. No. 6.8e+02;
0; Mismatches 2; Indels
   h 35.5%;
Similarity 81.8%;
9; Conservative C
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   Query Match
Best Local Similarity
Matches 9; Conserv
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Oligonucleotide primer SEQ ID NO 307721 for detecting SNP TSC0022653. ABI07748 standard; DNA; 12 BP. (first entry) 22-FEB-2002 ABI07748

SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2.

18-OCT-2001.

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG

Berlin K; Piepenbrock C, olek A,

WPI; 2001-657177/75

This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 307721; 29pp + Sequence Listing; German.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABF99989, ABH00010-ABH99899 and ABI00010-ABI32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ID ABI08342
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically prereated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 ABC9989, ABF00010 ABF99899, ABH00010 ABH99989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                               Oligonucleotide primer SEQ ID NO 335676 for detecting SNP TSC0038955.
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     ABI35703 standard; DNA; 12 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                               Length 12;
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Pred. No. 6.8e+02;
0; Mismatches 2;
Sequence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
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                                          Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
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Matches 9; Conservative
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Berlin K;

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                                      Gaps
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Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels
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Gaps

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737 AACAGAACACC 747

12 AAAATAACACC

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RESULT 1268 ABI35703

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Berlin K;

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Piepenbrock C, Berlin K;
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                        06-APR-2001; 2001WO-IB000713
                                  07-APR-2000; 2000DE-01019173
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                                                                                                                                                                                     Local Similarity 81.8
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                                                     Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                    (EPIG-) EPIGENOMICS AG
                                           (EPIG-) EPIGENOMICS
                                                                WPI; 2001-657177/75
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               18-OCT-2001
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35.5%; 81.8%;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide primer SEQ ID NO 314604 for detecting SNP TSC0026451.
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                                           Set of oligonucleotides, useful for diagnosis and cell typing, designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                  Claim 1; SEQ ID NO 311934; 29pp + Sequence Listing; German
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WPI; 2001-657177/75
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                                                                                                       methylation status.
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ABI14631/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, certral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00001-ABC09089, ABR00010-ABP9989, ABR0010-ABB182073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The cligomers are also used for detecting cell type differentiation. ABC0010-ABE99989, ABF00010-ABE99989 and ABI00010-ABE3073 tepresent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at fib. wipo.int/pub/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                       Oligonucleotide primer SEQ ID NO 350261 for detecting SNP TSC0046575.
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                                 ABI50288 standard; DNA; 12
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Matches 9, Conservative
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RESULT 1273
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                  ABI50288/
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22-FEB-2002 (first entry)

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35.5%; Score 7.8; DB 1; Length 12; llarity 81.8%; Pred. No. 6.8e+02; Conservative 0; Mismatches 2; Indels

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                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                   Oligonucleotide primer SEQ ID NO 352121 for detecting SNP TSC0047678.
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WO200177384-A2

18-OCT-2001.

Homo sapiens

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC09989, ABF0010-ABF99989, ABH0010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2
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                                                 This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but
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                   Claim 1; SEQ ID NO 373922; 29pp + Sequence Listing; German.
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central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                         Length 12;
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35.5%; Score 7.8; DB 1;
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2;
was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic
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                                                                                                                            Oligonucleotide primer SEQ ID NO 295102 for detecting SNP TSC0016434
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ABH95109 standard; DNA; 12 BP
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central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Matches 9; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                             Piepenbrock C,
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ABH72581;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oligonucleotide primer SEQ ID NO 296213 for detecting SNP ISC0016960.
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                                                                                              Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                              Claim 1; SEQ ID NO 321163; 29pp + Sequence Listing; German.
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                       Berlin K;
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Best Local Similarity
Matches 9; Conserva
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                   olek A,
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ABH96220/c
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

Claim 1; SEQ ID NO 296213; 29pp + Sequence Listing; German.

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and cytosine methylation status in chemically pretreated genomic DNA. The oligomicleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The cligomers are also used for detecting cell type differentiation. ABCC0010-ABC99899, ABF00010-ABF99899, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, Control of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but ftp.wipo.int/pub/published_pct_sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                              Length 12;
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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81.8%;
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Best Local Similarity 81.6-
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22-FEB-2002 (first entry)
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ABH97940;
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                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                        Gaps
                                                                                                                                                                                          Oligonucleotide primer SEQ ID NO 322725 for detecting SNP TSC0031029.
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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ilarity 81.8%;
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                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonucleotide primer SEQ ID NO 297933 for detecting SNP TSC0017835.
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8 g ABH97940 standard; DNA; 12 BP.

RESULT 1285 ABH97940/c ID ABH97941 XX

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                                                                                                                                       Olek A, Piepenbrock C,
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a rarge of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. Abconoto
                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                          Oligonucleotide primer SEQ ID NO 324263 for detecting SNP TSC0031917.
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    (first entry)
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22-FEB-2002
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Oligonucleotide primer SEQ ID NO 324193 for detecting SNP TSC0031856.

(first entry)

22-FEB-2002

ABI24220;

BP.

ABI24220 standard; DNA; 12

Berlin

Piepenbrock C,

Olek A,

WPI; 2001-657177/75.

07-APR-2000; 2000DE-01019173. 06-APR-2001; 2001WO-IB000713

WO200177384-A2.

18-OCT-2001

(EPIG-) EPIGENOMICS AG

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
Set of oligonuclectides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                             Claim 1; SEQ ID NO 324193; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                35.5%; Score 7.8; DB 1;
81.8%; Pred. No. 6.8e+02;
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Best Local Similarity 81.8%,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part to of the printed specification, but was obtained in electronic format from WIPO at the printed specification ftp.wipo.int/pub/published_pot_sequences
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                                                                                                                                                                                                                                                                                           35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; arive 0; Mismatches 2; Indels
                                                                                                                                                                                                                          Seguence 12 BP; 1 A; 0 C; 3 G; 8 T; 0 U; 0 Other;
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Best Local Similarity 81...
Best Local 9; Conservative
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                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                 Oligonucleotide primer SEQ ID NO 301731 for detecting SNP TSC0019628.
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RESULT 1290
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABF9989, ABF00010-ABF9989, ABF00010-ABF9989, ABF9989, ABF9989, ABF9989, ABF9989, ABF9989, ABF9989, ABF9989, ABF99989, ABF99989, ABF9999, ABF9999, ABF9999, ABF9999, ABF9999, ABF9999, ABF9999, ABF
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                                                             (EPIG-) EPIGENOMICS AG
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                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oycosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABC0010-ABE9989, ABR0010-ABH9989 and ABI00010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from MIPO at the printed specification, but typ.wipo.int/pub/published_pct_sequences
      This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC09989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide primer SEQ ID NO 278354 for detecting SNP TSC0005920.
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                                                                                                                                                                                                                                                                                                                        35.5%; Score 7.8; DB 1; Length 12; ilarity 81.8%; Pred. No. 6.8e+02; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                  Sequence 12 BP; 0 A; 5 C; 1 G; 6 T; 0 U; 0 Other;
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF99999, ABH00010-ABF99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                   35.5%; Score 7.8; DB 1; L
81.8%; Pred. No. 6.8e+02;
ative 0; Mismatches 2;
                     Sequence 12 BP; 2 A; 0 C; 3 G; 7 T; 0 U; 0 Other;
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Matches 9; Conserv
                                                                                          Query Match
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ABIO 55124/2

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RESULT 1296

Berlin K;

Olek A, Piepenbrock C,

WPI; 2001-657177/75

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06-APR-2001; 2001WO-IB000713 07-APR-2000; 2000DE-01019173

WO200177384-A2 Homo sapiens.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                 Oligonucleotide primer SEQ ID NO 331734 for detecting SNP TSC0036439.
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Best Local Similarity 81.8
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Best Local Similarity 81.8%,
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Berlin K;

Olek A, Piepenbrock C,

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ABH84458 standard; DNA; 12
                                                                          WO200177384-A2
                                                                       Homo sapiens
                                                           22-FEB-2002
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acid (PNA) oligomers for detecting single mucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC001010-ABR99989, ABR0010-ABR9989, ABR0010-ABR99899, ABR0010-ABR9989999, ABR0010-ABR99899999, ABR0010-ABR998999999, ABR0010-ABR99989, ABR0010-ABR99989, ABR0010-ABR99989, ABR0010-ABR99989, ABR0010-ABR99989, ABR0010-ABR99989, ABR0010-ABR999899, ABR0010-ABR99989, ABR0010-ABR99989, ABR0010-ABR99989, ABR0010-ABR99989, ABR0010-ABR99989, ABR0010-ABR99989, ABR0010-ABR99989999, ABR0010-ABR999899, ABR0010-ABR99989, ABR0010-ABR99989, ABR0010-ABR99989, ABR0010-ABR99989, ABR0010-ABR99989, ABR0010-ABR998999, ABR0010-ABR99989, ABR0010-ABR99989, ABR0010-ABR99989, ABR0010-ABR99989, ABR0010-ABR99989, ABR0010-ABR99989, ABR0010-ABR999899, ABR0010-ABR99989, ABR0010-ABR99989, ABR0010-ABR99989, ABR0010-ABR99989, ABR0010-ABR99989, ABR00010-ABR99989, ABR00010-ABR99989
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WPI; 2001-657177/75
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Gaps
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35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02;
                           2; Indels
                           0; Mismatches
                           9; Conservative
                                                     734 AGAAACAGAAC 744
                                                                                N
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             Local Similarity
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(first entry)

Oligonucleotide primer SEQ ID NO 284451 for detecting SNP TSC0011838

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG.

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 284451; 29pp + Sequence Listing; German.

acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a This invention describes novel oligonucleotide primers or peptide nucleic

35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02;

Best Local Similarity

Query Match

Sequence 12 BP; 7 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

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range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The coligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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22-FEB-2002 (first entry)
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                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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methylation status.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99899, ABF00010-ABE99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                             Claim 1; SEQ ID NO 290385; 29pp + Sequence Listing; German.
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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81.8%;
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Best Local Similarity 81.0.
Best Local 9, Conservative
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35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; ative 0; Mismatches 2; Indels

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                       Oligonucleotide primer SEQ ID NO 347885 for detecting SNP TSC0045323
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                                                               ABI47912 standard; DNA; 12
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AB147912
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                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide primer SEQ ID NO 344195 for detecting SNP TSC0043437.
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Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                           Query Match
35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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                                                               Sequence 12 BP; 1 A; 1 C; 2 G; 8 T; 0 U; 0 Other;
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ftp.wipo.int/pub/published_pct_sequences
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                                       This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting call type differentiation. ABC00010-ABC99889, ABF00010-ABH89989, ABF00010-ABH89989, ABF00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but typ.wipo.int/pub/published_pct_sequences
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Claim 1; SEQ ID NO 347885; 29pp + Sequence Listing; German.
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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acid, cytosine methylation; cardiovascular; primer; ss; system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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                                                                                             06-APR-2001; 2001WO-IB000713.
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Best Local Similarity 81.8%;
Matches 9; Conservative 0
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ABI50966 standard; DNA; 12
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peptide nucleic
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range of diseases including immune system, gastroinfestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABC0010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at the printed specification, but the wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes novel oligonucleotide primers or peptide nucleic acid (PRA) oligoners for detecting single nucletide polymorphisms (SNP) and cytosine methylation status in chemically pretreated general DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                    Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 350939; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12 BP; 0 A; 1 C; 3 G; 8 T; 0 U; 0 Other;
                                                                  Berlin K;
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Best Local Similarity 81.8
Matches 9; Conservative
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                                                               Piepenbrock C,
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(EPIG-) EPIGENOMICS AG
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                                                                  olek A,
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This invention describes novel oligonucleotide primers or peptide nucleic

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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide primer SEQ ID NO 355036 for detecting SNP TSC0000340.
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ABIS5063
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Sequence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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   Length 12;
Score 7.8; DB 1; Length 12
Pred. No. 6.8e+02;
); Mismatches 2; Indels
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81.8%;
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Best Local Similarity 81.8.
Since 9; Conservative
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      Query Match
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Matches
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XX ABI77
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99899, ABH0010-ABF99899 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPD at
                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                Oligonuclectide primer SEQ ID NO 371181 for detecting SNP TSC0058636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 371181; 29pp + Sequence Listing; German.
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                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         methylation status.
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                  ABI71208
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC90989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine

Berlin K;

(EPIG-) EPIGENOMICS AG Piepenbrock

WPI; 2001-657177/75.

olek A,

methylation status.

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173

WO200177384-A2

18-OCT-2001

Claim 1; SEQ ID NO 358169; 29pp + Sequence Listing; German.

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                       Oligonucleotide primer SEQ ID NO 358908 for detecting SNP TSC0051375.
                                                                                                                                                                                                                                                                                                                              Berlin K;
                                                        ABI58935 standard; DNA; 12 BP.
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Gaps

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WPI; 2001-657177/75

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

Oligonucleotide primer SEQ ID NO 358169 for detecting SNP TSC0050979.

ABI58196 standard; DNA; 12 BP.

735 GAAACAGAACA 745

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Matches

GAAACAATACA 2

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22-FEB-2002 (first entry)

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Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels

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Sequence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other;

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                                                                                                                         This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99999, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                  Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                          Claim 1; SEQ ID NO 358908; 29pp + Sequence Listing; German
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oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99889, ABH0010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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81.8%; Pred. No. 6.8e+02;
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llarity 81.8%;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonucleotide primer SEQ ID NO 320124 for detecting SNP TSC0029574.
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ABH75051; Query Match RESULT 1322 Matches 8 X C C C C C C C C C C C C X S 원 ਨੇ ô This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) eligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The eligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, entrain ervous system, cardiovascular and metabolic disorders. The eligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABF00010-ABF9989 and ABI0010-ABF82073 represent the eligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at SNP, single nucleotide polymorphism, human, diagnosis, PNA, cancer, CNS, peptide nucleic acid, cytosine methylation, cardiovascular, primer; ss; central nervous system; gastrointestinal, respiratory, immune; metabolic. Oligonucleotide primer SEQ ID NO 298260 for detecting SNP TSC0017996. Gaps Set of oligonuclectides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status. Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status. . 0 Claim 1; SEQ ID NO 271141; 29pp + Sequence Listing; German. Query Match
35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels Sequence 12 BP; 8 A; 4 C; 0 G; 0 T; 0 U; 0 Other; ftp.wipo.int/pub/published\_pct\_sequences Berlin K; Berlin K; ABH98267 standard; DNA; 12 BP. 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173. 07-APR-2000; 2000DE-01019173 (first entry) 736 AAACAGAACAC 746 Piepenbrock C, Olek A, Piepenbrock C, 1 AAACAACACAC 11 (EPIG-) EPIGENOMICS AG (EPIG-) EPIGENOMICS AG WPI; 2001-657177/75. WPI; 2001-657177/75 WO200177384-A2 Homo sapiens 22-FEB-2002 18-OCT-2001. ABH98267 Olek A, 

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published\_pct\_sequences SNP; single nuclectide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 275038 for detecting SNP TSC0003769. Gaps Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status. . 0 Claim 1; SEQ ID NO 298260; 29pp + Sequence Listing; German. Claim 1; SEQ ID NO 275038; 29pp + Sequence Listing; German. 35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; rive 0; Mismatches 2; Indels Seguence 12 BP; 7 A; 3 C; 0 G; 2 T; 0 U; 0 Other; Berlin K; BP. 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173 ABH75051 standard; DNA; 12 (first entry) 9; Conservative 737 AACAGAACACC 747 AACATAATACC 11 Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG WPI; 2001-657177/75. Best Local Similarity WO200177384-A2. Homo sapiens. 18-OCT-2001. 22-FEB-2002

Page 578

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo int/pub/published_pct_sequences
                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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designed to detect single-nucleotide polymorphisms and cytosine
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ABH76553 standard; DNA; 12 BP.
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                                                ABI01553 standard; DNA; 12
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Best Local Similarity 81.8
Matches 9; Conservative
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ABH76553/c
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                                                                                       Match 15; Score 7.8; DB 1; Length 12; Local Similarity 81.8%; Pred. No. 6.8e+02; es 9; Conservative 0; Mismatches 2; Indels
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                                                Sequence 12 BP; 1 A; 1 C; 2 G; 8 T; 0 U; 0 Other;
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Local 9, Conservative
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABF00010-ABF99899, ABH00010-ABH999999 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but two int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                               Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                    Claim 1; SEQ ID NO 276696; 29pp + Sequence Listing; German.
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Berlin K;
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Piepenbrock C,
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olek A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                            Oligonucleotide primer SEQ ID NO 309158 for detecting SNP TSC0023389.
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designed to detect single-nucleotide polymorphisms and cytosine
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Best Local Similarity 81...
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733 GAGAAACAGAA 743
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                                 12 GACAAACAAAA 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 methylation status.
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                                                                                                                                                            ABI09185;
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ID ABI0
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AC ABI0
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22-FEB-2002

18-OCT-2001

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WFPO at
                                                                                                                                                                                                                                                 Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 335745; 29pp + Sequence Listing; German.
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                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                              Oligonucleotide primer SEQ ID NO 309298 for detecting SNP TSC0023469.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Set of oligonuclectides, useful for diagnosis and cell designed to detect single-nucleotide polymorphisms and methylation status.
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                         (first entry)
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Best Local Similarity 81.0
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Gaps

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
Oligonucleotide primer SEQ ID NO 311185 for detecting SNP TSC0024345.
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WO200177384-A2

Homo sapiens.

22-FEB-2002

ABI35772;

RESULT 1331 ABI35772,

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99889, ABH00010-ABH99989 and ABI00010-ABH82073 are present the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
detect single-nucleotide polymorphisms and cytosine
                                                                         Claim 1; SEQ ID NO 311185; 29pp + Sequence Listing; German.
designed to detect methylation status.
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Sequence 12 BP; 0 A; 1 C; 3 G; 8 T; 0 U; 0 Other;

/ Match 35.5%; Score 7.8; DB 1; Length 12; Local Similarity 81.8%; Pred. No. 6.8e+02; tes 9; Conservative 0; Mismatches 2; Indels 736 AAACAGAACAC 746 AAACGAAACAC 1 11 ઠે d

ABI11567 standard; DNA; 12 BP ABI11567; 

22-FEB-2002 (first entry)

Oligonucleotide primer SEQ ID NO 311540 for detecting SNP TSC0024547.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2

18-OCT-2001

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173,

(EPIG-) EPIGENOMICS AG

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonuclectides, useful for diagnosis and cell typing, idesigned to detect single-nuclectide polymorphisms and cytosine methylation status. Claim 1; SEQ ID NO 311540; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, artdiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABF00010-ABF99989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABF82073

·; represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences Gaps ; Score 7.8; DB 1; Length 12; Pred. No. 6.8e+02; 0; Mismatches 2; Indels Sequence 12 BP; 2 A; 0 C; 4 G; 6 T; 0 U; 0 Other; 75.5%; Local Similarity 81.8%; Local Similarity 81.8%; Les 9; Conservative 736 AAACAGAACAC 746 11 AAACATAACCC 1 Query Match Best Local RESULT 1334 Matches 8 X G G G G ò g

ABI13745 standard; DNA; 12 BP.

ABI13745;

(first entry) 22-FEB-2002

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Oligonuclectide primer SEQ ID NO 313718 for detecting SNP TSC0025933.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2.

18-OCT-2001

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG

Berlin K; Piepenbrock C, olek A,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 313718; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences 

Sequence 12 BP; 0 A; 0 C; 5 G; 7 T; 0 U; 0 Other;

Gaps ö h 35.5%; Score 7.8; DB 1; Length 12; Similarity 81.8%; Pred. No. 6.8e+02; 9; Conservative 0; Mismatches 2; Indels Query Match Best Local Similarity Matches 9; Conserv

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                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                        Oligonucleotide primer SEQ ID NO 288923 for detecting SNP TSC0013731.
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                                                      ABH88930 standard; DNA; 12
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Matches 9; Conservative
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12 AAACACAACCC
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic discorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE99989, ABF00010-ABE99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence 12 BP; 0 A; 0 C; 3 G; 9 T; 0 U; 0 Other;
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Best Local Similarity 81.8%;
Matches 9; Conservative C
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                                                                                                               Berlin K;
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                                              (EPIG-) EPIGENOMICS AG.
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Score 7.8; DB 1; Length 12; Pred. No. 6.8e+02; 0; Mismatches 2; Indels

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PMA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                Oligonuclectide primer SEQ ID NO 347970 for detecting SNP TSC0045385.
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Claim 1; SEQ ID NO 347243; 29pp + Sequence Listing; German.

Berlin K;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically prereated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99899, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                         Oligonucleotide primer SEQ ID NO 372540 for detecting SNP TSC0059450.
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ABI72567 standard; DNA; 12 BP.
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                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                     Length 12;
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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Sequence 12 BP; 1 A; 0 C; 2 G; 9 T; 0 U; 0 Other;
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ABI72567/c
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 374499 for detecting SNP TSC0060741. AB174526
ID AB174526
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DE Oligonucleotide primer SEQ ID
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, aardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic formmat from WIPO at fire printed specification, but fire wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                            Set of oligonucleotides, useful for diagnosis and cell typing, addesigned to detect single-nucleotide polymorphisms and cytosine
                                                                                                                                 Claim 1; SEQ ID NO 268953; 29pp + Sequence Listing; German
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WPI; 2001-657177/75.
                                                                                         methylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically prefreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99899, ABF00010-ABE99899, ABF00010-ABE99899, ABF00010-ABE99899 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                    ligonucleotides, useful for diagnosis and cell typing, it o detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12 BP; 7 A; 4 C; 0 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                               Berlin K;
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                                                                                                              06-APR-2001; 2001WO-IB000713.
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Best Local Similarity 81.0
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                                                                                                                                                                                                                                                                                                                                                                                 methylation status.
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Set of

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory,
    typing, i
                                                                                                                                                                          Claim 1; SEQ ID NO 294352; 29pp + Sequence Listing; German.
oligonucleotides, useful for diagnosis and cell ed to detect single-nucleotide polymorphisms and
                                               designed to detect methylation status.
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Olek A, Piepenbrock C, Berlin K;

(EPIG-) EPIGENOMICS AG

06-APR-2001; 2001WO-IB000713 07-APR-2000; 2000DE-01019173

WO200177384-A2

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide primer SEQ ID NO 269723 for detecting SNP TSC0001860.
                                                                                                                                                                                        Gaps
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                                                                                                                                                         Length 12;
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81.8%; Pred. No. 6.8e+02;
tive 0; Mismatches 2; Indels
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE99989, ABF00010-ABE99989, ABH00010-ABE99989 and ABI00010-ABI32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but twipo.int/pub/published_pot_sequences
                                                                                                                                                      SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                           Oligonucleotide primer SEQ ID NO 270025 for detecting SNP TSC0001962.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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Best Local Similarity 81.8%;
Matches 9; Conservative
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                              ABH70048 standard; DNA; 12
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Berlin K;

Piepenbrock C,

olek A,

(EPIG-) EPIGENOMICS AG

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173.

Mon Oct 18 14:40:07 2004

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
          Oligonucleotide primer SEQ ID NO 295186 for detecting SNP TSC0016477.
                                                                                                                                                                                                                                                   Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 295186; 29pp + Sequence Listing; German.
                                                                                                                                          06-APR-2001; 2001WO-IB000713.
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                                                                                                                                                                                                           Piepenbrock C,
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Berlin K;

ô This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABR00010-ABE9989, ABR00010-ABE9989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from NIPO at Gaps õ 35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; ive 0; Mismatches 2; Indels Sequence 12 BP; 6 A; 5 C; 0 G; 1 T; 0 U; 0 Other; ftp.wipo.int/pub/published\_pct\_sequences Sest Local Similarity Query Match

9; Conservative 737 AACAGAACACC 747 Matches ò

1 AACAAAACCCC 11 Db

ABH97185 standard, DNA; 12 BP (first entry) 22-FEB-2002 ABH97185 RESULT 1348 ABH97185/c 

Oligonucleotide primer SEQ ID NO 297178 for detecting SNP TSC0017472.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2

18-OCT-2001.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                 Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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ftp.wipo.int/pub/published_pct_sequences
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                                                                                  This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                Claim 1; SEQ ID NO 297824; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; rive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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central nervous system; gastrointestinal; respiratory; immune; metabolic
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                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; SS; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                            Oligonucleotide primer SEQ ID NO 298300 for detecting SNP TSC0018015
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Pred. No. 6.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligonuclectide primer SEQ ID NO 274703 for detecting SNP TSC0003649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12 BP; 1 A; 0 C; 3 G; 8 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 737 AACAGAACACC 747
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12 AAAAAACACC 2
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretraeted genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010 ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formant from WIPO at Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine Claim 1; SEQ ID NO 274703; 29pp + Sequence Listing; German. methylation status.

Ϋ, Berlin

Olek A, Piepenbrock C,

WPI; 2001-657177/75.

(EPIG-) EPIGENOMICS

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173.

18-OCT-2001

Seguence 12 BP; 2 A; 4 C; 0 G; 6 T; 0 U; 0 Other;

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173.

WO200177384-A2

18-OCT-2001.

Homo sapiens

(EPIG-) EPIGENOMICS AG

Oligonuclectide primer SEQ ID NO 303263 for detecting SNP TSC0020412.

(first entry)

22-FEB-2002

ABI03290;

Page 592

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                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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           Score 7.8; DB 1; Length 12;
Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                Berlin K;
                                                                                                                                          ABI01737 standard; DNA; 12 BP.
           35.5%;
81.8%;
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                                                                                                                                                                                        22-FEB-2002 (first entry)
Query Match
Best Local Similarity 81.0.
Local 9; Conservative
                                                        732 GGAGAAACAGA 742
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                                                                                                                                                                                                                                                                                                                                                                                                         (EPIG-) EPIGENOMICS AG
                                                                                12 GGAGATAAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonuclectide primer SEQ ID NO 278680 for detecting SNP TSC0006264.
                                                                                                    Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                 Claim 1; SEQ ID NO 303263; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; tive 0; Mismatches 2; Indels
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  Berlin K;
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  Piepenbrock C,
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                                                      WPI; 2001-657177/75
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olek A,
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Matches
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WO200177384-A2

ABI03290 standard; DNA; 12 BP.

RESULT 1358 ABI03290/c ID ABI03290 XX

GAAAAACAAAA

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schultz1-727.rng

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                ligonuclectides, useful for diagnosis and cell typing, it detect single-nuclectide polymorphisms and cytosine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                  Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Berlin K;
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ABH79704 standard; DNA; 12 BP.
                                                                               07-APR-2000; 2000DE-01019173.
                                               06-APR-2001; 2001WO-IB000713
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                                                                                                                                                                                                                  Set of oligonucleotides,
                                                                                                                                                  Piepenbrock C,
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                                                                                                                 (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                  designed to detect
methylation status.
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                                                                                                                 This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073 targresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                    Match 35.5%; Score 7.8; DB 1; Length 12; Local Similarity 81.8%; Pred. No. 6.8e+02; see 9; Conservative 0; Mismatches 2; Indels
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                                                                                Claim 1; SEQ ID NO 279697; 29pp
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RESULT 1363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but fur wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data_for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification for the wipo.int/pub/published_pct_sequences
                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide primer SEQ ID NO 309200 for detecting SNP TSC0023411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Set of oligonuclectides, useful for diagnosis and cell typing, i
designed to detect single-nuclectide polymorphisms and cytosine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 309200; 29pp + Sequence Listing; German.
                                                                                                              35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; ive 0; Mismatches 2; Indels
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                                                                                    Seguence 12 BP; 8 A; 3 C; 1 G; 0 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                          ABI09227 standard; DNA; 12 BP.
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but two but wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                        Oligonucleotide primer SEQ ID NO 334498 for detecting SNP TSC0038193.
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designed to detect single-nucleotide polymorphisms and cytosine
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ABI34525 standard; DNA; 12 BP.
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ABH87869 standard; DNA; 12
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Conservative

Oligonucleotide primer SEQ ID NO 287862 for detecting SNP TSC0013282.

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schultz1-727.rng

07-APR-2000; 2000DE-01019173

ĸ, Berlin

Piepenbrock C,

Olek A,

WPI; 2001-657177/75

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Set of oligonuclectides, useful for diagnosis and cell typing, is designed to detect single-nuclectide polymorphisms and cytosine methylation status. Claim 1; SEQ ID NO 287862; 29pp + Sequence Listing; German. Berlin K; 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173. Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG WPI; 2001-657177/75. WO200177384-A2 18-OCT-2001 Homo

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metaboolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

0; Gaps Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels Sequence 12 BP; 1 A; 0 C; 6 G; 5 T; 0 U; 0 Other; 

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ABI13118 standard; DNA; 12 (first entry) ABI13118; RESULT 1365 

BP.

Oligonucleotide primer SEQ ID NO 313091 for detecting SNP TSC0025474.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

WO200177384-A2 Homo sapiens.

18-OCT-2001

06-APR-2001; 2001WO-IB000713

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989, ABH00010-ABE99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status. Claim 1; SEQ ID NO 313091; 29pp + Sequence Listing; German. 

Sequence 12 BP; 5 A; 7 C; 0 G; 0 T; 0 U; 0 Other;

Gaps ., Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels

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737 AACAGAACACC 747 1 AACCCAACACC 11 셤

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ABI53296 standard; DNA; 12 BP ABI53296; RESULT 1366
ARI53296
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AC ABI53296
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(first entry) 22-FEB-2002 Oligonucleotide primer SEQ ID NO 353269 for detecting SNP TSC0048413.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

W0200177384-A2

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG.

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 353269; 29pp + Sequence Listing; German

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Score 7.8; DB 1; Length 12; Pred, No. 6.8e+02; 0; Mismatches 2; Indels

Query Match 35.5%; Best Local Similarity 81.8%; Matches 9; Conservative

736 AAACAGAACAC 746

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11 AAACAAAACC 1

Sequence 12 BP; 1 A; 0 C; 4 G; 7 T; 0 U; 0 Other;

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo int/pub/published_pct_sequences
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81.8%;
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ABI53718/C
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ABI53718/C
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SNP; sin
KW POPLide
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invantion. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                       ABI54744 standard; DNA; 12
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RESULT 1136
AB1547447(
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11 GAGGAATAGAA

RESULT 1369

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNB) and oytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic discorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF99999, ABF00010-ABF99999, ABF00010-ABF99999 and ABI00010-ABF32073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but two obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 362148; 29pp + Sequence Listing; German.
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Pred. No..6.8e+02;
0; Mismatches 2; Indels
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Best Local Similarity 81.8%;
Matches 9; Conservative
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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                              Oligonucleotide primer SEQ ID NO 354911 for detecting SNP TSC0049361.
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35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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                        ABI54938 standard; DNA; 12 BP
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AB154938/c
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RESULT 1370

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                      Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 363052; 29pp + Sequence Listing;
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Matches 9; Conservative
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ВР.

Score 7.8; DB 1; Length 12; Pred. No. 6.8e+02; 0; Mismatches 2; Indels

35.5%;

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range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers as also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fire printed specification, but ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Length 12;

Score 7.8; DB 1; Pred. No. 6.8e+02;

35.5%;

Query Match Best Local Similarity

Berlin K;

Matches

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF9989, ABH0010-ABF9989 and ABI0010-ABI82073 the preparent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide primer SEQ ID NO 297286 for detecting SNP TSC0017504.
                                             Oligonucleotide primer SEQ ID NO 296894 for detecting SNP TSC0017337.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        set or oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 296894; 29pp + Sequence Listing, German.
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-rac 2; Indels
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22-FEB-2002 (first entry)
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Matches 9; Conservative
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                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                      Oligonucleotide primer SEQ ID NO 380436 for detecting SNP TSC0063822.
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Matches 9; Conservative
  9; Conservative
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                                          733 GAGAAACAGAA 743
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ABH96901/C ID ABH9690 XX AC ABH9690

RESULT 1375

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useful for diagnosis and cell typing, is

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but fire wipo int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                  designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 297286; 29pp + Sequence Listing; German.
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                06-APR-2001; 2001WO-IB000713
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Matches 9; Conservative
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                                                                    This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989, ABH00010-ABE99989 and ABI00010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP: single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                    Claim 1; SEQ ID NO 323067; 29pp + Sequence Listing; German.
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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methylation status.
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Best Local Similarity
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ABH99118
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Score 7.8; DB 1; Length 12; Pred. No. 6.8e+02; 0; Mismatches 2; Indels

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide primer SEQ ID NO 275389 for detecting SNP TSC0003880.
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                                                                                Seguence 12 BP; 6 A; 6 C; 0 G; 0 T; 0 U; 0 Other;
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                                                                                                                     Score 7.8; DB 1;
Pred. No. 6.8e+02;
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Best Local Similarity 81.8%;
Matches 9; Conservative
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Matches 9; Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12 BP; 7 A; 1 C; 2 G; 2 T; 0 U; 0 Other;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                 Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                   claim 1; SEQ ID NO 326225; 29pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12 BP; 0 A; 0 C; 5 G; 7 T; 0 U; 0 Other;
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(EPIG-) EPIGENOMICS AG
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                                                                                                                     designed to detect amethylation status.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
peptide nucleic acid, cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oligonucleotide primer SEQ ID NO 326225 for detecting SNP TSC0032964.
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nes 9; Conservative
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                                                     Homo sapiens.
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acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides eu used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory. central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABC0010-ABH99889 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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81.8%; Pred. No. 6.8e+02;
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Best Local Similarity 81.0
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 330600 for detecting SNP TSC0035613. 22-FEB-2002 (first entry) 

Homo sapiens.

WO200177384-A2

18-OCT-2001

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG.

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 330600; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99899, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 12 BP; 8 A; 2 C; 0 G; 2 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                            Oligonuclectide primer SEQ ID NO 285246 for detecting SNP TSC0012209.
                                      Gaps
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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Query Match
Best Local Similarity
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18-OCT-2001.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                               Oligonuclectide primer SEQ ID NO 310947 for detecting SNP TSC0024237.
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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                                                22-FEB-2002 (first entry)
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Best Local Similarity 81...
9, Conservative
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
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                                                            06-APR-2001; 2001WO-IB000713.
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Best Local Similarity 81.8
Matches 9; Conservative
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WPI; 2001-657177/75

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretracted genemic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF99889 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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                 Set of oligonucleotides, useful for diagnosis and cell typing, addesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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oligomers are also used for detecting cell type differentiation. ABC00010 -ABC99989, ABF00010-ABF9989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at fig. wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and oytosite methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic formmat from WIPO at fitted specification, but fitp.wipo.int/pub/published_pct_sequences
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                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Oligonucleotide primer SEQ ID NO 352289 for detecting SNP TSC0047796.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                              Berlin K;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, cantral nervous system, cardiovascular and merabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE99989, ABF00010-ABE99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPD at
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                      Oligonuclectide primer SEQ ID NO 364768 for detecting SNP TSC0054707.
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                                                 ABI64795 standard; DNA; 12
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RESULT 1397
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AB16,735

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                             Score 7.8; DB 1; Length 12;
Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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                                                 Sequence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
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81.8%;
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nes 9; Conservative
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Best Local Similarity
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                                                                                                      Query Match
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonucleotide primer SEQ ID NO 318029 for detecting SNP TSC0028403

736 AAACAGAACAC 746

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AAACACAACTC 12

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ ID NO 318617 for detecting SNP TSC0028770. oligonucleotides, useful for diagnosis and cell typing, is to detect single-nucleotide polymorphisms and cytosine . 0 Claim 1; SEQ ID NO 318029; 29pp + Sequence Listing; German. Ouery Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels Sequence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other; BP. 06-APR-2001; 2001WO-IB000713. 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173. 07-APR-2000; 2000DE-01019173 ABI18644 standard; DNA; 12 (first entry) 736 AAACAGAACAC 746 Olek A, Piepenbrock C, 2 AAACAATACAC 12 (EPIG-) EPIGENOMICS AG (EPIG-) EPIGENOMICS WPI; 2001-657177/75 Set of oligonucleot: designed to detect amethylation status. WO200177384-A2 WO200177384-A2 sapiens. Homo sapiens. 22-FEB-2002 18-OCT-2001 18-OCT-2001 ABI18644; Ношо ABI18644/ ò ద

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

Sequence 12 BP; 0 A; 0 C; 6 G; 6 T; 0 U; 0 Other;

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Berlin K;

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Piepenbrock

olek A,

WPI; 2001-657177/75

Claim 1; SEQ ID NO 318617; 29pp + Sequence Listing; German.

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                               Gaps
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/ Match 12; Score 7.8; DB 1; Length 12; Local Similarity 81.8%; Pred. No. 6.8e+02; see 9; Conservative 0; Mismatches 2; Indels
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Matches
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Pred. No. 6.8e+02; 0; Mismatches 2;

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Sequence 12 BP; 1 A; 1 C; 2 G; 8 T; 0 U; 0 Other;
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35.5%; Score 7.8; DB 1; Length 12;

Query Match

ABH75097;

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Best Local Similarity 81.8
Matches 9; Conservative
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oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligoners are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, AHH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE09989, ABF00010-ABE99989, ABF00010-ABE99989, ABF00010-ABE99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at
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                                                                                                                                                                                     ABH74220 standard; DNA; 12
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12 GAAACACAATA 2
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABF00010-ABF99989, ABM0010-ABF99899 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                         SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                        Oligonucleotide primer SEQ ID NO 275084 for detecting SNP TSC0003780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                  22-FEB-2002 (first entry)
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Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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ABI26253 standard; DNA; 12 BP. (first entry) 22-FEB-2002 ABI26253; 1404 

Oligonucleotide primer SEQ ID NO 326226 for detecting SNP TSC0032965

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

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WO200177384-A2

06-APR-2001; 2001WO-IB000713. 18-OCT-2001 

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75

Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 326226; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA)/oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at

Sequence 12 BP; 7 A; 4 C; 0 G; 1 T; 0 U; 0 Other;

0; Gaps Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No: 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels

736 AAACAGAACAC 746

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ABI02575 standard; DNA; 12 BP. ABI02575; RESULT 1405 

(first entry) 22-FEB-2002 Oligonucleotide primer SEQ ID NO 302548 for detecting SNP TSC0020056.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WOZ00177384-A2.

18-OCT-2001

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS

Olek A, Piepenbrock C,

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Berlin

WPI; 2001-657177/75

Set of oligonuclectides, useful for diagnosis and cell typing,

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989 and ABI00010-ABI82073
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                                  methylation status.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE09989, ABF00010-ABE99989 and ABE10010-ABE3073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published_pct_sequences
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represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                  Length 12;
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Pred. No. 6.8e+02;
0; Mismatches 2;
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Best Local Similarity 81.8%;
Matches 9; Conservative
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                                                                                                                                                                                     This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but fur wipo int/pub/published_pct_sequences
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designed to detect single-nucleotide polymorphisms and cytosine
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Score 7.8; DB 1; Length 12; Pred. No. 6.8e+02; 0; Mismatches 2; Indels

Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative (

735 GAAACAGAACA 745 ||| || || |||

Seguence 12 BP; 1 A; 1 C; 3 G; 7 T; 0 U; 0 Other;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, coligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                            Oligonucleotide primer SEQ ID NO 306974 for detecting SNP TSC0022276.
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ftp.wipo.int/pub/published_pct_sequences
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ABI07001 standard; DNA; 12
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Matches 9; Conservative
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12 GAACCATAACA
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Claim 1; SEQ ID NO 287131; 29pp + Sequence Listing; German.
                                                                        Claim 1; SEQ ID NO 336561; 29pp + Sequence Listing; German
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Matches 9; Conservative
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                   Piepenbrock C,
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                                WPI; 2001-657177/75
                                                           methylation status.
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Berlin K;

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but two, int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                            This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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designed to detect single-nuclectide polymorphisms and cytosine
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonucleotide primer SEQ ID NO 316351 for detecting SNP TSC0027404.

(first entry)

22-FEB-2002

ABI16378

ABI16378 standard; DNA; 12 BP

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Sequence 12 BP; 8 A; 4 C; 0 G; 0 T; 0 U; 0 Other;
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                                                                 Score 7.8; DB 1;
Pred. No. 6.8e+02;
0; Mismatches 2;
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Query Match
Best Local Similarity '81.8',
Best Local Similarity '81.8',
Best Local Similarity '81.8',
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                                Query Match
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI32073 data for this patent did not form part of the printed specification, but the blub published prefrom WIPO at

Sequence 12 BP; 6 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Berlin K;

Olek A, Piepenbrock C,

(EPIG-) EPIGENOMICS

WPI; 2001-657177/75.

06-APR-2001; 2001WO-IB000713 07-APR-2000; 2000DE-01019173

WO200177384-A2. Homo sapiens.

18-OCT-2001

Claim 1; SEQ ID NO 316351; 29pp + Sequence Listing; German

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                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                  Gaps
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35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; rive 0; Mismatches 2; Indels
                                                                                                                                                                          BP.
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                Best Local Similarity 81.8 Matches 9; Conservative
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736 AAACAGAACAC 746

AAACAAAACCC 12

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RESULT 1414 ABI16378

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory,
                                                                                                                               This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                             ides, useful for diagnosis and cell typing, single-nucleotide polymorphisms and cytosine
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                                                                                                     Claim 1; SEQ ID NO 342496; 29pp + Sequence Listing; German.
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Matches 9; Conservative
                                    oligonucleotides,
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WPI; 2001-657177/75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-4BC99989, ABF00010-ABF9989, ABF00010-ABF9989 and ABI00100-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels

Berlin K;

Piepenbrock C,

olek A,

WPI; 2001-657177/75

(EPIG-) EPIGENOMICS AG

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99899, ABF00010-ABF99899, ABH00010-ABH999989 and ABI00010-ABI82073 trepresent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
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                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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              Oligonucleotide primer SEQ ID NO 364679 for detecting SNP TSC0054651.
                                                                                                                                                                                                                                                                                                                                                                                    ligonucleotides, useful for diagnosis and cell typing, it o detect single-nucleotide polymorphisms and cytosine
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Pred. No. 6.8e+02;
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF99989, ABH0010-ABF99989, and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formmat from WIPO at this published_pot_sequences
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                            This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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          Claim 1; SEQ ID NO 380433; 29pp + Sequence Listing; German.
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Pred. No. 6.8e+02;
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was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
central nervous system; gastrointestinal; respiratory; immune; metabolic.
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ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                       SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                       ABI20393 standard; DNA; 12 BP
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                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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olek A, RESULT 1425
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COLT-CEBCOL ABH73762;

Query Match

Matches

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Gaps

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typing, is

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABH99999 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at oet or oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status. Claim 1; SEQ ID NO 275474; 29pp + Sequence Listing; German. Sequence 12 BP; 9 A; 3 C; 0 G; 0 T; 0 U; 0 Other; Piepenbrock C, WPI; 2001-657177/75 Á olek 

Berlin

Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels 734 AGAAACAGAAC 744

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ABI28569 standard; DNA; 12 BP. (first entry) 22-FEB-2002 RESULT 1428 

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Oligonucleotide primer SEQ 1D NO 328542 for detecting SNP TSC0034382.

Homo sapiens.

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB000713

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG.

Berlin Olek A, Piepenbrock C,

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WPI; 2001-657177/75.

typing, i Set of oligonuclectides, useful for diagnosis and cell designed to detect single-nuclectide polymorphisms and methylation status.

Claim 1; SEQ ID NO 328542; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC39989, ABF00010-ABF9989, ABF00010-ABF9989, ABF00010-ABF9989 and ABI00010-ABF82073 represent the oligomers described in the invention. NOTE: The sequence was obtained in electronic format from WIPO at the printed specification, but the wipo.int/pub/published\_pct\_sequences 883000000000088

Seguence 12 BP; 9 A; 0 C; 2 G; 1 T; 0 U; 0 Other;

Gaps . 0 Length 12; Query Match 35.5%; Score 7.8; DB 1; Length 12
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels

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735 GAAACAGAACA 745 GAAAAAGAAAA 12 N

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AEH79548 standard; DNA; 12 BP

22-FEB-2002 (first entry)

0; Gaps

Oligonucleotide primer SEQ ID NO 279541 for detecting SNP TSC0007466.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2.

18-OCT-2001.

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173.

(EPIG-) EPIGENOMICS AG.

Berlin K; Olek A, Piepenbrock C,

WPI; 2001-657177/75.

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 279541; 29pp + Sequence Listing; German.

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNB) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 the represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at was obtained in electronic format from Wi ftp.wipo.int/pub/published\_pct\_sequences ABH79548/A
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Sequence 12 BP; 0 A; 0 C; 2 G; 10 T; 0 U; 0 Other;

RESULT 1430 ABH80335/c

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                             SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                         Oligonucleotide primer SEQ ID NO 280455 for detecting SNP TSC0008655.
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ABI05650 standard; DNA; 12
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es 9; Conservative
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ABI05650/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Score 7.8; DB 1; Length 12;
Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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  Query Match
Best Local Similarity 81.6
Matches 9; Conservative
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Matches 9; Conservative
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WO200177384-A2.

Homo sapiens

ABH80462/c ID ABH80462 standard; DNA; 12 BP. XX

RESULT 1431

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligomucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, contral nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ö SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Gaps Oligonucleotide primer SEQ ID NO 306155 for detecting SNP TSC0021828. Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine methylation status. o; Claim 1; SEQ ID NO 305623; 29pp + Sequence Listing; German. Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels Sequence 12 BP; 1 A; 3 C; 0 G; 8 T; 0 U; 0 Other; Berlin K; Berlin K; BP. 06-APR-2001; 2001WO-IB000713. 06-APR-2001; 2001WO-IB000713 07-APR-2000; 2000DE-01019173 07-APR-2000; 2000DE-01019173 .182/c ABI06182 standard; DNA; 12 22-FEB-2002 (first entry) 733 GAGAACAGAA 743 Olek A, Piepenbrock C, Olek A, Piepenbrock C, 12 GAGAAATAAAA 2 (EPIG-) EPIGENOMICS AG (EPIG-) EPIGENOMICS WPI; 2001-657177/75. WPI; 2001-657177/75 WO200177384-A2 Homo sapiens. 18-OCT-2001 18-CCT-2001 ABI06182; RESULT 1433 à g

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                 Claim 1; SEQ ID NO 306155; 29pp + Sequence Listing; German
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ABI32093 standard; DNA; 12 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
-ABC99989, ABF00010-ABF99989, ABH00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide primer SEQ ID NO 284544 for detecting SNP TSC0011875.
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                                                                                                                                                      Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 91.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                     Sequence 12 BP; 1 A; 6 C; 0 G; 5 T; 0 U; 0 Other;
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                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                         Oligonucleotide primer SEQ ID NO 313448 for detecting SNP TSC0025771.
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designed to detect single-nucleotide polymorphisms and cytosine
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                                    ABI13475 standard; DNA; 12
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Oligonucleotide primer SEQ ID NO 290443 for detecting SNP TSC0014352.

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Gaps

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35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; trive 0; Mismatches 2; Indels

Local Similarity 81.8

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735 GAAACAGAACA 745

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but fire wipo.int/pub/published\_pct\_sequences SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic. Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status. Claim 1; SEQ ID NO 290443; 29pp + Sequence Listing; German. Seguence 12 BP; 5 A; 5 C; 0 G; 2 T; 0 U; 0 Other; Berlin K; 06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173 Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG WPI; 2001-657177/75 WO200177384-A2 Homo sapiens 

35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; ive 0; Mismatches 2; Indels Query Match
Best Local Similarity 81.0

ò g RESULT 1438

ABI15662 standard; DNA; 12 BP ABI15662; 

(first entry) 22-FEB-2002

Oligonucleotide primer SEQ ID NO 315635 for detecting SNP TSC0027012.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2

18-OCT-2001

06-APR-2001; 2001WO-IB000713

07-APR-2000; 2000DE-01019173

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ÅĞ. (EPIG-) EPIGENOMICS ĸ Berlin Piepenbrock C, olek A,

WPI; 2001-657177/75

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Claim 1; SEQ ID NO 315635; 29pp + Sequence Listing; German.

This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABE99989, ABF00010-ABE99989, ABF00010-ABE99989 and ABI00010-ABE3073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPO at 

Sequence 12 BP; 6 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

0; Gaps Length 12; 35.5%; Score 7.8; DB 1; Length 12 81.8%; Pred. No. 6.8e+02; ive 0; Mismatches 2; Indels Query Match
Best Local Similarity 81.8

Bost Local 9; Conservative

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736 AAACAGAACAC 746 AAACTTAACAC 12

ઠે g RESULT 1439

ВР. ABI49818 standard; DNA; 12

ABI49818;

22-FEB-2002 (first entry)

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Gaps

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Oligonucleotide primer SEQ ID NO 349791 for detecting SNP TSC0046328.

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Homo sapiens

WO200177384-A2.

18-OCT-2001

06-APR-2001; 2001WO-IB000713.

07-APR-2000; 2000DE-01019173

(EPIG-) EPIGENOMICS AG.

Olek A, Piepenbrock C,

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WPI; 2001-657177/75.

Set of oligonuclectides, useful for diagnosis and cell typing, is designed to detect single-nuclectide polymorphisms and cytosine methylation status. 

Claim 1; SEQ ID NO 349791; 29pp + Sequence Listing; German.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF99889, ABH00010-ABH99889 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at the printed specification, but fire wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Pred. No. 6.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide primer SEQ ID NO 352679 for detecting SNP TSC0048031.
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                                Score 7.8; DB 1; Length 12; Pred. No. 6.8e+02; 0; Mismatches 2; Indels
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Sequence 12 BP; 1 A; 0 C; 3 G; 8 T; 0 U; 0 Other;
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABC0010-ABE99899, ABM0010-ABE99899 and ABI00010-ABE8073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but twipo.int/pub/published\_pct\_sequences

Claim 1; SEQ ID NO 352030; 29pp + Sequence Listing; German.

RESULT 1442

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99999, ABF00010-ABH99999 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                                                                                          Oligonucleotide primer SEQ ID NO 353148 for detecting SNP TSC0048333.
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                     ABI53175 standard; DNA; 12 BP
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The cligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The coingomers are also used for detecting cell type differentiation. ABC0010-ABC99889, ABF00010-ABF99899, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

Sequence 12 BP; 1 A; 0 C; 3 G; 8 T; 0 U; 0 Other;

Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.

Berlin K;

Olek A, Piepenbrock C,

(EPIG-) EPIGENOMICS

WPI; 2001-65717/75.

06-APR-2001; 2001WO-IB000713

WO200177384-A2

18-OCT-2001

Homo sapiens

07-APR-2000; 2000DE-01019173

Claim 1; SEQ ID NO 376788; 29pp + Sequence Listing; German.

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                                 Gaps
                                                                                                                                                                                                         Oligonucleotide primer SEQ ID NO 378343 for detecting SNP TSC0062733.
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        35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; rive 0; Mismatches 2; Indels
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                                                                                                                                      ABI78370 standard; DNA; 12 BP
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German.

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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide primer SEQ ID NO 378374 for detecting SNP TSC0007374.
                                               Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                Claim 1; SEQ ID NO 378343; 29pp + Sequence Listing;
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               WPI; 2001-657177/75
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range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABF00010-ABF99989, ABF00010-ABF99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic former from WIPO at
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Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81 8%; Pred No. 6.8e+02;

Sequence 12 BP; 1 A; 0 C; 6 G; 5 T; 0 U; 0 Other;

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oliconucleotides are used for diagnosis and/or prognosis of cancer and a

Claim 1; SEQ ID NO 378374; 29pp + Sequence Listing; German.

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                               SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                               Oligonuclectide primer SEQ ID NO 317667 for detecting SNP TSC0028158.
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Pred. No. 6.8e+02;
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Best Local Similarity 81.8%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide primer SEQ ID NO 382008 for detecting SNP TSC0009339.
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                                                                                                                                                                                                                                                                                                                   ABI82035 standard; DNA; 12 BP.
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                                                                                                                                      12 AACATACCACC 2
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RESULT 1448

à 셤 ABI17694 ID ABI1 XX AC ABI1 XX

22-FEB-2002 (first entry)

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Gaps

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Indels

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Mismatches

; 0

9; Conservative

Matches

ò 유 1447

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Gaps

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Claim 1; SEQ ID NO 294498; 29pp + Sequence Listing; German.

methylation status.

Page 630

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically prefreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99999, ABF00010-ABF99999, ABH00010-ABH99999 and ABI00010-ABF82073 data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; SS; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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                                                                                                                                                                    ligonucleotides, useful for diagnosis and cell typing, it o detect single-nucleotide polymorphisms and cytosine
                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 292984; 29pp + Sequence Listing; German.
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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81.8%;
               06-APR-2001; 2001WO-IB000713.
                                             07-APR-2000; 2000DE-01019173
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                                                                                                                                                                         of oligonucleotides,
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                                                                                                            Piepenbrock C,
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                                                                                                                                           WPI; 2001-657177/75
                                                                                                                                                                                        designed to detect a methylation status.
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but typ.wipo.int/pub/published_pot_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide primer SEQ ID NO 295687 for detecting SNP TSC0016687.
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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81.8%;
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RESULT 1453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pot_sequences
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                                                                                                                                                         Query Match
35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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                                                                                                       Sequence 12 BP; 1 A; 6 C; 0 G; 5 T; 0 U; 0 Other;
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ABH/17751

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ABH/177
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Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.

Berlin K;

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(EPIG-) EPIGENOMICS

Olek A, Piepenbrock C,

WPI; 2001-657177/75.

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173

WO200177384-A2. Homo sapiens.

18-OCT-2001.

Claim 1; SEQ ID NO 272307; 29pp + Sequence Listing; German.

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                              Gaps
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35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                  BP.
                                                                                                                                                ABI23966 standard; DNA; 12
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               Best Local Similarity 81.8
Matches 9; Conservative
                                                      737 AACAGAACACC 747
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    Query Match
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ABI23966
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0; Gaps

736 AAACAGAACAC 746

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2 AAACAAATCAC 12

This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically prereated genomic DNA. The oligomicleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989, ABH00010-ABE99989 and ABI00010-ABE82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the wipo.int/pub/published\_pct\_sequences

Sequence 12 BP; 8 A; 3 C; 0 G; 1 T; 0 U; 0 Other;

SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonucleotide primer SEQ ID NO 272307 for detecting SNP TSC0002774.

(first entry)

22-FEB-2002

ABH72328;

BP.

ABH72328 standard; DNA; 12

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, ardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; Ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                      Berlin K;
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                                      Piepenbrock C,
(EPIG-) EPIGENOMICS AG
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                                                                              WPI; 2001-657177/75
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Best Local Similarity
Matches 9; Conserv
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                                   olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1456
ABH76081/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
  peptide nucleic acid, cytosine methylation; cardiovascular; primer; ss, central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligonucleotide primer SEQ ID NO 274781 for detecting SNP TSC0003674.
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                                                                                                                                                                                                                                                                                                                                                                                Set of oligonucleotides, useful for diagnosis and cell typing, is designed to detect single-nucleotide polymorphisms and cytosine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 323939; 29pp + Sequence Listing; German.
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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81.8%;
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Best Local Similarity 81.0
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                                                                                                                                                                                                                                                                (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                                                                                                                          methylation status
                                                                                                     WO200177384-A2.
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                                                               Homo sapiens
                                                                                                                                           18-OCT-2001
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Gaps

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Length 12;

Score 7.8; DB 1; Length 12 Pred. No. 6.8e+02; 0; Mismatches 2; Indels

35.5%; 81.8%;

Query Match Best Local Similarity 81.8 Matches 9; Conservative

733 GAGAAACAGAA 743

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1 GCGAAACAAAA 11

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acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABCC0010-ABC99989, ABF0010-ABF99989, ABR0010-ABH99989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligonuclectide primer SEQ ID NO 326688 for detecting SNP TSC0033234.
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                      Sequence 12 BP; 0 A; 0 C; 4 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                          ABI26715 standard; DNA; 12 BP.
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Best Local Similarity 81.0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Olek A, Piepenbrock C,
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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.

Oligonucleotide primer SEQ ID NO 302632 for detecting SNP TSC0020091.

(first entry)

22-FEB-2002

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ABI02659;

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ABI02659 standard; DNA; 12

RESULT 1458

ABI02659

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; ive 0; Mismatches 2; Indels
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ABI03308
ID ABI03308 standard, DNA, 12
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8
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, aradiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC99899, ABF00010-ABF99899, ABH00010-ABH99999 and ABI00010-ABI82073 targement the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at

BP.

er.

Sequence 12 BP; 8 A; 2 C; 2 G; 0 T; 0 U; 0 Other;

ftp.wipo.int/pub/published\_pct\_sequences

oligonucleotides, useful for diagnosis and cell typing, ied to detect single-nucleotide polymorphisms and cytosine

Berlin K;

Olek A, Piepenbrock C,

WPI; 2001-657177/75

designed to detect methylation status.

Set of

(EPIG-) EPIGENOMICS AG

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173.

WO200177384-A2. Homo sapiens.

18-OCT-2001.

Claim 1; SEQ ID NO 302632; 29pp + Sequence Listing; German.

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                             Oligonucleotide primer SEQ ID NO 328938 for detecting SNP TSC0034660.
                                                                                                                                                                                                                                                                                                          965/c
ABI28965 standard; DNA; 12
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                                                                                                                                                                                                                                                                                 AATAAAACACC
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     ABI03308
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35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; ive 0; Mismatches 2; Indels

Best Local Similarity 81.8 Matches 9; Conservative

Matches

Query Match

736 AAACAGAACAC 746

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Sequence 12 BP; 1 A; 0 C; 5 G; 6 T; 0 U; 0 Other;

ftp.wipo.int/pub/published\_pct\_sequences

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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                           SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                          Oligonuclectide primer SEQ ID NO 303281 for detecting SNP TSC0020420.
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ftp.wipo.int/pub/published_pct_sequences
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22-FEB-2002 (first entry)
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This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a reange of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC0010-ABC9989, ABF0010-ABH99989 and ABI0010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at

Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.

Berlin K;

Piepenbrock C,

olek A,

WPI; 2001-657177/75

EPIG-) EPIGENOMICS

06-APR-2001; 2001WO-IB000713. 07-APR-2000; 2000DE-01019173.

WO200177384-A2.

18-OCT-2001

Claim 1; SEQ ID NO 328938; 29pp + Sequence Listing; German.

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                             Oligonucleotide primer SEQ ID NO 279799 for detecting SNP TSC0007838
                                                                                                                                                                                                                                                                                                                                              Berlin K;
                                                           ABH79806 standard; DNA; 12 BP.
                                                                                                                                                                                                                                                                         06-APR-2001; 2001WO-IB000713.
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                                                                                                        (first entry)
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12 AAACACCACAC
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                                                                                                                                                                                                     Homo sapiens.
                                                                                                        22-FEB-2002
                                                                                 ABH79806;
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                                    RESULT 1461
                                               ABH79806
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(first entry)

WPI; 2001-657177/75

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                                                                                                                           This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99889, ABF00010-ABF9989, ABF00010-ABF9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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              Set of oligonucleotides, useful for diagnosis and cell typing, idesigned to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                            Claim 1; SEQ ID NO 279799; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                        35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; ive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Conservative
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oligomers are also used for detecting cell type differentiation. ABC00010-ABC39989, ABF00010-ABH39989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Oligonucleotide primer SEQ ID NO 309521 for detecting SNP TSC0023558.
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WO200177384-A2 Homo sapiens.

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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Claim 1; SEQ ID NO 288670; 29pp + Sequence Listing; German.
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                                                                                                                                                              This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989, ABH00010-ABH99989 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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Best Local Similarity 81.8
Matches 9; Conservative
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(first entry)

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SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                           Oligonucleotide primer SEQ ID NO 346435 for detecting SNP TSC0044583.
                             ABI46462 standard; DNA; 12 BP.
                                                                                                                                                                                                                                                                             06-APR-2001; 2001WO-IB000713.
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                                                        ABI46462;
olek A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABE99989, ABF00010-ABE99989, ABH00010-ABE99989 and ABI00010-ABE3073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format from WIPD at
                                                                                                                                                                                                                                                                                                                 SNP; single nuclectide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                    Gaps
                                                                                                                                                                                                                                                                                          Oligonuclectide primer SEQ ID NO 345246 for detecting SNP TSC0000735.
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                                                     Score 7.8; DB 1; Length 12;
Pred. No. 6.8e+02;
0; Mismatches 2; Indels
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                              Sequence 12 BP; 8 A; 4 C; 0 G; 0 T; 0 U; 0 Other;
  ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                           ABI45273 standard; DNA; 12 BP
                                                        35.5%;
81.8%;
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                                                     Query Match
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                             736 AAACAGAACAC 746
                                                                                                                                       2 AAACAAAACCC 12
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methylation status.
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Berlin K;

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                                          Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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81.8%; Pred. No. 6.8e+02;
ative 0; Mismatches 2;
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Best Local Similarity 81.8-
Local 9, Conservative
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Gaps

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Query Match
35.5%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 6.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels

733 GAGAAACAGAA 743

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Berlin K;

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Olek A, Piepenbrock C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes novel oligonucleotide primers or peptide nucleic acid (PNA) oligoners for detecting single nucleotide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genomic DNA. The oligonucleotides are used for diagnosts and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, entrain parvous system, ardiovascular and metabolic disorders. The oligoners are also used for detecting cell type differentiation. ABC00010-ABC99899, ABH00010-ABH99989 and ABI0010-ABH82073 the person of this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  was obtained in electronic format from WI ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
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                                                               Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
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                                                                                                                                                                                                                          Claim 1; SEQ ID NO 349429; 29pp + Sequence Listing; German.
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Query Match

Seguence 12 BP; 1 A; 2 C; 0 G; 9 T; 0 U; 0 Other;

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range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers ealso used for detecting cell type differentiation. ABC0010-ABC99889, ABC0010-ABR99889 and ABI00010-ABI82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form par of the printed specification, but was obtained in electronic format from WIPO at fire wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes novel oligonuclectide primers or peptide nucleic acid (PNA) oligomers for detecting single nuclectide polymorphisms (SNP) and cytosine methylation status in chemically pretreated genemic DNA. The oligonuclectides are used for diagnosis and/or prognosis of cancer and a range of diseases including immune system, gastrointestinal, respiratory, central nervous system, cardiovascular and metabolic disorders. The oligomers are also used for detecting cell type differentiation. ABC00010-ABC99989, ABF00010-ABH99989 and ABI00010-ABH82073 represent the oligomers described in the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
  oligonucleotides are used for diagnosis and/or prognosis of cancer and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide primer SEQ ID NO 368604 for detecting SNP TSC0057109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Set of oligonucleotides, useful for diagnosis and cell typing, i designed to detect single-nucleotide polymorphisms and cytosine methylation status.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 368604; 29pp + Sequence Listing; German.
                                                                                                                                                                                                                             35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                        Seguence 12 BP; 0 A; 0 C; 5 G; 7 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВР.
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                                                                                                                                                                                                                                                                        9; Conservative
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                                                                                                                                                                                                                                                                                                                                               11 AAACAAAACCC 1
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                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS; peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss; central nervous system; gastrointestinal; respiratory; immune; metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oligonucleotide primer SEQ ID NO 357951 for detecting SNP TSC0050892.
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                                                                 Indels
Pred. No. 6.8e+02;
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                                    81.8%;
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                                Best Local Similarity 81.8
Matches 9, Conservative
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AB157976

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Grassmann
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        Strobel I,
                                                                                                                                                                                                            Sequence 12 BP; 0 A; 5 C; 2 G; 0 T; 5 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                               Modified 3' RNA region of Influenza A virus #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Steinkasserer A,
         Steinkasserer A,
                                                                                    Disclosure; Page 5; 33pp; English
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                                                                                                                                                                                                                                        Local Similarity 81.8
nes 9; Conservative
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         Hobom G,
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                          WPI; 2002-418777/45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
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         Schuler G,
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                                                                                                                                                                                                                                        Human leukocyte antigen typing by amplifying a sample followed by sequence specific oligonucleotide hybridization with labeled oligonucleotide probes that hybridize with a series of known control DNA
                                                                                                                                                                                                                                                                                                           The present invention relates to human leukocyte antigen (HLA) typing. The method involves detecting polymorphic residues by sequence specific oligonucleotide probe hybridization (SSOPH) with labeled oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytostatic; antiviral; tumour associated antigen; TAA; dendritic cell; virus-associated antigen; VAA; recombinant influenza virus; vaccine; viral infection; immune; wild-type; influenza C virus; ss.
                                              Human; leukocyte antigen; HLA; typing; sequence specific probe; SSOPH;
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3' conserved RNA region of wild-type influenza C virus.
                                                                                                                                                                                                                                                                                                                                                           Sequence 12 BP; 4 A; 3 C; 4 G; 1 T; 0 U; 0 Other;
                          Mutilple allele detection probe #4.
                                                                                                                                                                                                                                                                                        Example, Col 22-23; 16pp; English
                                                                                                                                                                                 (BLOO-) BLOOD CENT RES FOUND INC.
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                                                                                                                                                    90US-00544218.
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                                                                                                                                  97US-00000805
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Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                                                                                                     Baxter-Lowe LA, Gorski JA;
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AAL37779 standard; RNA; 12
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         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Influenza virus
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                                                                          Homo sapiens
                                                                                             US6194147-B1
                                                                                                                                  30-DEC-1997;
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         16-MAY-2001
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The invention relates to a method for the expression of tumour associated antigens (TAA) or virus-associated antigens (VAA) by dendritic cells comprising; preparing a recombinant influenza virus containing a nucleotide sequence confidence of the TAA or VAA; and infecting dendritic cells with the recombinant virus. The method is used for expressing TAA or VAA in dendritic cells. The cells are used for preparing a medicament for treating tumours or viral infections. A vaccine can be created by using dendritic cells presenting tumour antigens to induce an immune response. This polymucleotide sequence represents a 3' conserved RNA region of the wild-type influenza C virus of the invention The invention relates to a method for the expression of tumour associated antigens (TAA) or virus-associated antigens (VAA) by dendritic cells comprising: preparing a recombinant influenza virus containing a nucleotide sequence coding for the TAA or VAA; and infecting dendritic Cytostatic, antiviral; tumour associated antigen; TAA; dendritic cell; virus-associated antigen; VAA; recombinant influenza virus; vaccine; viral infection; immune; Influenza A virus; ss. Gaps Expressing tumor or viral associated antigens by dendritic cells, use for treating tumors or viral infections, comprises using recombinant influenza virus containing nucleic acid encoding the antigens. Expressing tumor or viral associated antigens by dendritic cells, use for treating tumors or viral infections, comprises using recombinant influenza virus containing nucleic acid encoding the antigens. 0 Grassmann 35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; rive 0; Mismatches 2; Indels

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cells with the recombinant virus. The method is used for expressing TAA or VAA in dendritic cells. The cells are used for preparing a medicament for treating tumours or viral infections. A vaccine can be created by using dendritic cells presenting tumour antigens to induce an immune response. This polymucheotide sequence represents a modified 3' RNA region of the Influenza A virus of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detection; classification; identification; toxin detection; protease; ADP-ribosylating toxin; cytotoxic phospholipase; exfoliative toxin; toxic threat agent; ds.
                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                       / Match 35.5%; Score 7.8; DB 1; Length 12; Local Similarity 81.8%; Pred. No. 6.8e+02; nes 9; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                    Seguence 12 BP; 1 A; 3 C; 1 G; 0 T; 7 U; 0 Other;
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99US-0122152P.
99US-013399P.
99US-015171.
99US-015177P.
99US-00398965.
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P-PSDB; ABG94454.
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26-FEB-1999;
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                                                                                                                                                                                                                                                                                 Query Match
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The invention describes methods of automated detection, classification and identification comprising treating cells containing luminescent reporter molecules (I) in array of locations with a test substance, where (I) are detectors, classifiers or identifiers, imaging cells in each location to obtain luminescent signals and converting optical information into digital date to interpret presence of toxins in the test substance. The method are useful for detection of toxins chosen from proteases, ADP-ribosylating toxins, cytotoxic phospholipases, and exfoliative toxins.

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The present invention describes a human influenza virus (I) comprising an RNA-sequence encoding a modified RNA-polymerase that differs from the wild-type RNA-polymerase of the human influenza virus in that at least 1 of the amino acid residues distinguishing the wild-type RNA-polymerase of the human influenza virus from FPV Bratislava RNA-polymerase of corresponding amino acid residue(8) as present in FPV Bratislava RNA-polymerase of Bratislava RNA-polymerase of CC Bratislava RNA-polymerase. (I) has virucide, cytostatic, anti-HIV, hepatociropic, anti-inflammatory and immunomodulator activities and can be used in gene therapy and vaccines. The influenza virus is useful for preparing agents for: (a) gene transfer into cells, preferably into mammalian cells, particularly into human cells, by viral infection; (b) gene transfer into antigen-presenting cells, and the use of the obtained companded to including therapeutic and prophylactic vaccination; in vivo vaccination, including therapeutic and prophylactic vaccination; (c) eliciting an immune response, including the induction of a T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human influenza virus comprising an RNA-sequence encoding a modified RNA-polymerase, useful for preparing agents for therapeutic and prophylactic vaccination, or treating a growing tumor or a chronic infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Influenza virus; transcription; replication; RNA polymerase; vaccine; gene therapy; cytostatic; anti-HIV; hepatotropic; antiinflammatory; immunomodulator; virucide; infectious disease; ss.
Three classes of cell-based luminescent reporter molecules such as detectors, classifiers and identifiers are described and serve as reporters of toxic threat agents. The first two levels of characterisation ensure a rapid readout of toxin class without sacrificing the ability to detect many new mutant toxins or dissect several complex mixtures of known toxins. This sequence encodes a protease bissensor recognition site used in the cell-based screening
                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified influenza virus A 3' conserved region SEQ ID NO:4.
                                                                                                                                                                                                                                      Score 7.8; DB 1; Length 12;
Pred. No. 6.8e+02;
                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                              Sequence 12 BP; 6 A; 1 C; 3 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABQ75462 standard; RNA; 12 BP.
                                                                                                                                                                                                                                      35.5%;
81.8%;
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                                                                                                                                                                                                                                                                                 9; Conservative
                                                                                                                                                                                                                                                                                                                         732 GGAGAACAGA 742
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                                                                                                                                                                                                                                                               Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Influenza virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABQ75462;
                                                                                                                                                                                                                                           Query Match
                                                                                                                                                          system
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gene transfer into antigen-presenting cells, and the use of the obtained product for ex vivo immunotherapy; in vivo somatic gene therapy; in vivo vaccination; including therapettic and prophylactic vaccination; (c) vaccination; including therapettic and prophylactic vaccination; (d) casponse; including the induction of a T-cell response; (d) treating a growing tumour or a chronic infectious disease; (e) immunotherapy, preferably for autologous immunotherapy; (f) transfer and expression of foreign genes into cells infected by such viruses; or (g) transfer and expression of RNA molecules into cells infected by such viruses; preferably the RNA molecules into cells infected by such viruses; preferably the RNA molecules collusar antisease equences or double-strand sequences relative to the target cellular mRNA molecules, and/or the agent is suitable for sequence-specific gene silencing, preferably by antisense RNA or RNA interference mechanisms such as riboxyme cleavages of target RNAs. The recombinant viruses can be made for use in vaccines against HNV, hepatitis B or C virus, herpes viruses or papilloma viruses. The present sequence represents a 3' conserved region of a wild type influenza virus, given in the

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Gaps

0;

Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels

731 AGGAGAAACAG 741

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Sequence 12 BP; 0 A; 5 C; 2 G; 0 T; 5 U; 0 Other;

exemplification of the present invention

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response, (d) treating a growing tumour or a chronic infectious disease, (e) immunotherapy, preferably for autologous immunotherapy; (f) transfer and expression of foreign genes into cells infected by such viruses, or (g) transfer and expression of RNA molecules into cells infected by such viruses, preferably the RNA molecules to be expressed are antisense sequences or double-strand sequences relative to the target celluar mRNA molecules, and/or the agent is suitable for sequence-specific gene silencing, preferably by antisense RNA or RNA interference mechanisms made for use in vaccines against HIV, hepatitis B or C virus, herpes viruses or papilloma viruses. The present sequence represents a modified a conserved region of an influenza virus, given in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human influenza virus comprising an RNA-sequence encoding a modified RNA-polymerase, useful for preparing agents for therapeutic and prophylactic vaccination, or treating a growing tumor or a chronic infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Influenza virus, transcription, replication, RNA polymerase, vaccine, gene therapy, cytostatic, anti-HIV; hepatotropic, antiinflammatory, immunomodulator; virucide; infectious disease, ss.
                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                         Length 12;
                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Influenza virus C 3' conserved region SEQ ID NO:3.
                                                                                                                                                                                                                          Sequence 12 BP; 1 A; 3 C; 1 G; 0 T; 7 U; 0 Other;
                                                                                                                                                                                                                                                      Score 7.8; DB 1;
Pred. No. 6.8e+02;
                                                                                                                                                                                                                                                                                       0; Mismatches
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ABQ75461 standard; RNA; 12 BP.
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                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                          the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Influenza virus.
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The invention relates to a replicase complex comprising a hepatitis C virus (HCV) NSBs replicase protein, a linear nucleic acid template and a complementary nucleic acid primer which is annealed to the 3' terminus of the template, where the template is at least three nucleotides and the primer is two or three nucleotides, and the template and primer do not form a stable duplex in solution in the absence of the HCV NSSB protein. The complex is useful for detecting HCV replicase activity and permits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel replicase complex comprising hepatitis C virus NS5B replicase, a 3 nucleotide-long template to which a 2 nucleotide-long primer is annealed, and template and primer which do not form a stable duplex in the absence
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus (HCV) NS5B replicase RNA synthesis template #20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus; HCV; NS5B replicase; ss; RNA polymerase
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                                                                                                                                                                                                         ABK99290 standard; RNA; 12 BP.
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AGCAGAAGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HONG/) HONG Z.
(FERR/) FERRARI E.
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                                                                                                                                                                                                                                                                                                                                                                           21-OCT-2002
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12
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The present invention describes a human influenza virus (I) comprising an RNA-sequence encoding a modified RNA-polymerase that differs from the wild-type RNA-polymerase of the human influenza virus in that at least 1 of the amino acid residues distinguishing the wild-type RNA-polymerase of the human influenza virus from FPV Bratislava RNA-polymerase of replaced with the corresponding amino acid residue(s) as present in FPV Bratislava RNA-polymerase. (I) has virucide, cytostatic, anti-HIV, hepatotropic, antiinflammatory and immunomodulator activities and can be used in gene therapy and vaccines. The influenza virus is useful for preparing agents for: (a) gene transfer into cells, preferably into mammalian cells, particularly into human cells, by viral infection; (b)

Disclosure; Page 15; 172pp; English.

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          and evaluate antiviral inhibitors and to improve the specificity and efficacy of the inhibitors. The complex is also useful in the development of a reliable system for determining kinetic and thermodynamic constants of HCV NSSB-catalysed nucleotide incorporation and investigation of mechanistic inhibitors for mis-incorporation or chain termination. Specifically, the short RNA template and primer pairs are useful in screening assays which are used for determining kinetic, thermodynamic and mechanistic properties of NSSB replication and ultimately in the development of inhibitors of NSSB in Newly identified inhibitors of replicase activity may be used for development and ultimately in the replicase activity may be used for development and inhibitors of SSB seplication and ultimately in the seplicase activity may be used for development of inhibitors of seplicase RNA synthesis
sensitive RNA-dependent RNA polymerase assays to screen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant influenza virus for transfer and expression of foreign genes and RNA molecules into cells and for preventing, treating influenza, has biscistronic viral RNAs coding for two genes in tandem arrangement.
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Influenza C; tandem RNA segment; TRS; gene expression; influenza; vaccine; somatic gene therapy; expression vector; immunotherapy; autologous immunotherapy; gene silencing; ss.
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                    Sequence 12 BP; 8 A; 2 C; 1 G; 0 T; 1 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wild type influenza C, 3' conserved region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Meyer-Rogge S;
                                                                                                                                                                                                                                                                     35.5%;
81.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABK15139 standard; RNA; 12
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                                                                                                                                                                                                                                                                                                       9; Conservative
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Best Local Similarity
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antisense or double-stranded sequences relative to the target cell cellular mRNA molecules, and/or the agent is suitable for sequence-specific gene silencing, preferably by antisense RNA or RNA interference mechanisms. (I) gives high-yield expression for foreign genes. This sequence represents the 3' conserved region of influenza C virus, described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant vector containing sequence for small nuclear RNA, useful e.g. for identifying variant snRNA that suppresses expression of transcription products.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a recombinant vector which comprises DNA, consisting of an insertion cassette contained between at least two insertion sites, that encodes a small nuclear (sn) RNA. The invention used to identify snRNA modifications that inhibit expression of transcription products (and the identified snRNA are used to suppress expression) for delivering antisense sequences to the nucleus and to create transcenic animals. The present sequence is Luc (ludiferase)-1547/10+2 construct DNA. (Updated on 07-AUG-2003 to correct OS field.)
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                                                                                                                                              35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; Arive 0; Mismatches 2; Indels
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Pred. No. 6.8e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12 BP; 7 A; 5 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                  Sequence 12 BP; 0 A; 5 C; 2 G; 0 T; 5 U; 0 Other;
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81.8%;
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(first entry)
                                                                                                                                   Query Match
Best Local Similarity 81.0.
Best Local 9, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transgenic animal;
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22-OCT-2002
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Best Local S
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The invention describes a recombinant influenza virus (I), stable in the absence of any helper virus, that has a viral RNA segment being a biscistronic RNA molecule coding for two genes in tandem arrangement (tandem RNA segment, TRS). (I) is useful for expression of incorporated foreign gene(s) and RNA molecules in cells. (I), preferably a recombinant influenza A virus is useful for: preventing and/or treating influenza, and for preparing a medicament for vaccination purposes; somatic gene therapy, and as immunopen for inducing antibodies; as an expression vector for producing proteins or glycoproteins; preparing agents for somatic gene therapy; immunotherapy, preferably autologous immunotherapy; transfer and expression of foreign genes and RNA molecules into cells infected by such viruses, where the RNA molecules to be expressed include

Disclosure; Page 6; 39pp; English

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Expression which comprises binding complexes, formed between a single-
expression which comprises binding complexes, formed between a single-
expression which comprises binding complexes, formed between a single-
extranded gene product and an individual primer, or many different
primers, to a surface in a random arrangement. Cyclic extension of the
complementary strand of the gene product is then performed using one or
more polymerases by treating the bound complexes with a solution
containing a polymerase and 1-4 modified nuclectides (NTX), labeled with
fluorescent dyes. NTX are base-modified nuclectides (NTX), labeled with
fluorescent dyes. NTX are base-modified so that if one NTX is
incorporated by polymerase then a second can not be incorporated into the
same strand. The method is used for quantitative analysis of the
carpression of many genes, e.g. for identifying genes involved in
carpression of many genes can be bound to any position on the
surface, eliminating the need for synthesis of different oligonucleotides
at specific positions. Analysis is performed on a standardised surface,
are succession of unknown genes can be detected, only small amounts
of starting material are required (mRNA from a single cell) and all steps
are suitable for automation. Only short sequences (10-50 nucleotides)
need to be determined for identification of genes, if their sequences are
cavailable in databases. This sequence represents an oligonucleotide used
to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parallel analysis of gene expression, useful e.g. for identifying genes involved in tumorigenesis, by cyclical extension of randomly arranged primers using modified nucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parallel analysis; gene expression; tumorigenesis; detection; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12 BP; 6 A; 6 C; 0 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Page 54; 107pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing oligonucleotide #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-APR-2002; 2002WO-EP004657.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-APR-2001; 2001DE-01020798.
                                                                                                       ABQ77279 standard; DNA; 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GENO-) GENOVOXX GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-183838/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200288381-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tcherkassov D;
                                                                                                                                                                                                                                                                                                           25-APR-2003
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                                                                                                                                                                                                         ABQ77279;
RESULT 1485
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                                                        0; Gaps
Query Match 35.5%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 6.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                        737 AACAGAACACC 747
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BP. RESULT 1486

à

ABQ77340 standard; DNA; 12 ABQ77340;

08-MAY-2003 (first entry)

Parallel sequencing associated oligonucleotide SEQ ID

Parallel sequencing; cyclical extension; ds.

Synthetic.

40200288382-A2

07-NOV-2002

26-APR-2002; 2002WO-EP004659

27-APR-2001; 2001DE-01020797

(GENO-) GENOVOXX GMBH

WPI; 2003-183839/18.

Parallel sequencing of nucleic acid fragments, useful e.g. for analysis of single-nucleotide polymorphisms, by cyclical extension of primers with modified nucleotides.

Example 4; Page 59; 121pp; German.

This invention describes a novel method for parallel sequencing of nucleic acid fragments which comprises: (i) binding fragments of about 50 nucleic acid fragments which comprises: (i) binding fragments of about 50 complex with an individual primer, or many different primers, to a a complex with an individual primer, or many different primers, to a complex with an individual primer, or many different primers, to a complementary strand of the mucleic acid fragment is then performed using complementary strand of the mucleic acid fragment is then performed using containing polymerases and 1-4 modified nucleotides rate used, then fluorescent signals from each can be measured separately, (ii) then modified nucleotides are used, then fluorescent signals from each can be cleaved and the modification in the nucleotides is a clavable sterically bulky ligand, (iv) the surface incorporated by a polymerase then a second can not be incorporated into the nucleotides is a clavable sterically bulky ligand, (iv) the surface in incorporated nucleotides are detected from a fluorescent dye and the cut of the nucleotides are removed from complementary strand is extended by one unincorporated modification in the nucleotide, then washed to remove unincorporated modification in the nucleotide, then washed to remove unincorporated modification in the nucleotide, then washed to remove unincorporated modification in the nucleotide, then washed to remove unincorporated modification of the surface, simultaneously for all signals in the sequence of the nucleotide and the sequence of the nucleot acid fragment and the sequence of the nucleot acid fragment in the method provides a chaper, quicker and more acid percently for mutational analysis and for detection of alteranatively conferent analysis of sequences, many sequences can be determined in a percented the sequences, and all single-nucleotide polymorphisms in a sequence, and all separated with a surface and post in any order and and it is inmaterial if synthesis of a molecules rather tha population. This sequence illustrate the method of t

Sequence 12 BP; 6 A; 6 C; 0 G; 0 T; 0 U; 0 Other;

0; 35.5%; Score 7.8; DB 1; Length 12; llarity 81.8%; Pred. No. 6.8e+02; Conservative 0; Mismatches 2; Indels Local Similarity nes 9; Conserv Query Match Matches

ö

737 AACAGAACACC 747

EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat; polymorphic marker prediction of ubiquitous simple sequences; POWPOUS; Rep.-K; human; genetic disease; drug-treatment; Machado-Joseph; Haw River syndrome; Huntington's disease; fragile-X syndrome; Fredreich's ataxis; myotonic dystrophy; hyperandrogenemia; spinal atrophy; bulbar atrophy; spinocerebellar ataxia.

EST polymorphic DNA repeat polynucleotide #59.

(first entry)

17-APR-2003

ABX79734 standard; cDNA; 12 BP.

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The invention discloses a method for identifying a candidate polymorphic repeat within a coding sequence (expressed sequence tag, EST), which comprises detecting tandem repeats in a target coding sequence, scoring the repeats for polymorphic probability and generating a dataset correlating the repeats with polymorphic probability to identify a candidate polymorphic repeat. The computational methods (polymorphic repeat in the computational methods (polymorphic marker prediction of ubiquitous simple sequences, PoMPOUS, and Rep-X) are useful for identifying and detecting candidate polymorphic repeats in human genes, which can be used to understand, treat or eliminate genetic diseases, predispositions or adverse drug-treatment reactions. Examples of diseases linked to nucleotide repeats are Machado-Joseph, Haw River syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxis, myotonic dystrophy, hyperandrogensemia, spinal and bulbar atrophy and spinocereballar ataxia. The sequences presented in ABX79676-ABX80022 are the polymorphic repeats identified for a search of human ESTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying a candidate polymorphic repeat within a coding sequence, understanding or treating genetic disease, comprises detecting tandem repeats in a target coding sequence and scoring the repeats for
                                                                                                                                                                                                                                                                                          EST; expressed sequence tag; ss; polymorphic repeat, tandem repeat, polymorphic marker prediction of ubiquitous simple sequences; POMPO Rep-X; human; genetic disease; drug-treatment; Machado-Joseph; Haw River syndrome; Huntington's disease; fragile-X syndrome; Predreich's atexis; myotonic dystrophy; hyperandrogenaemia; spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.5%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 6.8e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12 BP; 0 A; 7 C; 0 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                     EST polymorphic DNA repeat polynucleotide #329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example; Col 1163; 588pp; English.
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                                                                                                                                 ABX80004 standard; cDNA; 12 BP.
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                                                                                                                                                                                                               17-APR-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polymorphic probability.
Wren JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-208818/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US6472154-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-OCT-2002,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Garner HR,
                                                                                                                                                                        ABX80004,
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Fondon JW;

Identifying a candidate polymorphic repeat within a coding sequence, i understanding or treating genetic disease, comprises detecting tandem repeats in a target coding sequence and scoring the repeats for

Example; Col 267; 588pp; English

for tandem

polymorphic probability.

Fondon JW;

Minna JD,

Wren JD,

Garner HR,

WPI; 2003-208818/20

(TEXA ) UNIV TEXAS SYSTEM

99US-00475947 99US-00475947

31-DEC-1999;

31-DEC-1999;

Homo sapiens

US6472154-B1

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The invention discloses a method for identifying a candidate polymorphic repeat within a coding sequence (expressed sequence tag, EST), which comprises detecting trandem repeats in a target coding sequence, scoring the repeats for polymorphic probability and generating a dataset correlating the repeat. The computational methods (polymorphic repeat.) are useful for identifying and detecting candidate polymorphic repeats in human genes, which can be used to understand, treat or eliminate genetic diseases, predispositions or adverse durg-treatment reactions. Examples of diseases linked to nucleotide repeats are Machado-Joseph, Haw River syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxis, myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and spinocereballar ataxia. The sequences presented in ABX79676-ABX80022 are the polymorphic repeats identified for a search of human ESTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12 BP; 6 A; 4 C; 2 G; 0 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 7.8; DB 1;
Pred. No. 6.8e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADA18488 standard; DNA; 12 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.5%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 81.8
es 9; Conservative
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(first entry)

20-NOV-2003

0

Gaps

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Conservative GGAGAAACAGA 742

Local Similarity

Best Loc Matches

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GGAGAGAGAGA

RESULT 1488

ABX79734

732 12

à g

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ADC22510 standard; DNA; 12 BP.

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This invention described a novel method for parallel sequencing analysis of nucleic acids in which single-stranded fragments, of 50-1000 bases, are generated, representing overlapping fragments of a complete sequence. The fragments are then attached, as a complex with one or primers, in random fashion to a reaction surface. The complementary strand of the single stranded fragment is constructed using one or more DNA polymerases on a cycle involving incubating the bound complex with a least one of in a cycle involving incubating the bound complex with a fluorescent dye, different for each modified nucleotide so that they can be distinguished. Individual incorporated modified nucleotides can be detected from the contracteristic fluorescence, with simultaneous detection of the relative positions of the complex on the surface and optionally repeating the entire cycle. Detection in is by broad-field epifluorescence, laser-contracted in successive cycles. Bach fragment includes a primar binding sequences are determined through specific correlation of the signal detected in successive cycles. Bach fragment includes a primar binding site (BBS), one in each strand for double-stranded sequences, and this site is the same for all fragments. The method is used (i) to identify mutations, particularly all single-nucleotide polymorphisms in a gene and (ii) for analysis of gene expression. Compared with known methods, this process is less expensive, quicker and more efficient, especially it allows many fragments to short fragments for mutational analysis, in the same process single nucleic acid molecules can be detected, the risk of errors through failure of synchronization in a population and work and process of the nucleic acid to not need to be made (eliminating conjuge of the nucleic acid to not need to be made (eliminating conjuge of the nucleic acid to not need to be made (eliminating and a trips of and PCN). Even weakly expressed, or unknown, genes can be sequenced and conty a trip a gene and even weakly macunt of start
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parallel sequencing of nucleic acid fragments, useful e.g. for detecting mutations, comprises sequential single-base extension of immobilized fragment-primer complex.
                                           parallel sequencing; fluorescence; detection; mutational analysis; NSKF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 56; 114pp; German.
                                                                                                                                                                                                                                                             28-AUG-2002; 2002WO-EP009614.
                                                                                                                                                                                                                                                                                                              29-AUG-2001; 2001DE-01042256.
NSKF target DNA sequence
                                                                                                                                                                                                                                                                                                                                                         (GENO-) GENOVOXX GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-290205/28.
                                                                                                                                                               WO2003020968-A2.
                                                                                                                                                                                                                                                                                                                                                                                                         Tcherkassov D;
                                                                                                                  Unidentified.
                                                                                                                                                                                                             13-MAR-2003
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Score 7.8; DB 1; Length 12;
Pred. No. 6.8e+02;
0; Mismatches 2; Indels
Sequence 12 BP; 6 A; 6 C; 0 G; 0 T; 0 U; 0 Other;
                                     35.5%;
                                     Query Match
Best Local Similarity 81.8
Matches 9; Conservative
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RESULT 1490 ADC22510/c

RESULT 1491

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The present invention describes a recombinant fusion protein (I) for detecting binding of a molecule of interest. (I) comprises: (a) a detecting binding of a molecule of interest. (I) comprises: (a) a detection domain, on binding domain for the molecule of interest. The detection domain, the first localisation domain and the binding domain for the molecule of interest are operably linked. The binding domain for the molecule of interest are operably linked. The binding domain for the molecule of interest are operably linked. The binding domain for the molecule of interest use separated from the first localisation domain by 0 comming of a molecule of interest is separated from the first localisation domain by 0 comming of a molecule of interest both do not occur in a single non-recombinant protein with the same spacing as in the recombinant fusion protein, of protein for detecting binding of a molecule of interest. Also described.

(1) a recombinant moleic acid encoding the recombinant fusion protein, or sequences operably linked to the recombinant mucleic acid control sequences operably linked to the recombinant mucleic acid control sequences operably linked to the recombinant mucleic acid control expression vector; (4) a kit for detecting binding of the molecule of interest; and (5) a method for identifying compounds that alter the binding of the molecule of interest. The recombinant fusion protein is useful for detecting binding of a molecule of interest. The recombinant protein and enables the monitoring of biochemical eventment in live, intact con the interest is used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant fusion protein comprising detection and first localization domains and a binding domain for the molecule of interest, useful for detecting binding of a molecule of interest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                       recombinant fusion protein; fusion protein; binding; detection; localisation domain; binding domain; subcellular compartment localisation; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                  Protein binding domain nucleotide sequence SEQ ID NO:359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12 BP; 0 A; 3 C; 3 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 359; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen Y;
                                                                                                                                                                                                                                                                                                                                                                      01-AUG-2002; 2002WO-US024572
                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-2001; 2001US-0309395P.
13-DEC-2001; 2001US-0341589P.
                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bright G, Premkumar DR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CELL-) CELLOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 AGACAGAACGC
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                                                                            (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; ADC22511
                                                                                                                                                                                                                                                                                402003012068-A2.
                                                                                                                                                                                                                                             Homo sapiens.
                                                                            18-DEC-2003
                                                                                                                                                                                                                                                                                                                              13-FEB-2003
                                     ADC22510;
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ds; cell based toxin; luminescent reporter molecule; biosensor; microchip; drug discovery; MAP4; epitope; affinity tag; protease recognition site; caspase; target domain. Protease recognition site for caspase-6 DNA #1. ADC18377 standard; DNA; 12 BP. 18-DEC-2003 (first entry) Giuliano K, Kapur R; WPI; 2003-786988/74. US2003096322-A1. Unidentified. 01-DEC-1999; 25-FEB-2000; 27-FEB-1997; 22-MAY-2003 31-AUG-1999 17-SEP-1999 08-MAR-1999 ADC18377; ADC18377 

97US-00810983. 98US-00031271 99US-0123399P. 99US-0123399P. 99US-0151797P. 99US-010388965 99US-0168408P. 19-MAR-2002; 2002US-00100957.

(CELL-) CELLOMICS INC.

P-PSDB; ADC18378

Cell based toxin characterization method for e.g. in drug discovery paradigm, involves treating cells possessing luminescent reporter molecules with fluorescence based molecules reagents to detect presence of toxins.

Example 10; SEQ ID NO 65; 98pp; English.

the invention relaters to characterising cell based ucknish, where the Cell possessing luminescent reporter molecules (biosensors) are provided on a microchip, and are treated with fluorescence based molecular reagents.

The cells are photographed with fluorescence optics, and the optical information is converted into digital data. The presence of the toxin in information is converted into digital data, based on changes in the classifier in each cell. Also included are a computer readable storage medium storing a cell based toxin characteristing or cell based toxin detection. The method is used for characterishing or detecting a biological cell based toxin that affect particular biological functions and for preparing molecular biochemical arrays for new drug discovery paradigm. It is also used in automated DNA sequencing, capplication, positional cloning, Mybridisation by combining many cell carget validation and candidate optimisation by combining many cell carget validation and candidate optimisation by combining many cell carget validation and candidate optimisation by combining many cell carget times and faster evaluation of promising drug candidates. The capent and test compounds required in each assay. The biosensor comprises a signal component (fluorescence protein (fuse escent protein (fuse escent protein (fuse escent protein) and a tester the mine and test compounds required in each assay. The biosensor centering it to microtubules) or detectable signal (epitope or affinity tethering it to microtubules) or detectable signal (epitope or affinity tethering it to microtubules) or detectable signal (epitope or affinity tethering it to microtubules) or detectable signal (epitope or affinity tethering it to microtubules) or detectable signal (compartment). The present encodes a protease recognition site (e.g. for a caspase protein) and a compartment). The present encodes a protease recognition site (e.g. for a dapase recognition. The invention relates to characterising cell based toxins, where the cell

Gaps . 0 Score 7.8; DB 1; Length 12; Pred. No. 6.8e+02; 0; Mismatches 2; Indels Sequence 12 BP; 6 A; 1 C; 3 G; 2 T; 0 U; 0 Other; . 0 35.5%; 81.8%; Query Match
Best Local Similarity 81.8
Matches 9; Conservative 732 GGAGAAACAGA 742 1 GTAGAAATAGA 11 g

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Search completed: October 18, 2004, 14:07:21 Job time : 8 secs

AZ386064

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/lab host="B. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/clone_lib="Wouse 10kb plasmid UUGCIM library"
/note="Vector: FWD42Iv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was hydrodynamically sheared by repeated from an originate to the blunt ends in high molar excess. The
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli XII0-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                  Mus musculus (house mouse)

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

R Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Rellam,H., Longacre,S., Mahmoul,M., Meenen,E., Pedersen,T.,

Rellam,H., Rose,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

AL Unpublished (2000)

AL Unpublished (2000)

AL Unpublished (2000)

R University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
AZ386064 linear GSS 02-OCT-2000 linear GSS 02-OCT-2000 lM0145C04F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0145C04 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0145 row: C column: 04
Seg primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
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/db xref="taxon:1000"
/clone="UUGCIM0145C04"
                                                                   AZ386064.1 GI:10499860
GSS.
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84112, USA
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Matches 13; C
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ACCESSION: B07312
ACCESSION: B0587766
ACCESSION: C6771120
ACCESSION: AL394689
ACCESSION: C7311011
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ACCESSION: CR2989850
ACCESSION: CR304450
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ACCESSION: CR308889
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ACCESSION: CF318771
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ACCESSION: CF3794554
ACCESSION: CF313731
ACCESSION: CF31350
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ACCESSION: CF301888
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ACCESSION: CA794225
ACCESSION: CA851674
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                                                                                                      October 18, 2004, 14:39:47; Search time 0.001 Seconds (without alignments) 38.836 Million cell updates/sec
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   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 27 summaries
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Match Length DB
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73
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Perfect score:
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No.
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5

ò Gaps . 0 17.0%; Score 12.4; DB 1; Length 19; 92.9%; Pred. No. 1.3; 1:ve 0; Mismatches 1; Indels . 918 TCTTTGCCTTTTAT 931 4 rerrrecerrrage 17 Similarity 92.9

ALIGNMENTS

RESULT 2 BQ589768

RESULT

TITLE

schultz1-899 rst

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To (bases 1 to 13)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
plant J. 32 (5), 845-857 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pCMVSPORT6; Site_1: Sall; Site_2: NotI; ontDA library from sugar beet, ILbrary provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sall-NotI, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B07312 G360T3 WVAT4 sheared genomic library Trypanosoma brucei rhodesiense genomic clone G360, genomic survey sequence.
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I (bases 1 to 12)
El-Sayed, N.M.A. and Donelson, J.E.
A survey of the Trypanosoma brucei rhodesiense genome using shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     orientation:
SP6-SalI-CCACGCTCCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
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Trypanosoma brucei rhodesiense
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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Pred. No. 3.4;
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                                                                                                                                                                                                                                                                                                                                                  Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 13 Std Error: 0.00
Plate: 1 row: J column: 02
Seq primer: SP6; CATACGATTAGGTGACACTATAG.
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97237559
                           Caryophyllales; Amaranthaceae; Beta.
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/organism="Beta vulgaris"
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Contact: El-Sayed NMA
John Donelson's Laboratory
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B07312.1 GI:1667053
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E012680-024-020-D03-SP6 MPIZ-ADIS-024-storage root Beta vulgaris
cDNA clone 024-020-D03 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                           Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; eudicotyledons; core eudicots; Caryophylales; Amaranthaceae; Beta.

1 (bases 1 to 13)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., and Radelof,U.

Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="storage root"
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/note="vector: pcMvSPORT6; Site_3: NotI; Site
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SP6-Sall-CCACGCGTCCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
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E012207-024-001-J02-SP6 MPIZ-ADIS-024-inflorescence Beta vulgaris
cDNA clone 024-001-J02 5-PRIME, mRNA sequence.
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0
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ADIS DNA core facility at WPIZ
ADIS DNA core facility at WPIZ
MAX-Planck-Institute for Plant Breeding Research
Carl-Von-Linne Weg 10, 50829 Koeln, Germany
Fax: 049221506281,
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 13 Std Error: 0.00
Plate: 20 row: D column: 03
Seq primer: SP6; CATACGATTAGGTGACACTATAG.
Location/Qualifiers
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Pred. No. 2;
0; Mismatches 2; Indels
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                                                                                                                                 BQ589768.1 GI:26119351
EST.
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Best Local Similarity 84.6
Matches 11; Conservative
                                                                                                                                                                                                                               Beta vulgaris
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/note="Vector: pCMVSPORT6; Site_1: Sall; Site_2: Not1; Onte="Vector: pCMVSPORT6; Site_1: INterry provided by KWS Kleinwarzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sall-Not1, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSS 03-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SP6-Sall-CCACGCGTCCG-Sprime-cDNa-polya-CC-Not1-T7; Note: Sequencing granted in the context of the GAB1-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GAB1-Primary database:http://gabi.rzpd.de"
                                       cultivar="KWS2320 (double haploid, monogerm breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="leaves"
/dev_stage="shoot"
/lab_host="k. coli strain DHSalpha"
/clone lib="tmf"
/note="Vector: PCR 4Blunt-TOP; 0.8-1.2 kb methylation
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1. (bases 1 to 12)

Li,W., Zhang,P., Fellers,J., Friebe,B. and Gill,B.S. Sequence composition, organization and evolution of a basic Unpublished (2003)
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Dr. Biram S. Gill's Lab
Wheat Genetics Resource Center, Kansas State University
4024 Throckmorton, Manhattan, KS 66506-5502, USA
Tel: 785-532-1108
Fax: 785-552-5692
Email: wli@ksu.edu
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Pred. No. 4.6;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                      /lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-leaf"
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/mol_type="genomic DNA"
/strain="AL 6/78"
/db xref="taxon:37682"
/clone="tmf17C15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             filtered genomic DNA library"
                                                                                                                                      /db_xref="taxon:161934"
/clone="024-010-M01"
/tissue_type="leaf"
                                                                                                      /db xref="GABI:185095"
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ilarity 81.8%;
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CG677120
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                                                                                                                                                                                                                                                                                                                                                                                           /organism="Trypanosoma brucei rhodesiense"
/mol type="genomic DNA"
/sub_species="rhodesiense"
/db_xref="taxon:1286"
/db_xref="taxon:1286"
/dlone="0360"
/dev_stage="Bloodstream form"
/done lib="WMAT4 sheared genomic library"
/clone lib="WMAT4 sheared genomic library"
/clone lib="WMAT4 sheared genomic library"
/clone lib="WMAT4 sheared genomic Lypranosomes reexpressing the WMAT4
/clone library construction, the DNA was mechanically shotgun library construction, the DNA was mechanically shotgun library construction, the DNA was mechanically shotsun library construction, the DNA was mechanically shotsunt-ended with T4 DNA polymerase. Following dephosphorylation with Shrimp Alkaline Phosphatase, DNA fragments were cloned into the pCR-Script vector
(Stratagene)."
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E012340-024-010-M01-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone
024-010-M01 5-PRIME, mRNA sequence.
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Bukaryota, Varidiplantae, Streptophyta, Embryophyta, Tracheophyta,
Bukaryota, Wardoliophyta, eudicotyledons, core eudicots;
Caryophyllales, Amaranthaceae, Beta.
1 (Bases 1 to 12)
1 (Bases 1 to 12)
1 (Bases 1 to 12)
2 (Bases 1 to 12)
2 (Bases 1 to 12)
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Howard Hughes Medical Institute
300 EMRB, Dept. of Biochemistry, University of Iowa, Iowa City,
52242
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Pred. No. 3.4;
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ADIS DNA core facility at MPIZ
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Max-Von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: Weisshaa@mpiz-koeln.mpg.de
Insert Length: 12 Std Brror: 0.00
Plate: 10 row: M column: 01
Seq primer: SP6; CATACGATTTAGGATGATAGG.
                                                                                                                               Tel: 319 335 6918
Fax: 319 335 6764
Email: nelsayed@vaxa.weeg.uiowa.edu
Insert Length: 700 Std Error: 200.00
Seq primer: T3 primer
Class: shotgun.
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    .12
    /organism="Beta vulgaris"
    /mol_type="mRNA"

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BQ587766.1 GI:26117348
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Matches 9; Conservative
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CK298980
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                                                                                                                                                        CNSO6E5N 1 inear GSS 17-JUN-2001
T3 end of clone AROAA018H04 of library AROAA from strain CBS 732 of
Zygosaccharomyces rouxii, genomic survey sequence.
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                                                                                                                                                                                                                                                                                           Sygosaccharomyces rouxii
Zygosaccharomyces rouxii
Zygosaccharomyces rouxii
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
Baccharomycetels; Ascomycota; Saccharomycetes;
Saccharomycetels; Saccharomycetacee; Zygosaccharomyces.

(bases 1 to 9)
Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malperuw, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaia, T. Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Mincher, P., Atraub, M., Potier, S., Tekaia, F., Dujon, B., Wincker, P., Ariguenave, F. and Souciet, J.

Genomic exploration of the hemiascomycetous yeasts: 8.
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FEBS Lett. 487 (1), 3-12 (2000)
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FEBS Lett. 487 (1), 52-55 (2000)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Enhartoideae; Spermatophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

E (bases 1 to 10)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTS

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyengai, Korea

Tal: 82 31 330 6193

Fax: 82 21 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Oryza sativa"
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CF311011

ABF--06-B02.b1 ABF3-overexpressing transgenic rice plasmid CDNA Library (ABF) Oryza sativa CDNA clone ABF--06-B02, mRNA sequence.
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1 (bases 1 to 10)

Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B., Staskantoz,B., Jin,H. and Baker,B.

Graskantoz,B., Jin,H. and Baker,B.

Unpublished (2003)

Coher_ESTS: ESTY6163

Contact: Robin Buell

The Institute for Genomic Research
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Location/Qualifiers
                                                                                                                             CF311011.1 GI:33682772
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7LEAF--04-A13.g1 Rice leaf plasmid cDNA linear EST 15-AUG-2003
sativa_cDNA clone 7LEAF--04-A13, mRNA sequence.
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae, Oryza,
1 (bases 1 to 11)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Rim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                              orientation:
SP6-SalI-CCACGCGCCCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
SP6-SalI-CCACGCGCCCG-Sprime-cDNA-polyA-CC-NotI-T7;
Sequencing granted in the context of the GABI-Beet
project, local Pi: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
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Contact: Nature 1.8.7.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

Yorgin, KyeongGi, Korea
Tel: 82 31 330 6193
Fax: 82 31 320 6193
Fax: 82 31 320 6195
Fax: bhnahm@bio.myongji.ac.kr.

Location/Qualifiers
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/organism="Oryza sativa"
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cold-stress of leaves (50 hr, one pathogen challenged leaves (50 hr, one syringae py tomato 12 hr;
Xanthomonas campestris py campestris 12 hr, 18hr;
Pseudomonas syringae py phaseolicola 18hr, and Xanthomoas campestris py vesicatoria 18hr). RNA was isolated from these tissues and pooled in approximately equal molar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BQ585171 11 bp mRNA linear EST 06-DEC-2002 S014222-024-001-J02-SP6 MPIZ-ADIS-024-inflorescence Beta vulgaris cDNA clone 024-001-J02 5-PRIME, mRNA sequence.
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Beta vulgaris
Beta vulgaris
Beta vulgaris
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Caryophyllales; Amaranthaceae; Beta.
1 (Bases I to 11)
1 (Bases I to 11)
1 (Bases I to 11)
2 Ebases I to 11)
2 Drungowski, M.; Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M., Drungowski, M.; Schulz, B., Wurck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.
Cinstruction of a 'unigene' cDNA clone set by oligonucleotide
Gingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
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/organism="Beta vulgaris"
/mol type="mRNA"
/cultivar="KW82320 (double haploid, monogerm breeding
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9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: GTA ATA CGA CTC ATA AGG C.
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Pred. No. 3.6;
0; Mismatches 1; Indels
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ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 11 Std Error: 0.00
Plate: 1 row: J column: 02
Seg primer: SP6; CATACGATTTAGGTGACCTATAG.
                                                                                                                                                                                                                                                                   /organism="Nicotiana benthamiana"
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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ACCESSION VERSION KEYWORDS

RESULT 12 CF304450/c LOCUS DEFINITION

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CF543159 11 bp mRNA linear BST 22-SEP-2003 S014678-024-030-006-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone 024-030-006 5-PRIME, mRNA sequence.
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Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
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                               Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Wector: pCR4-TOPO, Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
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/dev stage="14 days after germination"
/dev stage="14 days after germination"
/lab_host="8.coli DH10B"
/clone lib=#ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
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/mol type="mRNA"
/culTivar="KWS2320 (double haploid, monogerm breeding
line)"
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                                                                                                                                                                                                                                                      Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr
Location/Qualifiers
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Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: wetsshaadmpiz-koeln.mpg.de
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Plane: 30 row: 0 column: 06
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/clone="ABF--04-E09"
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/cultivar="Nackdong"
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Unpublished (2003)
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ABF--04-E09.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--04-E09, mRNA sequence.
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Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Large-scale Sequencing Analysis of Rice ESTs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongJin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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/lab host="s.col; SOLR"
/lab host="s.col; SOLR"
/clone lib="ABF3-overexpressing transgenic rice lambda
phage CDNA library (ABF1)"
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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TITLE

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CFZ77997

B bp mRNA linear EST 14-AUG-2003
GTYZA SALIVA CDNA clone 14ETL--03-L19, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (Dases 1 to 8)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Large scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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Oryża sativa
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonuclectides and then used as templates for RT-PCR."
                                                                                                             Gaps
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fragments were cloned into the pCR-Script vector (Stratagene)."
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Cultivar="Nackdong"

db xref="taxon:4530"

clone="14ETL-03-L19"

fissus _Vype="laaf"

dev stage="14 days after

flab_nost="E_coli DH108"
                                                                   Score 7.4; DB Pred. No. 5.6;
                                                                                                             0; Mismatches
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87.5%; Pred. No. 39;
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CF301888.1 GI:33673649
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                                                                     10.1%;
88.9%;
                                                  Query Match
Best Local Similarity 88.5%
Best Local 8; Conservative
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CF301888/c
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CF277997
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                                             Trypanosoma.
1 (bases 1 to 12)
El-Sayed,N.M.A. and Donelson,J.E.
A survey of the Trypanosoma brucei rhodesiense genome using shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 bp DNA linear GSS 26-MAR-1997 G360T3 WVAT4 sheared genomic library Trypanosoma brucei rhodesiense genomic clone G360, genomic survey sequence.
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Howard Hughes Medical Institute
300 EMRB, Dept. of Biochemistry, University of Iowa, Iowa City, IA
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/clone_lib="MVAT4 sheared genomic library"
/clone=lib="MVAT4 sheared genomic library"
/note="Wector: pCR-Script Amp SK(+) (Stratagene), Site_1:
Srf I; Genomic DNA was isolated from a cloned population
of bloodstream trypanosomes reexpressing the MVAT4
metacyclic variant surface glycoprotein (VSG). For the
shotgun library construction, the DNA was mechanically.
sheared to give a tight size distribution, then
blunt-ended with T4 DNA polymerase. Following
dephosphorylation with Shrimp Alkaline Phosphatase, DNA
                                                                                                                                                                                                                 SP6-Sall-CCACGCGTCCG-Sprime-cDNA-polyA-CC-Not1-T7; Note:
                                                                                                                                                                                                                                     Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"
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Eukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                       Query Match
10.1%; Score 7.4; DB 1; Length 11;
Best Local Similarity 88.9%; Pred. No. 4.6;
Matches 8; Conservative 0; Mismatches 1; Indels
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/organism="Trypanosoma brucei rhodesiense"
/organism="Trypanosoma brucei rhodesiense"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
/db_xref="taxon:31286"
/clone="G360"
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Mol. Biochem. Parasitol. 84 (2), 167-178 (1997)
97237559
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Fax: 319 335 6764
Fax: 319 335 6764
Insert Length: 700 Std Error: 200.00
Seg primer: T3 primer
Class: shotgun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trypanosoma brucei rhodesiense
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Contact: E1-Sayed NMA
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/clone lib="Rice leaf plasmid cDNA library II (7LEAF)" /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and Then used as templates for RT-PCR."
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8.8%; Score 6.4; DB
Best Local Similarity 87.5%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches
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mol_type="mRNA"

cultivar="NacKdong"

/db xref="taxon:4530"

/clone="ABF--08-L15"
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CF312818.1 GI:33684579
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7LEAF--08-MO7.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
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1 (Bases 1 to 8)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbbio.com, bhnahm@bio.myongji.ac.kr.
                                                                                                                                                                                                                                                 Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yonglin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
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/tissue_type="leaf"
/tissue_type="leaf"
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/clone lib="Rice leaf plasmed cDNA library II (7LEAF)"
/note="Wector: pCR4-TOPO; Site_1: BCORI; mRNA was capped notes"wector: pCR4-TOPO; Site_1: BCORI; mRNA was capped notes"wector: pCR4-TOPO; Site_1: BCORI; mRNA was capped notes"wector: pCR4-TOPO; Site_1: BCORI; mRNA was capped notes for many considerations of the property of t
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartcideae; Oryzeae; Oryza.

1. (bases 1 to 8)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
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    Location/Qualifiers
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/clone="7LEAF"-08-M07"
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/dev_stage="7 days after_germination"
/lab_host="E.coli DH108"
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/mol_type="mRNA"
/cultivar="Nackdong"
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/organism="Oryza sativa"
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CF302851.1 GI:33674612
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CA794225 9 bp mRNA linear EST 05-DEC-2002 Cac_BL_1208 Cac_BL (Bean and Leaf from Amelonardo type Cacao) Theobroma cacao cDNA clone Cac_BL_1208 5', mRNA sequence. CA794225, GA794225.1 GI:26051301
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ABF--08-L15.g1 ABF3-overexpressing transgenic rice plasmid CDNA library (ABF) Oryza sativa CDNA clone ABF--08-L15, mRNA sequence.
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Oryza sativa

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Burartodaea; Oryzeae; Oryza.

Enrhartoideae; Oryzeae; Oryza.

I bases 1 to 8)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Mn,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTS

Umpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bloscience and Bloinformatics, MyongJi University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried for Zhrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression
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/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
                                                                      Gaps
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Score 6.4; DB 1; Length 8; Pred. No. 39;
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8.8%; Score 6.4; DB 1; Length 8;
Best Local Similarity 87.5%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 1; Indels
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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location/Qualifiers
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Best Local Similarity 87.5%;
Matches 7; Conservative
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Alkharouf, N.W., Khan, R. and Matthews, B.F.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARC, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CA851674 9 bp mRNA linear EST 01-AUG-2003 DIGCIO_F22_05.abl cDNA Peking library 2, 4 day SCN3 Glycine max cDNA clone_D16C10_5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Theobroma cacao"
/mol_type="mRNA"
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/db_xref="taxon:3641"
/clone="cac_BL_1208"
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/cell_type="Whole organ"
/dev_stage="maturity"
/lab_host="XL-1 Blue MRP'"
/clone_lib="Cac_BL (Bean and Leaf from Amelonardo type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ediaryora; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                            Tracheophyta;
                                                                                                               Theobroma.

1 (bases 1 to 9)

Jones, E.G., Allaway, D., Gilmour, D.M., Harris, C., Rankin, D.,

Retzel, E.R. and Jones, C.A.

Gene discovery and microarray analysis of cacao (Theobroma cacao L.) varieties

Planta 216 (2), 255-264 (2002)
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                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheol
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;
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3d Dundee Road, Slough, Berkehire, UK, SL1
Tel: +44 1664 416644
Email: Paul.Jones@eu.effem.com
Seg primer: T3
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Best Local Similarity 87.5%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 1.
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Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.
                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                    Theobroma cacao (cacao)
Theobroma cacao
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CA851674.1 GI:33388467
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Glycine max (soybean)
Glycine max
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CA851674/c
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CF312817

9 bp mRNA linear BST 15-AUG-2003
ABF--08-L15.b1 ABF3-overexpressing transgenic rice plasmid cDNA
ABF--08-L15, mRNA sequence.
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta,
Spermatophyta, Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaee; Oryzae.

1 (bases 1 to 9)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
                   /mol_trye="mcMa"
/mol_trye="mcMa"
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/db_xcs="taxon:3847"
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/dev_stage="Seedlings"
/dow_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
Genomics and Bioinformatics, MyongJi University
YongJi, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 635
Exax: 82 31 321 635
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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                                                                                                                                                                                                                                                                                        Score 6.4; DB 1; Length 9; Pred. No. 35; 0; Mismatches 1; Indels
organism="Glycine max"
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schultz1-899.rst

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of Bioscience and Bioinformatics, MyongJi University
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CA794554/c
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Enrhartoideae; Oryzeae; Oryza.

I (bases 1 to 9)
S. Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
YongIn, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
                                                             9 Dp mRNA linear EST 15-AUG-2003 HD--09-A13.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--09-A13, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="callus"
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/clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
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Xim,J.S., Vun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large scale Sequencing Analysis of Rice ESTS
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA library (HD)"

Another "Vector: pCR4-TOPO, Site_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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clone="HD--09-A13"
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Best Local Similarity 87.5
Matches 7; Conservative
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Gac_BL_1496 Cac_BL (Bean and Leaf from Amelonardo type Cacao)
Theobroma cacao cDNA clone Cac_BL_1496 5', mRNA sequence.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;
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Jones, P.G., Allaway, D., Gilmour, D.M., Harris, C., Rankin, D.,
Retral, B.R. and Jones, C.A.
Gene discovery and microarray analysis of cacao (Theobroma cacao
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
Tel: +44 1664 416644
Seq primer: T3.
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Planta 216 (2), 255-264 (2002)
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resistant soybean

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1. (bases 1 to 8)
Alkharouf,N.W., Khan,R. and Matthews,B.F.
Analysis of expressed sequence tags from roots of resistant soybea:
infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
                                                                                                                                                                                                                                                                                                                                                                             / organism="Glycine max"
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extracted from Peking roots 2 and 4 days past invasion."
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                                                                                                                                                                                                                                                       USA
Tel: 301 504 5750
Fax: 301 504 5726
Email: alkharon@ba.ars.usda.gov.
Location/Qualifiers
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enthartoideae; Oryzeae; Oryza.

Enthartoideae; Oryzeae; Oryza.

Enthartoideae; Oryzeae; Oryza.

S Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTS

Lonbublished (2003)

Conteat: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, KyengGi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Oryza sativa"
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HD--01-P12.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Agnoliophyta; eudicotyledons; core eudicots;
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8.2%; Score 6; DB 1; Length 8; 100.0%; Pred. No. 39; Aztive 0; Mismatches 0; Indele
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1,92,96,89,89,44,11,11,11,19,41,00,10,1,40,84,941,188,841,141,19,9,9,9,9,9,11	Thence 2 Thence 1 Thence 1 Thence 1 Thence 1 Thence 1 Thence 2 Thence 3 Thence 3 Thence 3 Thence 3 Thence 3 Thence 4 Thence 3 Thence 4 Thence 3 Thence 3 Thence 3 Thence 3 Thence 3 Thence 3 Thence 3 Thence 4 Thence 3 Thence 4 Thence 4 Thence 3 Thence 4 Thence 4 Thence 3 Thence 4 Thence 4 Thence 4 Thence 5 Thence 6 Thence 6 Thence 6 Thence 6 Thence 6 Thence 6 Thence 7 Thence 6 Thence 7 Thence 6 Thence 6 Thence 7 Thence 6 Thence 7 Thence 6 Thence 7 Thence
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14.8 15 1 US-08-894-922h-1 Sequence 2.14.8 15 1 US-08-585-684B-271 Sequence 2.14.8 15 1 US-09-038-037-271 Sequence 2.14.8 15 1 US-09-038-073-271 Sequence 2.14.2 12 1 US-09-038-073-271 Sequence 2.14.2 12 1 US-08-101-032-201-85 Sequence 2.14.2 12 1 US-08-101-92-945 Sequence 2.14.2 15 1 US-08-101-948-418 Sequence 2.14.2 15 1 US-08-101-948-418 Sequence 2.14.2 15 1 US-08-101-948-419 Sequence 2.14.2 16 1 US-08-101-948-419 Sequence 2.14.2 16 1 US-08-101-948-419 Sequence 2.14.2 10 US-08-101-948-419 Sequence 2.14.2 10 US-08-101-948-219 Sequence 2.14.2 1 US-08-101-948-219 Sequence 2.14.3 1 US-08-101-948-219 Sequence 2.13.4 1 US-0	13.4 14 105-08-535-249-29 Sequence 20 13.4 14 105-09-874-601-110 Sequence 113.4 14 105-09-874-601-110 Sequence 113.4 14 105-09-874-601-110 Sequence 113.4 15 105-09-874-601-113 Sequence 113.4 15 105-07-744-282C-123 Sequence 113.4 15 105-07-744-282C-123 Sequence 113.4 15 105-08-319-492B-73 Sequence 113.4 15 105-08-319-492B-73 Sequence 113.4 15 105-08-319-492B-170 Sequence 113.4 15 105-08-319-492B-170 Sequence 113.4 15 105-08-319-492B-436 Sequence 113.4 15 105-08-319-492B-436 Sequence 2113.4 15 105-08-311-486C-75 Sequence 2113.4 15 105-08-311-486C-75 Sequence 778-08-311-486C-75 Sequence
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1 US-08-388-353-181 Sequence 188 (198-08-388-353-228) Sequence 228 (198-08-388-353-228) Sequence 228 (198-08-388-353-228) Sequence 228 (198-08-388-353-231) Sequence 228 (198-08-388-353-324) Sequence 238 (198-08-388-353-304) Sequence 238 (198-08-388-353-304) Sequence 238 (198-08-388-353-304) Sequence 238 (198-08-388-3518-234) Sequence 238 (198-08-388-3518-234) Sequence 238 (198-08-388-3518-234) Sequence 238 (198-08-388-3518-234) Sequence 238 (198-08-388-3518-394) Sequence 238 (198-08-5518-394) Sequence 238 (198-08-5618-304) Sequence 238 (198-08-5618-304) Sequence 238 (198-08-5618-304) Sequence 238 (198-08-150-1564-2) Sequence 248 (198-08-150-1564-4) Seq	108 591B-8 Sequence 8	2 1 US-08-770-565-4 Sequence 4, 2 1 US-08-478-239A-26 Sequence 26
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                                                                                                 RESULT 1

VESULT 1

VESULT 1

SEQUENCE 54, Application US/09106038A

SEQUENCE 1 (0.00794ATION:
PATENTIN NO. 6007995

TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 91
CORRESPONDENCES: 91
CORPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COUNTRY: U.S.A.
ZIP: 92008
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COUNTRY: U.S.A.
ZIP: 92008
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORPUTER: MINT SYSTEM: Windows NT
SOFTWARE: Microsoft Word 97
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US(0.9) 106,038A
FILING DATE: Unne 26, 1998
CLIASSIFICATION NUMBER: RTS-0004
TELESTHOME: (760) 911-9200
TELESTHOME: REPARACTERISTICS:
LENGTH. 18
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US-09-106-038A-55/C

is Sequence 55, Application US/09106038A

is Patent No. 607395

is GENERAL INFORMATION:
APPLICANT: Brenda F. Baker and Lex M. COWSERT

i TITLE OF INVENTION: ANTISENSE MODULATION OF THERI

I TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 91

CORRESPONDENCE ADDRESS:
ADDRESSEE: Isis Pharmaceuticals, Inc.
STREET: 2292 Faraday Avenue
CITY: Carlsbad
COMPUTER READABLE FORM:
COUNTRY: U.S.A.

ZIP: 92008

COMPUTER READABLE FORM:
MODIUM TYPE: 3.5 inch disk, 1.44 Mb

COMPUTER: IBM PC compatible

MODERATING SYSTEM: Windows NT
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STRANDEDNESS: single
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TOPOLOGY: linear
US-09-106-038A-54
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Sequence 13, Appl
Sequence 13, Appl
Sequence 31, Appl
Sequence 24, Appl
Sequence 26, Appl
Sequence 136, Appl
Sequence 136, Appl
Sequence 137, Appl
Sequence 27, Appl
Sequence 28, Appl
Sequence 27, Appl
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US-08-545-785-2
US-08-441-887A-91
US-08-661-330A-94
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US-08-173-489C-295
US-08-173-130A-15
US-08-174-13
US-09-231-303-84
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US-09-231-303-85
US-09-231-303-85
US-09-231-303-85
US-09-175-65-31
US-09-175-65-25
US-09-874-601-135
US-09-874-601-135
US-09-874-601-137
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Query Match

24.7%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 18; Conservative 0; Mismatches 0; Indels
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Sequence 58, Application US/09106038A

Patent No. 600799

GENERAL INFORMATION:
APPLICANT: Brenda F. Baker and Lex M. Cowsert

TITLE OF INVENTION: EXPRESSION

TITLE OF INVENTION: EXPRESSION

NUMBER OF SEQUENCES: 91

CORRESPONDENCE ADDRESS:
ADDRESSEE: Tais Pharmaceuticals, Inc.
STREET: 2292 Faraday Avenue
CITY: Carlsbad
                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT:
Brenda F. Baker and Lex M. Cowsert
APPLICANT:
Brenda F. Baker and Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF THERI
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSE: Isis Pharmaceuticals, Inc.
STREET: 2292 Faraday Avenue
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FORTH OF PATION WINDER: US/09/106,038A FILING DATE: June 26,1998
CLASSIFICATION S14
ATTORNEY/AGENT INFORMATION:
NAME: LAUVEL SPEAT BEFINETEIN NAME: LAUVEL SPEAT BEFINETEIN NUMBER: 37,280
REFERENCE/DOCKET NUMBER: 37,280
REFE
                                                                                                                                                                                          US-09-106-038A-57/c
; Sequence 57, Application US/09106038A
; Patent No. 6007995
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DEDNESS: single
GY: linear
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ZIP: 92008
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 incl
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US-09-106-038A-57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: 15M PC comparable
OPERATING SYSTEM: Windows NT
SOFTWARE: Microsoft Word 97
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/106,038A
FILING DATE: June 26, 1998
CLASSIFICATION: 514
ATTORNEY AGENT INFORMATION:
NAME: LAURE! Spear Bernstein
REGISTRATION NUMBER: 37,280
REGISTRATION NUMBER: 37,280
REGISTRATION NUMBER: AS-0004
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
                                                                                                                   CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Laurel Spear Bernetin
REGISTRATION NUMBER: 37,280
REFERENCE/DOCKET NUMBER: 87,280
TELECOMONICATION INFORMATION:
TELEPHONE: (760) 931-9200
TELEFAX: (760) 603-3820
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
SOFTWARE: Microsoft Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,038A
FILLING DATE: June 26, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            911 TCTTTGGTCTTTGCCTTT 928
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
US-09-106-038A-55
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US-09-106-038A-56
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
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Score 15.4; DB 1; Length 17; Pred. No. 17; 0; Mismatches 1; Indels
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APPLICANT: Pavco, Pamela
APPLICANT: Pavco, Pamela
APPLICANT: Stinchcomb, James
APPLICANT: Stinchcomb, James
APPLICANT: Stinchcomb, James
APPLICANT: Stinchcomb, Jame
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: GROWTH PACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: SUICE 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: LOS ANGELS
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Btorage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WAPPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/0854,040
FILING DATE: January 11, 1996
CTASSIFTATION: 5.4
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: COCLOBE: 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 26, 1995
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (213) 955-040
TELEFAX: (213) 955-040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8

4.09-31-772B-3066/c

5.Sequence 3066, Application US/09371772B

; Patent No. 6566127
                                                                                                                                                                           US-08-584-040-7257/c
; Sequence 7257, Application US/08584040
; Patent No. 6346398
                                   952 ATGIATCGCTACCAACGG 969
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Best Local Similarity 94.1%;
Matches 16; Conservative (
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
US-08-584-040-7257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.7%; Score 18; DB 1; Length 18; 100.0%; Pred. No. 5.9; 0; Indels tive 0; Mismatches 0; Indels
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IS SEQUENCE 59, Application US/09106038A

SEQUENCE 50, Application US/09106038A

Patent No. 6007995

GENERAL INFORMATION:
APPLICANT: Brenda F. Baker and Lex M. Cowsert

TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSE: Isis Pharmaceuticals, Inc.
STREET: Carlsbad
STREET: Carlsbad
STATE: CA
COUNTRY: U.S.A.
COUNTRY: U.S.A.
COUNTRY: U.S.A.

ACOUNTRY: U.S.A.
COUNTRY: Windows NT
SOFTWARE: JS inch disk, 1.44 Mb
COMPUTER READBLE FORM:
MEDLUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OCHEMATING SYSTEM: Windows NT
SOFTWARE: Microsoft Word 97
CURRENT APPLICATION NUMBER: US/09/106,038A
FILING DATE: June 26, 1998
CLASSIFICATION NUMBER: RTS-0004
FILEPHONE: TELEPHONE: (760) 931-9200
TELEPHONE: (760) 603-3820
INPORMATION FOR SEQ ID NO: SP:
ENDUMPER: CRARETERISTICS:
ENDUMPER: CRARETERISTICS:
ENDUMPER: CRARETERISTICS:
ENDUMPER: CRARETERISTICS:
OPERATING SYSTEM: Windows NT
SOSTWARE: Microsoft Word 97
CURRENT APPLICATION DATA:
APPLICATION DATE: US 0.094106,038A
FILING DATE: Unne 26, 1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: LAURE! Spear Bernstein
REGISTRATTON NUMBER: ATS-0004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (760) 931-9200
TELEPHONE: (760) 931-9200
TELEPHONE: (760) 603-3820
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     935 TCCTCTTCATTGGTTTAA 952
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Matches 18; Conservative
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linear
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STRANDEDNESS: singl
                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-106-038A-58
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Gaps

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APPLICANT: Hall, Jeff G.
APPLICANT: Hall, Jeff G.
APPLICANT: Brow, Mary Ann D.
APPLICANT: Brow, Mary Ann D.
TITLE OF INVENTION: Defection Of Nucleic Acids By Multiple
TITLE OF INVENTION: Sequential Invasive Cleavages
NUMBER OF SEQUENCES: 163
CORRESPENDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, Lip
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STREET: California
COUNTRY: United States Of America
ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                        CIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: FIDPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
ATTOMNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E:
REGISTRATION NUMBER: 40,027
REPRENCE/DOCKET UNBER: FORS-02565
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ELBM PC compatible
COPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/823,516
FILING DATE: 24-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/01072
   NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
20.0%; Score 14.6; D
Best Local Similarity 81.0%; Pred. No. 31;
Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                 United States Of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       917 GTCTTTGCCTTTTATCCCTCC 937
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Patent No. 5994069
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                                                                                                                          San Francisco
California
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MOLECULE TYPE:
                                                                                                                                                                                 COUNTRY: Un
ZIP: 94104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-823-516-83
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APPLICANT: KANCO, FORM
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Scobedo, Jaim
APPLICANT: Escobedo, Jaim
APPLICANT: Escobedo, Jaim
APPLICANT: Escobedo, Jaim
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00, 876-J (237)198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR APPLICATION NUMBER: US 08/584,040
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US-09-068-319-5
i Sequence 5. Application US/09068319A
i Patent No. 6777560
i CENERAL INFORMATION:
APPLICANT: Jean-Marie Andrieu
APPLICANT: Wei Lu
ITILE OF INVENTION: METHOD AND KIT
FILE REFERENCE: 31736 PCT USA 072995
CURRENT FILING DATE: 1998-05-04
EARLIER APPLICATION NUMBER: US/09/068,319A
CURRENT FILING DATE: 1996-11-05
BARLIER FILING DATE: 1996-11-05
ARLIER FILING DATE: 1996-11-06
NUMBER OF SEQ ID NOS: 6
SOFTHARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
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Patent No. 5843669
GENERAL INFORMATION:
APPLICANT: Raiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Nataba Applicant: Invanione Cleavage Of TITLE OF INVENTION: Cleavage Of TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.1%; Score 15.7, 94.1%; Pred. No. 17; rive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Human Immunodeficiency Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            910 ITCTTTGGTCTTTGCCTTTTATC 932
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Best Local Similarity 94.1
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-3066
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 22-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/682,853
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/682,853
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,491
FILING DATE: 22-UL-1996
PRIOR APPLICATION NUMBER: US 08/599,491
FILING DATE: 24-UAN-1996
ATTONINY/AGRAT INFORMATION:
ANAME: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kaiser, Michael W.
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Improved Cleavage Agents
NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
ADDRESSER: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 20.0%; Score 14.6; D
Best Local Similarity 81.0%; Pred. No. 31;
Matches 17; Conservative 0; Mismatches
                       TATION ATTAINMENT OF A STANDARD OF A STANDAR
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REGISTATION NUMBER: 40,027
REPERENCE/DOCKET NUMBER: FORS-02575
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-758-314-119
; Sequence 119, Application US/08758314
; Patent No. 6090606
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            917 GICITIGCCITITATCCCTCC 937
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PRIOR APPLICATION DATA:
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20.0%; Score 14.6; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 31;
Matches 17; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
CONTRY: United States Of America
ZIP: 94104
COMPUTER: EDAPP GRA:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC c
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Sequence 119, Application US/08759038
Fatent No. 6090543
GENERAL INFORMATION:
APPLICANT: Prudent, James R.
APPLICANT: Hall, Jeff G.
APPLICANT: Brow, Wictor I.
APPLICANT: Brow, Mary Ann D.
APPLICANT: Dahlberg, James E.
TITLE OF INVENTION: Cleavage of Nucleic Acids
NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/759,038
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,314
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/756,386
FILING DATE: 29-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/682,853
FILING DATE: 12-JUL-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        917 GICTITGCCTTTTATCCCTCC 937
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 29-NOV-1996
21-JAN-1997
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Gaps
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US-09-684-938-119
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                                                                                                                                                    Length 21;
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                                                                                                                                                       DB 1;
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APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Lyamichev, Natasha
TITLE OF INVENTION: Lyamichev, Natasha
FILE REFRENCE: FORS-03755
CURRENT FAPLICATION NUMBER: US/09/308,825A
CURRENT FILING DATE: 1999-10-08
PRIOR PILING DATE: 1999-110-08
PRIOR APPLICATION NUMBER: 08/757,653
PRIOR PELING DATE: 1996-112-9
PRIOR PELING DATE: 1996-112-0
PRIOR PELING DATE: 1996-112-0
PRIOR PELING DATE: 1997-11-29
NUMBER OF SEQ ID NOS: 188
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 119, Application US/09684938
Sequence 119, Application US/09684938
Patent No. 655357
GENERAL INFORMATION:
APPLICANT: Edser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natshar
TITLE OF INVENTION: Improved Cleavage Agents
TITLE OF INVENTION: Improved Cleavage Agents
FILE REFERENCE: FORS 03755
CURRENT FILING DATE: 2000-10-06
FRIOR APPLICATION NUMBER: 08/756
FRIOR FILING DATE: 1999-05-25
FRIOR FILING DATE: 1999-05-25
FRIOR PELICATION NUMBER: 08/757, 653
FRIOR PELICATION NUMBER: 08/757, 653
FRIOR PELICATION NUMBER: 08/758, 314
FRIOR APPLICATION NUMBER: 08/758, 314
FRIOR PELING DATE: 1996-11-29
FRIOR PELING DATE: 1996-11-29
FRIOR PELING DATE: 1997-11-29
NUMBER OF SEQ ID NOS: 188
SOFTWARE PATENTIN VET: 2.0
                                                                                                                                                       Query Match 20.0%; Score 14.6; D
Best Local Similarity 81.0%; Pred. No. 31;
Matches 17; Conservative 0; Mismatches
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                          ENGTH: 21
TYPE: DNA
CRGANISM: Hepatitis B virus
US-09-306-420C-16
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Matches 17; Conserv
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US-09-684-938-119
SEQ ID NO 16
LENGTH: 21
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APPLICANT: BARTHOLOMBUSZ, ANGELINE I
APPLICANT: BARTHOLOMBUSZ, ANGELINE I
APPLICANT: BARTHOLOMBUSZ, ANGELINE I
APPLICANT: AYE, THEIN T
APPLICANT: DEMAN, ROBERT A
TITLE OF INVENTION: VIRAL VARIANTS AND METHODS FOR DETECTING SAME
FILE REFERENCE: 2551-28
CURRENT APPLICATION NUMBER: US/09/306,420C
CURRENT FILING DATE: 1990-05-06
PRIOR APPLICATION NUMBER: PCT/AU97/00520
PRIOR PILING DATE: 1997-06-15
PRIOR PILING DATE: 1996-11-08
NUMBER OF SEC ID NOS: 57
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APPLICANT: BARTHOLOWEUSZ, ANGELINE I
APPLICANT: BARTHOLOWEUSZ, ANGELINE I
APPLICANT: AYE, THEIN T
APPLICANT: AYE, THEIN T
APPLICANT: DEMAN, OLDERT A
TITLE OF INVENTION: UIRAL VARIANTS AND METHODS FOR DETECTING SAME
FILE REFERENCE: 2551-28
CURRENT APPLICATION NUMBER: US/09/306,420C
CURRENT FILING DATE: 1999-05-06
PRIOR PELICATION NUMBER: PCT/AU97/00520
PRIOR APPLICATION NUMBER: PO3519
PRIOR FILING DATE: 1996-11-08
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81.0%; Pred. No. 31
TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 119:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-08-758-314-119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 12, Application US/09306420C; Patent No. 6555311; GENERAL INFORMATION:
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NS-09-304-20C-16/c
; Sequence 16, Application US/09306420C
; Patent No. 6555311
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ORGANISM: Hepatitis B virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 81.0
Matches 17; Conservative
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SOFTWARE: Patentin Ve
SEQ ID NO 12
LENGTH: 21
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APPLICANT: LOCARNI
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US-09-306-420C-12
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US-09-377-309-87
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                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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APPLICANT: Wright, Jim A.
APPLICANT: Wright, Alping H.
TITLE OF INVENTION: ANTITUMOR ANTISENSE SEQUENCES DIRECTED
TITLE OF INVENTION: AGAINST RIBONUCLEOTIDE REDUCTASE
NUMBER OF SEQUENCES: 163
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                Ouery Match 20.0%; Score 14.6; DB 1; Length 21; Best Local Similarity 81.0%; Pred. No. 31; Matches 17; Conservative 0; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSE: KOHN & ASSOCIATES
STREET: 30500 No. 5998383thwestern Hwy. Suite 410
CITYET: 30500 No. 5998383thwestern Hwy. Suite 410
CITYET: Addresse:
COUNTRY: US
ZIP: 48344
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/904,901
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 0227.00004
FELECOMMUNICATION INFORMATION:
TELEFARAL (248) 539-5055
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                         RESULT 18
US-08-904-901-134/c
; Sequence 134, Application US/08904901
; Patent No. 5998383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
ANTI-SENSE: YES
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US-09-249-730-134/c
; Sequence 134, Application US/09249730
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                                                                                 ORGANISM: Artificial Sequence FEATURE:
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 119
LENGTH: 21
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Best Local Similarity
Matches 15; Conserv
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                                                                  TYPE: DNA
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NS-09-249-247-134/C

NS-09-249-247-134/C

Sequence 134, Application US/09249247

Patent No. 6593305;

GENERAL INFORMATION:

APPLICANT: WAGHT, Jim A.

APPLICANT: WIGHT, Jim A.

TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and TITLE OF INVENTION: R2 Components of Ribonuclectide Reductase

TITLE OF INVENTION: R2 Components of Ribonuclectide Reductase

TITLE OF INVENTION: R2 Components of Ribonuclectide Reductase

TITLE OF INVENTION: NAMBER: US 60/023,040

EARLIER PILING DATE: 1996-08-02

EARLIER FILING DATE: 1997-08-02

EARLIER FILING DATE: 1997-08-01

NUMBER OF SEQ ID NOS: 220

SOFWWARE: Patentin Ver. 2.0

SEQ ID NOS: 220
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APPLICANT: WRIGHT, Jim A.
APPLICANT: WRIGHT, Jim A.
APPLICANT: WRIGHT, Jim A.
APPLICANT: VOUNG, Alping H.
TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and TITLE OF INVENTION: R2 Components of Ribonucleotide Reductase FILE REFERENCE: 032396-040
CURRENT APPLICATION NUMBER: US/09/249,730
CURRENT FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 220
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 134
LENGTH: 20
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Patent No. 6258790
GENERAL INPORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Cowsert, Lex M.
TITLE OF INVENTION: ANTISENSE MODULATION OF INTEGRIN 4 EXPRESSION
FILE REFERENCE: ISPH-0390
CURRENT APPLICATION UMBER: US/09/377,309B
CURRENT FILING DATE: 1999-08-19
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Pred. No. 32;
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Best Local Similarity 93.8%;
Matches 15; Conservative
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Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Human
US-09-249-730-134
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CRGANISM: Human
US-09-249-247-134
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PRIOR APPLICATION NUMBER: JP 9-193207
PRIOR FILING DATE: 1997-07-03
PRIOR APPLICATION NUMBER: PCT/JP98/03016
PRIOR FILING DATE: 1998-07-03
NUMBER OF SEQ ID NOS: 20
SGFWARE: Patentin Ver: 2.1
ENGTHARE: 20
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ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                            ORGANISM: Artificial Sequence FEATURE:
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Best Local Similarity 80.0%;
Matches 16; Conservative
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity
Matches 16; Conserv
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US-09-198-452A-4603
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US-09-792-251-23/c
                                                                                                                                                                                           TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: PCR primer used in OTHER INFORMATION: 5' RACE method performed in Example 2 for amplifying the OTHER INFORMATION: 5' end of human MKK7
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                                                                                                                                                                                                                                                       18.6%; Score 13.6; DB 1; Length 20; 80.0%; Pred. No. 46; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: NISHIDA, Eisuke
APPLICANT: NISHIDA, Eisuke
APPLICANT: MORIGUCHI, Tetsuo
APPLICANT: MATGUCHI, Tetsuo
TITLE OF INVENTION: No. 6465618e1 MAPK Kinase
FILE REFERENCE: 98-102705
CURRENT APPLICATION NUMBER: UP 9-367640
PRIOR APPLICATION NUMBER: JP 9-193207
PRIOR APPLICATION NUMBER: JP 9-193207
PRIOR APPLICATION NUMBER: PP-17-07-03
PRIOR APPLICATION NUMBER: PCT/JP98/03016
PRIOR PILING DATE: 1997-07-03
PRIOR PILING DATE: 1998-07-03
NUMBER: PALENTING DATE: 1998-07-03
NUMBER: PALENTING DATE: 1998-07-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17, Application US/09446754
Patent No. 6465618
GENERAL INFORMATION
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL MATSUZAKI, Osamu
TITLE OF INVENTION:
GURRENT APPLICATION NUMBER: US/09/446,754
GURRENT APPLICATION NUMBER: US 9-12-7
FRIOR APPLICATION NUMBER: UP 9-367640
FRIOR FILING DATE: 1997-12-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.6%; Score 13.6; D
80.0%; Pred. No. 46;
iive 0; Mismatches
                                                                                                                                                                           , OTHER INFORMATION: antisense sequence
US-09-377-309-87
              09/166,203
                                                                                                                                                                                                                                                                                                                                                   945 IGGITTAATGTATCGCTACC 964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/09446754 Patent No. 6465618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   913 TTTGGTCTTTGCCTTTTATC 932
                                                                                                                                                                                                                                                                                                                                                                                    1 TGCTTTAGTGTTTCTCTACC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TITGGTCTCTTCCTGTGATC 20
           EARLIER APPLICATION NUMBER: 09/:
EARLIER FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 99
                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 80.0
Matches 16; Conservative
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Best Local Similarity 80.0
Matches 16, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 22
US-09-446-754-11
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US-09-446-754-17
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                                                                            SEQ ID NO 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 11
LENGTH: 20
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Sequence 4603, Application US/09198452A

Sequence 4603, Application US/09198452A

Sequence 4603, Application US/09198452A

Sequence 100, 6559294

GENERAL INFORMATION:

APPLICANT: Griffals, R.

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever TITLE OF INVENTION: and treatment of infection

FILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

CURRENT APPLICATION NUMBER: 1998-11-24

NUMBER OF SEQ ID NOS: 6849

LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 23, Application US/09792251
Sequence 23, Application US/09792251
Patent No. 6664074
GENERAL INFORMATION:
APPLICANT: Fritz, Christian
APPLICANT: Youngman, Philip
APPLICANT: Guzman, Luz-Maria
TITLE OF INVENTION: USE OF YACM AND YQEJ, ESSENTIAL BACTERIAL GENES AND FOLYPEPTIDES
TITLE OF INVENTION: UND THEIR USE
FILE REPERENCE: 06286-140001
CURRENT PILITG DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
SEQ ID NO 23
OTHER INFORMATION: Description of Artificial Sequence: 3' end primer used in OTHER INFORMATION: Example 2 for amplifying the sequence inbetween the 5' and OTHER INFORMATION: 3' sequences of human MKK7
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US-09-531-000-29
                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: David Spector

APPLICANT: David Spector

APPLICANT: Jacqueline Wyatt

TITLE OF INVENTION: ANTISENSE MODULATION OF SR-CYP EXPRESSION
FILE REPERBNCE: TST-0145

CURRENT APPLICATION NUMBER: US/09/706,197

NUMBER OF SEQ ID NOS: 87

LENGTH: 20
                                                                Query Match
18.6%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 46;
Matches 16; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
18.4%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 50;
Matches 14; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 29, Application US/09531000
| Patent No. 6461810
| GENERAL INPORMATION:
| APPLICANT: FRESCO, Jacques R.
| TITLE OF INVENTYON: TRIPLEX IN-SITU HYBRIDIZATION
| FILE REPERENCE: 2448-103
| CURRENT APPLICATION NUMBER: US/09/531,000
| CURRENT FILING DATE: 1090-11-10
| PRIOR APPLICATION NUMBER: PCT/US98/23765
| PRIOR FILING DATE: 1998-11-10
| PRIOR PELING DATE: 1998-11-10
| PRIOR FILING DATE: 1997-11-10
| SEQ ID NOS: 77
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO S: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
// OTHER INFORMATION: Antisense Oligonucleotide
US-09-706-197-77
                                                                                                                                                            905 TCATTTTCTTTGGTCTTTGC 924
                                                                                                                                                                                                                                                                                           US-09-706-197-77; Sequence 77, Application US/09706197; Patent No. 6475797
; OTHER INFORMATION: primer for PCR US-09-792-251-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
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US-09-531-000-29
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US-09-128-452A-2716/c

Sequence 2716, Application US/09198452A

Sequence 2716, Application US/09198452A

Sequence 2716, Application US/09198452A

GENERAL INFORMATION:
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999

FILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

CURRENT FILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 6849
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                                                                                                                                                   Sequence 24, Application US/08607384A

Patent No. 5849488

GENERAL INFORMATION:
APPLICANT: ALATOSAVA, JOUKO TAPANI
APPLICANT: TILSALA-TIMESJ RVI, AND KYLLIKKI
TILLE OF INVENTION: FROM A MILK SAMPLE
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS: 13
CORRESPONDENCE ADDRESS: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
18.1%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 51;
Matches 15; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA RElease #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/607,384A
FILING DATE: 27-FEB-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Staphylococcus epidermidis
STRAIN: ATCC 12228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 227-75
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       929 TATCCTCCTCTTTATTG 946
1 TTTCTCCTTTCTTCAT 18
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MOLECULE TYPE: DNA (genomic)
HYPOTHFICAL: NO
ORIGINAL SOURCE:
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                                                                                                      RESULT 28
US-08-607-384A-24/c
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少は一年 聖明 あいころ

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APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
ITILE OF INVENTION: Biallelic markers for use in constructing a high density...
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Best Local Similarity 87.5%; Pred. No. 58;
Matches 14; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Antisense Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.5%; Score 12.8; E
87.5%; Pred. No. 58;
iive 0; Mismatches
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US-09-422-978-10295/c
; Sequence 10295, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
                                                    Sequence 36, Application US/09205144; Patent No. 5958771; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               927 TITAICCICCICTIC 942
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                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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Best Local Similarity 87.5
Matches 14; Conservative
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; ORGANISM: Homo sapiens
US-09-267-423-8
                RESULT 31
US-09-205-144-36
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                                                                                                              Score 13.2; DB 1; Length 20;
Pred. No. 54;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                          RESULT 30

US-08-239-431A-8/c
Sequence 8, Application US/08239431A
Sequent No. 5716835
GENERAL INFORMATION:
APPLICANT: Regan, John W.
APPLICANT: Woodward, David F.
TITLE OF INVENTION: NOVEL HUMAN EP PROSTAGLANDIN RECEPTOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 12.8; D
Pred. No. 58;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/239,431A
FLING DATE: 05-MAY-1994
CLASSIFICATION 0: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                917 GICTITGCCTTTTATCCC 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 87.5%; Prv
Matches 14; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: ALR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
                                                                                                                                                                                                                                      18 Grerrigerecriarece 1
                                       TYPE: DNA
ORGANISM: Chlamydia pneumoniae
                                                                                                                   Query Match
Best Local Similarity 83.3%;
Matches 15; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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MOLECULE TYPE: CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAGMENT TYPE:

ORIGINAL SOURCE:
US-08-239-431A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                             US-09-198-452A-2716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92660
SEQ ID NO 2716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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APPLICANT: C. Frank Bennett
APPLICANT: C. Frank Bennett
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Lex M. Cowsert
APPLICANT: Lex M. Cowsert
IIIE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-2 EXPRESS)
FILE REFERENCE: RTS-0021
CURRENT APPLICATION NUMBER: US/09/205,144
CURRENT FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 36
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/09267423
; GENERAL INFORMATION:
    APPLICANT: Gil, Daniel W.
    APPLICANT: Woodward, David F.
    TITLE OF INVENTION: NO. 6395878el Human Prostaglandin EP Receptor
    FILE REFERENCE: 17023 DIV CIP
    CURRENT APPLICATION NUMBER: US/09/267,423
    CURRENT FILING DATE: 1999-02-05
    EARLIER FILING DATE: 1999-02-05
    EARLIER FILING DATE: 1998-02-05
    NUMBER OF SEQ ID NOS: 10
    SOFTWARE: PastSEQ for Windows Version 3.0
    SEQ ID NO 8
    LENTH: 18
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APPLICANT: Cunningham, Bruce A.
APPLICANT: CONDINGHAM, BRAINTON L.
AITLE OF INVENTION: CONTAINING FIBRONECTIN TYPE III REPEATS AND METHODS OF USE
NUMBER OF SEQUENCES: 77
OCRESPONDENCE ADDRESS:
ADDRESSE: The Scripps Research Institute
STREET: 10550 No. 6313265th Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: California
COUNTRY: U.S.
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            Gaps
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PCT-US95-07744A-32/c
Sequence 32, Application PC/TUS9507744A
Sequence 32, Application PC/TUS9507744A
GENERAL INFORMATION:
TITLE OF INVENTION: Plant Genes for Sensitivity to Ethylene
TITLE OF INVENTION: and Pathogens
NUMBER OF SEQUENCES: 82
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & Norris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 12.4; DB 1; Length 18;
Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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WEDIUM TYPE: Ploppy disk

WEDIUM TYPE: Ploppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/506,296B

FILING DATE: 24-JUL.1995

ATTONEY/AGENT INPORMATION:

NAME: PILING, Thomas

REGISTRATION NUMBER: 34,163

REGISTRATION NUMBER: 34,163

REGISTRATION NUMBER: 15RI 488.0

TELEPHONE: (619) 554-2937

TELEPHONE: (619) 554-2937

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

TOWATH: 18 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
            Mismatches
                                                                                                                                                                                                                                                                                                                                                ; Sequence 12, Application US/08506296B
; Patent No. 6313265
; GENERAL INFORMATION:
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                                                                                      933 CCTCCTCTTCATTG 946
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Best Local Similarity 92.99
Matches 13; Conservative
            Matches 13; Conservative
                                                                                                                                                           17 ccrccrcrraarra
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STRANDEDNESS: single
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HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-506-296B-12
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LOCATION: 1..19

1 COCATION: 1..19

1 COCATION: DESCRIPTION: downstream amplification primer 99-10966 for SEQ 2430, in complem

US-09-422-978-10295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-261-822A-32/c

) Sequence 32, Application US/08261822A,

Patent No. 5650553

) GENERAL INFORMATION:

APPLICANT: Ecker, Joseph R. et al.

TITLE OF INVENTION: Plant Genes for Sensitivity to Ethylene

TITLE OF INVENTION: and Pathogens

NUMBER OF SEQUENCES: 82

CORRESPONDENCE ADDRESS:

ADDRESSES: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5650553ris

STREET: One Liberty Place, 46th floor

CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
17.5%; Score 12.8; DB 1; Length 19;
Best Local Similarity 87.5%; Pred. No. 61;
Matches 14; Conservative 0; Mismatches 2; Indels
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/261,822A
FILING DATE: 17-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:

NAME: Beardell, Lori Y.

REGISTRATION NUMBER: 34,293
TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100
TELEPHONE: (215) 168-32:
SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CONA
HYPOTHETICAL: NO
                            CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US/09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER PILING DATE: 1998-11-23
EARLIER PILING DATE: 1998-11-23
EARLIER PILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
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STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPUTER: IBM 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          909 TTTCTTTGGTCTTTGC 924
FILE REFERENCE: GENSET.020CP1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 10295
LENGTH: 19
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US-08-261-822A-32
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DB 1; Length 17;
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                                                                                                                                                                                                             Sequence 65, Application US/08373124A

Sequence 65, Application US/08373124A

Patent No. 5646042

GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Braper, Kenneth
APPLICANT: Draper, Kenneth
APPLICANT: Draper, Kenneth
APPLICANT: Jarvis, Thale
ITILE OF INVENTION: TREATMENT OF RESTENOSIS AND
ITILE OF INVENTION: TREATMENT OF RESTENOSIS AND
ITILE OF SEQUENCES: 2627

CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fith Street
STREET: 633 West Fith Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
16.7%; Score 12.2; D
Best Local Similarity 41.2%; Pred. No. 70;
Matches 7; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: LOS ANGELES
CITY: LOS ANGELES
COUNTRY:
CALIFORNIA
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: STORAGE
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PETECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
FILING DATE: MAY 18, 1994
APPLICATION NUMBER: 08/245,466
FILING DATE: PEbruary 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: Pebruary 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: AUGUST 1092
APPLICATION NUMBER: 07/987,132
FILING DATE: AUGUST 26, 1992
ATTORNEY AGENT INFORMATION:
NAME: WASDLES RICHARD
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 39
US-08-435-628-65
; Sequence 65, Application US/08435628
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TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        910 TICITIGGICTITGCCT 926
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   917 GICTITGCCTTTTA 930
                                                                   19 Greirigecerria 6
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STRANDEDNESS: single
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US-08-373-124A-65
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US-09-422-978-7250/c
; Sequence 7250, Application US/09422978
; Patent No. 653751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Chumakov, Ilva
; APPLICANT: Chumakov, Ilva
; TILLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REPRENCE: GENERI 0200FP1
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT PILING DATE: 1999-10-20
; EARLIER PILING DATE: 1999-04-21
; EARLIER PILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 7250
; LENGTH: 199
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LOCATION: 1..19

OTHER INFORMATION: upstream amplification primer 99-3217 for SEQ 3316,

US-09-422-978-7250
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17.0%; Score 12.4; DB 1; Length 19;
Best Local Similarity 92.9%; Pred. No. 72;
Matches 13; Conservative 0; Mismatches 1; Indels
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COUNTRY: USA
ZIP: 19103
COMPUTER REDABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTE Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07744A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 12.4; DB
Pred. No. 68;
0; Mismatches
                                                                                                                                                                                                                                            UMBER: PCT/US95/07744A
15-JUNE-1995
                                                                                                                                                                                                                                                                     APPLICATION TO THE TABLE THE TABLE THE DELICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/261,822
FILING DATE: June 17, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
TELECHONE: (215) 568-3100
TELEPRAX: (215) 568-3100
TELEPRAX: (215) 568-3100
TELEPRAY: (215) 568-3100
TEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.0%;
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Best Local Similarity 92.94
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCT-US95-07744A-32
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APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions ReTITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions ReTITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor FILE REPERENCE: MEHBOO, 876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT APPLICATION NUMBER: US 60/005,974
PRIOR RILING DATE: 1995-10-26
RIOR RILING DATE: 1995-10-08
NUMBER OF SEQ ID NOS: 142225
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM POCDOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 31-JAN-1995

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Reed, Janet E.

REFERENCE/DOCKET NUMBER: 63076

TELEPHONE: (215) 563-4100

TELEPHONE: (215) 563-404

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPLICOSY: nucleic acid

STRANDEDNESS: single

TOPLICOSY: nucleic acid

STRANDEDNESS: single

TOPLICOSY: nucleic acid

HYPOTHETICAL: YES
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Best Local Similarity 29.4'
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: RNA
, ORGANISM: Homo sapiens
US-09-371-772B-5632
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ANTI-SENSE: YES
US-08-384-324-2
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GENERAL INFORMATION:
APPLICANT: SCINCHOCOND, Dan T.
APPLICANT: DETRICANCE, Remeth
APPLICANT: MCSW-1996.
APPLICANT: MCSW-1996.
APPLICANT: MCSW-1996.
APPLICANT: MCSW-1996.
TITLE OF INVENTION: TREATMENT OF RESTEROSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSES: Lyon & Lyon
STREET: Suite 4700
CITY: Los Angeles
STREET: Suite 4700
COMPUTER READABLE FORM:
MEDIUM TYPE: Storage
COMPUTER READABLE FORM:
MEDIUM TYPE: STORAGE
COMPUTER: MORADER: 08/245,628
FILING DATE: December 7, 1994
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: MAY 18, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: MORADER: 20/987,132
FILING 
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Best Local Similarity 41.2%; Pred. No. 70;
Matches 7; Conservative 7; Mismatches
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US-09-371-772B-5632
Sequence 5632, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.; APPLICANT: Rosviggen, Jim; APPLICANT: Stinchcomb, Dan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      910 TICTTIGGICTTIGCCT 926
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US-08-435-628-65
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; 0 Query Match
16.7%; Score 12.2; DB 1; Length 18;
Best Local Similarity 82.4%; Pred. No. 74;
Matches 14; Conservative 0; Mismatches 3; Indels

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APPLICANT: Cohen, Daniel
APPLICANT: Cohen, Daniel
APPLICANT: Cohen, Daniel
APPLICANT: Chumenfeld, Marta
APPLICANT: Chumenfeld, Marta
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
FILE REFERENCE: GENSET.020CP1
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-04-20
EARLIER FILING DATE: 1999-04-21
EARLIER FILING DATE: 1999-04-21
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-10-4-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 7176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: 1..18 -
; OTHER INFORMATION: upstream amplification primer 99-2636 for SEQ 3242,
US-09-422-978-7176
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; GENERAL INFORMATION:
, APPLICANT: University of Nebraska, Board of Regents
, APPLICANT: Gold, Barry I.
, TILL OF INVENTION: Synthetic Triple Helix-Forming Compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
16.7%; Score 12.2; D
Best Local Similarity 82.4%; Pred. No. 74;
Matches 14; Conservative 0; Mismatches
CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-11-23
EARLIER FILING DATE: 1998-11-3
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7776, Application US/09422978
Patent No. 6537751
GENERAL INFORMATION:
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Best Local Similarity 82.4%;
Matches 14; Conservative
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                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo Sapiens
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ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                       NAME/KEY: primer_bind LOCATION: 1..18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JS-09-422-978-7176/c
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                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: VAN DOORN, Leen-Jan et al.
APPLICANT: VAN DOORN, Leen-Jan et al.
TITLE OF INVENTION: Detection and identification of Human Papillomavirus by PCR and I TITLE OF INVENTION: Specific reverse hybridization.
FILE REPERENCE: 3501-0101P
CURRENT APPLICATION NUMBER: US/09/527,030G
CURRENT APPLICATION NUMBER: US/09/527,030G
SOFTWARE: PATING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 497
SOFTWARE: Patentin version 3.0
SEQ ID NO 108
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Type specific probe derived from the Human Papillomavirus (HPV) US-09-527-030G-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 44
US-094-422-978-5922/c
US-095-422-978-5922/c

y Sequence 5922, Application US/09422978

y Patent No. 6537751

y GENERAL INFORMATION:
   APPLICANT: Cohen, Daniel
   APPLICANT: Chen, Daniel
   APPLICANT: Chumakov, Ilya
   TITLE OF INVENDIANCON: Biallelic markers for use in constructing a high density...
   FILE REFERENCE: GENSET.020CP1
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Patent No. 6492173
GENERAL INFORMATION:
GAPLICANT: Lex M. COWEST
TITLE OF INVENTION: ANTISENSE MODULATION OF CYCLIN D2 EXPRESSION
FILE REFERENCE XTS-0275
CURRENT FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-920-760-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.7%; Score 12.2;
82.4%; Pred. No. 74;
                                                                                                                                                                        Sequence 108, Application US/09527030G Patent No. 6482588
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               TTTTCTTTGGTCTTTGC 924
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                                                         1 TTTTCTTTTTTTTTT 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Conservative
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Best Local Similarity
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Best Local Similarity
Matches 14; Conserv
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US-09-920-760-89/c
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US-09-527-030G-108
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LENGTH: 18
               908
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Sequence 6450, Application US/08584040

Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: Bacobedo, James
APPLICANT: Escobedo, James
APPLICANT: Escobedo, James
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: ALVORESPENDENCE ADDRESS:
ADDRESSE: LYON & LYON
STREET: 633 West Fifth Street
STREET: SALIC 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: SULLE #, voc
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: Storageible
COMPUTER: EM Compatible
COMPUTER: EM Compatible
COMPUTER: EM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: GOOD FORTER: DOOR FORTER: GOOD FOR
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PAPLICANT: WANG, ALICE M.; DOYLE, MICHAEL V.; MARK, DAVID F.

TITLE OF INVENTION: QUANTITION OF NUCLEIC ACIDS USING THE
POLYMERASE CHAIN REACTION
NUMBER OF SEQUENCES: 64

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/413,623

FILING DATE: 28-SEP-1989

PRIOR DATE: 28-SEP-1889

PRIOR PAPLICATION DATA:

APPLICATION DATA:

PILING DATE: 21-AUG-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 82.4
Matches 14; Conservative
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Best Local Similarity 82.4
Matches 14; Conservative
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO:64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ANTI-SENSE:
PCT-US96-01473-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 47
5219727-64
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RESULT 48

RESULT 49
US-09-371-772B-4106

Sequence 4106, Application US/09371772B

Sequence 4106, Application US/09371772B

Sequence 4106, Application US/09371772B

Sequence 4106, Application US/09371772B

Setent No. 6566127

GENERAL INFORMATION:

APPLICANT: Rinchcomp, Dan

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

APPLICANT: Stinchcomb, Dan

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

FILE REFERENCE: MBHB00, 876-J (237/198)

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Gaps

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Query Match 16.4%; Score 12; DB 1; Length 15; Best Local Similarity 50.0%; Pred. No. 66; Matches 6; Conservative 6; Mismatches 0; Indels

TYPE: nucleic acid STRANDEDNESS: single linear

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Pred. No. 76;
6; Mismatches 0; Indels
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APPLICANT: Pavco, Pamela
APPLICANT: Pavco, Pamela
APPLICANT: Stanchcomb, Dan T.
APPLICANT: Stanchcomb, Dan T.
APPLICANT: Stanchcomb, Dan T.
APPLICANT: Bscobedo, Jaime
TITLE OF INVENTION: NETHOD NUD REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3.6" Diskette, 1.44 Mb MEDIUM TYPE: 3.6" Diskette, 1.44 Mb MEDIUM TYPE: 1BM Compatible OPERATING SYSTEM: 1BM P.C. DOS 5.0 SOCTWARE: Word Perfect 5.1 CURRENT APPLICATION NUMBER: US/08/584,040 TILING DATE: January 11, 1996 CLASSIFICATION: 5.14 PRIOR APPLICATION NUMBER: 60/005,974 ATTORNEY AGENT INFORMATION: NAME: WALDENTY AGENT INFORMATION: NAME: WALDENTY MEDIES. 32,327, CONTINUAL MATTORNEY AGENT MINERED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . Sequence 1500, Application US/08584040 ; Patent No. 6346398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218/064
                      CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Guite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
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633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1499:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.0%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s uecucumeccu 16
    NUMBER OF SEQUENCES:
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STATE: California
COUNTRY: U.S.A.
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US-08-584-040-1500
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STREET:
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Sequence 5670, Application US/09371772B

Settle No. 6566127

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Stinchoomb, Dan

APPLICANT: Stinchoomb, Dan

APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor

TITLE OF INVENTION NUMBER: US/09/371,72B

CURRENT APPLICATION NUMBER: US 60/005,974

PRIOR FILING DATE: 1995-10-26

PRIOR FILING DATE: 1995-01-08

NUMBER OF SEQ ID NOS: 14225

SOFTWARE: PatentIn Version 3.0

LENGTH: 16
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Pred. No. 71;
6; Mismatches 0; Indels
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Pred. No. 66;
6; Mismatches 0; Indels
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; Patent No. 6346398
; GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Pavco. Pamela

APPLICANT: Stinchcomb, Dan T.

APPLICANT: Stinchcomb, Dan T.

TITLE OF INVENTION: METHOD AND REAGENT FOR THE

TITLE OF INVENTION: TREATMENT OF DISEASES OR

TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS

TITLE OF INVENTION: GROWTH FACTOR
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PATENTIN version 3.0
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                                                                                                                                                                                                                                                                                                                                16.4%;
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Best Local Similarity 50.v.
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Best Local Similarity 50.0
Matches 6; Conservative
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                                                                                                                                                                                                                                        TYPE: RNA
CORGANISM: Homo sapiens
US-09-371-772B-4106
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US-09-371-772B-5670
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US-08-584-040-1499
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LENGTH: 15
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REGERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELERAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1501:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-1501
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LENGTH: 17
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Sequence 1501, Application US/08584040

Sequence 1501, Application US/08584040

Patent No. 6346398

APPLICANT: Pavco, Pamela
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
TITLE OF INVENTION: METHOD AND REAGENT FOR THE TITLE OF INVENTION: METHOD AND REAGENT FOR THE TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 Weet Fifth Street
STREET: 631 Weet Fifth Street
STREET: 3011e 4700
CITY: Los Angeles
STREET: DOOLL-2066
COMPUTER: LOS Angeles
STREET: BM Compatible
COMPUTER: LEADABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: 3.5" DISKETC 5.1
CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005974
FILING DATE: OCCODER 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 16.4%; Score 12; DB 1; Length 17; Best Local Similarity 50.0%; Pred. No. 76; Matches 6; Conservative 6; Mismatches 0; Indels
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS S.O
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NAMBER: US/08/584,040
FILING DATE: Annuary 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNMER: 06/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: WAIDHUSE: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET WUMBER: 32,064
TELEFRAX: (213) 489-1600
TELERACTION FOR SEQ ID NO: 1500:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       915 TGGTCTTTGCCT 926
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US-08-584-040-1500
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REGISTRATION NUMBER: 32,327

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Sequence 44, Application US/09371772B

Sequence 44, Application US/09371772B

Sequence 44, Application US/09371772B

Sequence 44, Application US/09371772B

Sequence 40, Application

Sequence 40, Application

Sequence 41, Application

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Bacoco, Pam

APPLICANT: Bacoco, Jam

APPLICANT: Stinchcomb, Dan

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

TITLE OF INVENTION: WHERE: US/09/371,772B

CURRENT APPLICATION NUMBER: US 60/005,974

PRIOR FILING DATE: 1995-10-26

PRIOR FILING DATE: 1996-01-08

NUMBER OF SEQ ID NOS: 14225

SOFTWARE: PatentIn version 3.0
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US-09-371-772B-45
Squence 45, Application US/09371772B
Squence 45, Application US/09/371772B
Squence 45, Application US/09/371772B
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
CURRENT APPLICATION NUMBER: US/09/371,772B
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Length 17;
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Pred. No. 76;
6; Mismatches 0; Indels
Query Match
16.4%; Score 12; DB 1;
Best Local Similarity 50.0%; Pred. No. 76;
Matches 6; Conservative 6; Mismatches
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50.0%;
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                                                                                                                                                                                                                                                                                     RESULT 54
US-09-371-772B-44
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APPLICANT: Condon, Tom P.
APPLICANT: Condon, Tom P.
TITLE OF INVENTION: ANTISENSE MODULATION OF INTEGRIN 4 EXPRESSION FILE REFERENCE: ISPH-0323
CURRENT APPLICATION NUMBER: US/09/166,203A
CURRENT FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 60
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Pred. No. 76;
6; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR PILING DATE: 1995-01-08
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SCFTWARE: Patentin version 3.0
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTHER INFORMATION: antisense sequence US-09-166-203-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ), OTHER INFORMATION: antisense sequence US-09-377-309-21
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21, Application US/09166203A; Patent No. 5968826; GENERAL INFORMATION:
                                                                                                                                                                                                                                   16.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                            915 TGGTCTTTGCCT 926
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                                                                                                                                                                                                                               Query Match
Best Local Similarity 50.0
Matches 6; Conservative
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                                                                                                                                                       TYPE: RNA
CORGANISM: Homo sapiens
US-09-371-772B-4244
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US-09-377-309-21/c
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LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Estochedo, Jaine
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT APPLICATION NUMBER: US 60/005,974
PRIOR PILING DATE: 1995-00-06
PRIOR PILING DATE: 1995-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn Version 3.0
SEQ ID NO 46
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Paveo, Pare
APPLICANT: Paveo, Pane
APPLICANT: Paveo, Dan
APPLICANT: Stinchcomb, Dan
APPLICANTON: Cavels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBH800, 876-4 (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
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Pred. No. 76;
6; Mismatches 0; Indels
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  CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005, 974
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 46, Application US/09371772B Patent No. 6566127 GENERAL INFORMATION: APPLICANT: Ribozyme Pharmaceuticals, Inc. APPLICANT: Pavco, Pam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4244, Application US/09371772B Patent No. 6566127
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                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 50.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                915 TGGTCTTTGCCT 926
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                                                                                                                                                                                                 ORGANISM: Homo sapiens
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US-09-371-772B-4244
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US-09-371-772B-46
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                                                                                                                                                                           TYPE: RNA
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APPLICANT: Sanders, Jan W.
APPLICANT: Sanders, Jan W.
APPLICANT: Ledeboer, Adrianus M.
APPLICANT: Ledeboer, Adrianus M.
APPLICANT: Ledeboer, Adrianus M.
APPLICANT: Venema, Gerard
APPLICANT: Venema, Gerard
APPLICANT: Kok, Jan
TITLE OF INVENTION: Balt-Inducible Promoter Derivable from a Lactic Acid
TITLE OF INVENTION: Bacterium, and Its Use in a Lacctic Acid Bacterium for
TITLE OF INVENTION: Bacterium, and Its Use in a Lacctic Acid Bacterium for
TITLE OF INVENTION: Bacterium for DIRERS Senders Senders Portesin
TITLE OF INVENTION: PORDER: 1998-07-29
CURRENT FILING DATE: 1998-07-29
EARLIER APPLICATION NUMBER: EP 97200744/7
EARLIER FILING DATE: 1997-03-13
EARLIER FILING DATE: 1997-03-13
EARLIER FILING DATE: 1996-09-05
SOFTWARE: Patentin Ver. 2.0
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NAME/KEY: modified_base
COCATION: 16
COTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: that have xylose sugar linked via the o-xylene
OTHER INFORMATION: ring)"
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OTHER INFORMATION: Description of Artificial Sequence: primer NS3-10
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16.2%; Score 11.8; DB 1; Length 16;
Best Local Similarity 66.7%; Pred. No. 78;
Matches 10; Conservative 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                               LOCATION: 3 COTHER INFORMATION: /mod_base= OTHER OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 8..9 — OTHER INFORMATION: /mod_base= OTHER OTHER INFORMATION:
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TELEFAX: 415-327-250
TELEFAX: 415-327-250
TELEX: 706141
INPORMATION FOR SEQ ID NO: 98:
SEQUENCE CHRACTERISTICS:
LENGTH: 16 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
   'ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              918 TCTTTGCCTTTTATC 932
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ORGANISM: Artificial Sequence
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LOCATION: 14
OTHER INFORMATION: /mod_
OTHER INFORMATION:
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APPLICANT: Krawczyk, Steven
TITLE OF INVENTION: SEQUENCE-SPECIFIC NONPHOTOACTIVATED
TITLE OF INVENTION: CROSSLINKING AGENTS WHICH BIND TO THE MAJOR GROOVE OF
TITLE OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORTISON & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
COUNTRY: USA
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Fatent No. 6656731

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

TILLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity

FILE REFERENCE: MBH800-884-C

CURRENT FILING DATE: 2000-01-07

PRIOR APPLICATION NUMBER: US 09/444,209

PRIOR PLING DATE: 1999-11-19

PRIOR PLING DATE: 1999-11-19

PRIOR PLING DATE: 1999-09-22

PRIOR PLING DATE: 1998-09-22

PRIOR APPLICATION NUMBER: US 60/059,473

PRIOR PLING DATE: 1998-09-22

PRIOR DATE: 1998-09-22

PRIOR PLING DATE: 1998-09-22

PRIOR PLING DATE: 1998-09-22

PRIOR DATE: 1998-09-22

PRIOR DATE: 1998-09-22

PRIOR DATE: 1998-09-22

PRIOR DATE: 1998-09-22
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                     Query Match 16.4%; Score 12; DB 1; Length 18; Best Local Similarity 100.0%; Pred. No. 81; Matches 12; Conservative 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORPETATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/03680
FILING DATE: 19910524
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mureablige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4610-0011.40
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40.0%; Pred. No. 78;
tive 7; Mismatches
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                                                                                                                                       901 CTGGTCATTTTC 912
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Best Local Similarity 40.0
Matches 6; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                US-09-479-005A-303
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Matches 13; Conservative
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; ORGANISM: Homo sapiens
US-09-371-772B-419
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                         JS-09-371-772B-419
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                                                 DB 1; Length 17;
                                                                          2; Indels
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                                                                                                                                 us-08-584-040-1874
; Sequence 1874, Application US/08584040
; Patent No. 6346398;
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: Stinchomb, James
APPLICANT: Stinchomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: GROWTH PACTOR
NUMBER OF SEQUENCES: 8502
CORRESPENDENCE ADDRESS:
ADDRESSEE: Lyon F.T.
                                               16.2%; Score 11.8; D
86.7%; Pred. No. 83;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
16.2%; Score 11.8; D:
Best Local Similarity 53.3%; Pred. No. 83;
Matches 8; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
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Best Local Similarity 86.74
Matches 13; Conservative
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STRANDEDNESS: single
; NAME/KEY: primer bind; LOCATION: (1)..(17)
US-09-068-195-8
                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Los Angeles
STATE: California
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APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Pavco, Pam
APPLICANT: Bacched, Jam
APPLICANT: Bacched, Jam
APPLICANT: Bacched, Jame
APPLICANT: Bacched, Jame
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE REPERENCE: MBHB00,876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,7728
CURRENT FILING DATE: 1999-08-10
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: US 69/005,974
PRIOR FILING DATE: US 69/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1996-01-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09529812A
Sequence 4, Application US/09529812A
Patent No. 668230
GENERAL INFORMATION:
THILE OF INVENTION: NEW TRIPLEX FORMING OLIGONUCLEOTIDES AND THEIR USE IN TITLE OF INVENTION: ANTI-HBV
CURRENT APPLICATION NUMBER: US/09/529,812A
CURRENT FILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: CT/CN98/00248
PRIOR FILING DATE: 1998-10-19
PRIOR FILING DATE: 1997-10-21
NUMBER OF SEQ ID NOS: 18
SOCTWARR: PATENTIN Ver. 2.1
SEQ ID NO 4
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ORCANISM: Artificial Sequence
ORCANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Triplex
OTHER INFORMATION: forming oligonuclectide
OTHER INFORMATION: This oligo may or may not be 3'-monophosphorylated
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Best Local Similarity 53.3%; Pred. No. 83;
Matches 8; Conservative 5; Mismatches 2; Indels
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                                                                    GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
; Sequence 419, Application US/09371772B
; Patent No. 6566127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          924 CCTTTTATCCCTCCT 938
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Sequence 6620, Application US/09422978

1 Sequence 6620, Application US/09422978

2 Sequence 6620, Application US/09422978

3 Execut No. 6537751

3 APPLICANT: Chen, Daniel

3 APPLICANT: Chumakov, Ilya

4 TILE REFERENCE: GENSET.020CP1

5 TILE REFERENCE: GENSET.020CP1

5 CURRENT APPLICATION NUMBER: US/09/422,978

5 EARLIER FILING DATE: 1999-10-20

5 EARLIER FILING DATE: 1999-10-21

5 EARLIER FILING DATE: 1998-11-23

5 EARLIER FILING DATE: 1998-04-21

6 EARLIER FILING DATE: 1998-04-21

7 EARLIER FILING DATE: 1998-04-21

8 EARLIER FILING DATE: 1998-04-21
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LOCATION: 1..18
OTHER INFORMATION: upstream amplification primer 99-14093 for SEQ 2686,
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APPLICANT: McSwiggen, James
APPLICANT: Newton, Roger S.
APPLICANT: Newton, Roger S.
APPLICANT: Rambareack, Randy
TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF
TITLE OF INVENTION: PLASMA LIPOPROTEIN (a) [LP(a)] BY
TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΩB
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illarity 86.7%; Pred. No. 88;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                Query Match 16.2%; Score 11.8; I Best Local Similarity 86.7%; Pred. No. 88; Matches 13; Conservative 0; Mismatches
FILE REFERENCE: ISPH-0321
CURRENT APPLICATION NUMBER: US/09/167,109
CURRENT FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 228
SEGO ID NO 154
LENGTH: 18
                                                                                                                                                                                                                            ; OTHER INFORMATION: antisense sequence US-09-167-109-154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 77, Application US/08311760A, Patent No. 5599706, GENERAL INFORMATION:
                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                             909 TITCTTIGGICTITG 923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-422-978-6620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                 FEATURE:
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US-09-061-769A-21/C

Sequence 21, Application US/09061769A

Fatent No. 6239327

GENERAL INCRMATION:

APPLICANT: Cold spring Harbor Labs

TITLE OF INVENTION: use for Same
FILE REFERENCE: mea genes

CURRENT FILING DATE: 1998-04-16

PRIOR APPLICATION NUMBER: US/09/061,769A

CURRENT FILING DATE: 1998-04-16

PRIOR FILING DATE: 1998-04-16

NUMBER OF SEQ ID NOS: 21

SOSTWARE: Patentin Ver. 2.0

SEQ ID NO 21

LENGTH: 18
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CTHER INFORMATION: Description of Artificial Sequence: synthetic;
CTHER INFORMATION: primer
US-09-061-769A-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 16.2%; Score 11.8; DB 1; Length 18; Best Local Similarity 86.7%; Pred. No. 88; Matches 13; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
16.2%; Score 11.8; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 88;
Matches 13; Conservative 0; Mismatches 2; Indels
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Sequence 154, Application US/09167109

Patent No. 639227

GENERAL INFORMATION:

APPLICANT: Baker, Brenda F.

APPLICANT: Cowsert, Lex M.

APPLICANT: Monia, Brett P.

APPLICANT: XU, Xiaoxing S.

TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
                                                                                               APPLICANT: Lex M. Cowestt
APPLICANT: Lex M. Cowestt
APPLICANT: Lex M. Cowestt
APPLICANT: Ser M. O'Malley
TITLE OF INVENTION: ANTISENSE MODULATION OF SRA EXPRESSION
FILE REPRENCE: RTS-0048
CURRENT APPLICATION NUMBER: US/09/280,409
CURRENT FILING DATE: 1999-03-29
NUMBER OF SEQ ID NOS: 146
SEQ ID NO 72
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-280-409-72
                         US-09-280-409-72; Sequence 72, Application US/09280409; Patent No. 6107092
                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   935 TCCTCTTCATTGGTT 949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  924 CCTTTTATCCCTCCT 938
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APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: McWanggen, James
APPLICANT: Newton, Roger S.
APPLICANT: Newton, Roger S.
APPLICANT: Newton, Roger S.
APPLICANT: Newton, Roger S.
TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
TITLE OF INVENTION: PLASMA LIFOPROTEIN (a) [LP(a)] BY
TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 392
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: SMILE 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 11.4; D
Pred. No. 86;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Los Angeles
COUNTY: Los Angeles
COUNTY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 1.5" Diskette, 1.44 Mb
MEDIUM TYPE: SLOTAGE
COMPUTER: ENGRAGE
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASESEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/774, 310
FILING DATE: December 23, 1996
PRIOR APPLICATION NUMBER: 08/311,760
FILING DATE: September 23, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 223/229
TELECOMMUNICATION INFORMATION:
                                     SOFTWARE: FEBSEEQ VESTOR 1.3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,760A
FILING DATE: September 23, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Watburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/155
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHOME: (213) 955-0440
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
RRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 77, Application US/08774310
Patent No. 5877022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 46.2%;
Matches 6; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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TOPOLOGY:
US-08-311-760A-78
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US-08-3117-60A-78
US-08-3117-60A-78
Sequence 78, Application US/08311760A
Sequence 78, Application US/08311760A
Settle 78, Application US/08311760A
SELECTORIES SETTLE OF THE SETTLE OF THE OF INVENTION:
TITLE OF INVENTION: RELATED TO LEVELS OF TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN
STREET: 633 West fith Street
STREET: 634 West fith Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
15.6%; Score 11.4; D
Best Local Similarity 46.2%; Pred. No. 86;
Matches 6; Conservative 6; Mismatches
                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Fast SEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,760A
FILING DATE: September 23, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MAXDELS, Richard
REGISTRATION NUMBER: 32, 228/155
TELECOMMUTCATION INFORMATION:
TELEFROME: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
                                                    ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 933 CCTCCTCTTCATT 945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
     NUMBER OF SEQUENCES: 3
                                                                                                                     CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                           ZIP: 90071
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Gaps

Gaps

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ASSUBLT 1979-856-57/c
| Sequence 57, Application US/08929856
| Patent No. 6136584
| Patent No. 6136584
| Patent No. 6136584
| APPLICANT: Hiatt, Andrew APPLICANT: Hiatt, Andrew APPLICANT: Rose, Floyd TITLE OF INVENTION: DE NOVO POLYNUCLEOTIDE SYNTHESIS USING TITLE OF INVENTION: ROLLING TEMPLATES NUMBER OF SEQUENCES: 190
| CORRESPONDENCE ADDRESS: ADDRESSE: LERNER, DAVID, LITTENBERG, KRUMHOLZ & ADDRESSEE: MENTLIK STREET: 600 South, Avenue West CITY Westfield STATE: New Jersey
| COUNTRY: USA
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    Indels
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MEDIUM TYPE: RIOPPY disk
MEDIUM TYPE: RIOPPY disk
MEDIUM TYPE: ROMPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/929,856
FILING DATE: 15-SEP-1997
CLASSIFICATION: 536
ATTORNEY AGENT INFORMATION:
NAME: FOley, Shawn P.
REGISTRATION NUMBER: ROSE 3.0-057
FELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-7066
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
FORMIT : 15 base pairs
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.6%; Score 11.4; I 92.3%; Pred. No. 86; tive 0; Mismatches
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                                                                      : | | : | : : | | : : | 2 UCCUCUUCAUUUG 14
  6; Conservative
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STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 12; Conserv
  Matches
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APPLICANT: Stinchcomb, Daniel T.

APPLICANT: Stinchcomb, Daniel T.

APPLICANT: Mcswigen, James

APPLICANT: Newton, Roger S.

APPLICANT: Newton, Roger S.

APPLICANT: Ramharack, Randy

TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES

TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES

TITLE OF INVENTION: PLASMA LIPOPROTEIN (a) [LP(a)] BY

TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN

TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 392

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: Suite 4700

CITY: Los Angeles

STRTE: California

COUNTRY: U.S.A.
                                                                                                                                                                                                                                            15.6%; Score 11.4; DB 1; Length 15; 46.2%; Pred. No. 86; 1; Indels ive 6; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 11.4; DB 1;
Pred. No. 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: 1EM Compatible
OPERATING SYSTEM: IEM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/74,310
FILING DATE: Docember 23, 1996
FILING DATE: Docember 23, 1996
PRIOR APPLICATION DATA: 08/311,760
FILING DATE: September 23, 1994
APPLICATION NUMBER: 08/311,760
FILING DATE: September 23, 1994
APPLICATION NUMBER: 23, 1994
APPLICATION NUMBER: 23, 1397
FERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 223/229
FELEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 78:
ENGURATION FOR SEQ ID NO: 78:
LENGTH: 15 base pairs
ITARE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 73
US-08-774-310-78
Sequence 78, Application US/08774310
; Patent No. 5877022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.6%;
(213) 489-1600
(213) 955-0440
                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                      933 CCTCCTCTTCATT 945
                                                                                                                                                                                                                                                                                                                                                             2 CAUCCUCUUCAUU 14
                                                                                                                                                                                                                                                                   Best Local Similarity 46.2
Matches 6; Conservative
                                                                                                                                                                              linear
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Best Local Similarity
TELEPHONE:
TELEFAX: (
                                                                                                                                                                                                 US-08-774-310-77
                                                                                                                                                                                                                                                 Query Match
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PCT-US91-03680-96

Sequence 96, Application PC/TUS9103680

GENERAL INFORMATION:
APPLICANT: Matteucci, Mark D.
APPLICANT: Krawczyk, Steven
TITLE OF INVENTION: SEQUENCE-SPECIFIC NONPHOTOACTIVATED
TITLE OF INVENTION: OUTLEX DNA
TITLE OF INVENTION: DUDILEX DNA
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200 ADDRESSEE: Morrison & Foerster STREET: 545 Middlefield Road, Suite 200 CITY: Menlo Park

```
TITLE OF INVENTION: Therapy
FILE REPERENCE: 41984/78179
CURRENT APPLICATION NUMBER: US/09/270,542
CURRENT FILING DATE: 1999-03-17
EARLIER APPLICATION NUMBER: 09/221,222
SARLIER FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 207
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 186
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   937 CTCTTCATTGGTTTAA 952
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                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-270-542-186
                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 81.2*
...-rhes 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: RNA
CORGANISM: Homo sapiens
US-09-479-005A-176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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LENGTH: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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US-09-270-542-186
US-09-270-542-186
; Sequence 186, Application US/09270542
; Patent No. 6322976
; GENERAL INFORMATION:
; APPLICANT: Stituan, Timothy
; APPLICANT: Scott, James
; APPLICANT: Statton, Lawrence
; TITLE OF INVENTION: Compositions and Methods of Disease Diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.6%; Score 11.4; DB 1; Length 16; 80.0%; Pred. No. 92; tive 1; Mismatches 2; Indels
                                                                                                                                            CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/03680
FILING DATE: 19910524
CLASSIFICATION: 435
ATTORNEY/AGBNT INFORMATION:
NAME: MULASHIGE KALE H.
REGISTRATION NUMBER: 29,959
FEFERENCE/DOCKET NUMBER: 4610-0011.40
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-327-2951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: modified_base
LOCATION: 3
COTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /noce= "5-methylcytosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: modified_base
LOCATION: 9
COTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "5-methylcytosine"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mod_base= OTHER
/note= "5-methylcytosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRATURE:
NAME/KEY: modified_base
LOCATION: 8
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mod_base= OTHER
                                            ZIP: 94025
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415-327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         918 TCTTTGCCTTTTATC 932
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LOCATION: 16
OTHER INFORMATION: /mod_
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OTHER INFORMATION:
OTHER INFORMATION:
      California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity
Matches 12, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Sequence 48. Application US/08299849B
; Sequence 48. Application US/08299849B
; Patent No. $61220.
; Barent No. $61220.
; Patent No. $6120.
; Pate
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Sequence 176, Application US/09479005A

Palean No. 6665731

PAPLICANT: Ribozyme Pharmaceuticals, Inc.
TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
TITLE OF INVENTION: Nucleic Acid Catalysts with Endonuclease Activity
FILE REFERENCE: MHBHB00-884-C
CURRENT APPLICATION NUMBER: US/09/479,005A

PRIOR APPLICATION NUMBER: US 09/444,209

PRIOR FILING DATE: 1990-11-19

PRIOR FILING DATE: 1996-09-22

PRIOR FILING DATE: 1996-09-22

PRIOR FILING DATE: 1996-09-22

PRIOR FILING DATE: 1997-09-22

NUMBER OF SEQ ID NOS: 1208

SOFTWARE: PatentIn version 3.0
                                                                                                                                   Gaps
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15.3%; Score 11.2; DB 1; Length 16; 81.2%; Pred. No. 1e+02; ive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 80

US-08-373-124A-1012

Sequence 1012, Application US/08373124A

Patent No. 5646042

Patent No. 5646042

Patent No. 5646042

Patent No. 5646042

APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale

TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: TREATMENT OF RESTENOSIS

NUMBER OF SEQUENCES: 2627

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fitch Street
STREET: 633 West Fitch Street
STREET: 633 West Fitch Street
STREET: 631 West Fitch Street

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: Storage
COMPUTER: BM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING APPLICATION DATA:
PRIOR APPLICATION DATA:
                                  MEDIUM TYPE: storage—
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/73,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: December 7, 1994
APPLICATION NUMBER: 07/936,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: PERVARY 7, 1992
APPLICATION NUMBER: 20,7936,422
FILING DATE: AUGUST 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburgy Richard
RETERENCE/MOUNTGATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELECOMMUTICATION INFORMATION:
TELEFAX: (213) 955-0440
                          MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: storage
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US-08-373-124A-366
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordberfect
CURRENT APPLICATION NUMBER: US/08/299,849B
FILING DATE: 1-SEPTEMBER-1994
CLASSIFICATION NUMBER: US/037,230
FILING DATE: 26-WARCH-1993
PRIOR APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-WAY-1992
PRIOR APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION NUMBER: O1/807,043
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION NUMBER: O1/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION NUMBER: O1/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION NUMBER: O1/705,702
FILING DATE: 33-SEPTEMBER-1991
PRIOR APPLICATION NUMBER: O1/705,702
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION NUMBER: O1/705,702
FILING DATE: 23-SEPTEMBER-1091
PRIOR APPLICATION NUMBER: J0/946
REFERENCE/DOCKET NUMBER: J0/946
REFERENCE/DOCKET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 79
US-08-373-124A-366/C
is Sequence 366 Application US/08373124A
is APPLICANT: Stinctoomb, Dan T.
APPLICANT: Stinctoomb, Dan T.
APPLICANT: Darger, Kenneth
is APPLICANT: Darger, Kenneth
is APPLICANT: Darger, Thales
it TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ITILE OF INVENTION: TREATMENT OF RESTENCES: 2627
ITILE OF INVENTION: TREATMENT OF RESTENCES: 2627
INVENTION: ADDRESSES: Lyon & Lyon
is STREET: Salife 4700
CITY: Los Argeles
is STATE: California
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 927 TTTATCCCTCTTTC 942
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US-08-299-849B-48
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1012, Application US/08435628
; Batent No. 181796
; GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: Draper, Kenneth
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTIER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: ENORAGE S.0
SOFTWARE: WORD PETFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,628
FILING DATE: 05-MAY-1995
CLASSIFTCATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/215,466
FILING DATE: MANUBER: 08/215,466
FILING DATE: MANUBER: 08/192,943
FILING DATE: MANUBER: 08/192,943
FILING DATE: DECEMBER: 07/987,132
FILING DATE: DECEMBER: 07/987,132
FILING DATE: ABUNGER: 07/986,132
FILING DATE: AUGUST 7, 1992
APPLICATION NUMBER: 07/987,132
FILING DATE: AUGUST 7, 1992
APPLICATION NUMBER: 07/987,132
FILING DATE: AUGUST 7, 1992
APPLICATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
                                                                                                        MAME: Warburg, Richard

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 209/035

TELECOMMUNICATION INFORMATION:

TELEPAX: (213) 489-1600

TELEPAX: (213) 955-0440

TELEX: (7-3510

INFORMATION FOR SEQ ID NO: 366:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDENESS: single

US-08-435-628-366
                    07/936,422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  948 TITAAIGIAICGCIAC 963
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                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-435-628-1012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 366, Application US/08435628

Patent No. 5817796

GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Mary Javis, Thale
ITTLE OF INVENTION: TREATMENT OF RESTENOSIS AND
ITTLE OF INVENTION: TREATMENT OF RESTENOSIS AND
ITTLE OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
APPLICATION NUMBER: C., FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
APTONENZ/AGBNT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
FEFERENCE/DOCKET NUMBER: 209/035
FELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: storage COMPUTER: 1BM Compatible OPERATING SYSTEM: 1BM P.C. DOS 5.0 SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION IS 5.1 CLASSIFICATION: 5.14 PRIOR APPLICATION: 5.14 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/373,124 FILING DATE: MAY 18, 1995 APPLICATION NUMBER: 08/245,466 FILING DATE: MAY 18, 1994 APPLICATION NUMBER: 08/192,943 FILING DATE: February 7, 1994 APPLICATION NUMBER: 07/981,132 FILING DATE: Pebruary 7, 1994 APPLICATION NUMBER: 07/981,132 FILING DATE: December 7, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      913 TTTGGTCTTTGCCTTT 928
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Best Local Similarity 37.55
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 81
US-08-435-628-366/c
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US-08-373-124A-1012
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                                                                                                                                                                                                                                                                                                                                            15.3%; Score 11.2; DB 1; Length 17; 81.2%; Pred. No. 1.1e+02; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New York
COUNTRY: U.S.A.
ZIP: 10112-3801
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.50 inch, 720 Kb storage.
COMPUTER: IBM PS/V
COMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 47, Application US/08606505B
Fatent No. 6114601
Fatent No. 6114601
Fatent No. 6114601
FAPLICANT: KINCKAWA, Shigeto
APPLICANT: KINCKAWA, Shigeto
APPLICANT: SHIMADA, Yukihisa
APPLICANT: SHIMADA, Ritsuko
APPLICANT: SHIMADA, Ritsuko
APPLICANT: SHIMADA, Ritsuko
APPLICANT: SHIMADA, Ritsuko
FAPLICANT: SHIMADA, Ritsuko
APPLICANT: SHIMADA, Ritsuko
FAPLICANT: SHIMADA, RITSUKI GENES
FAPLICANT: SHIMADA, RITZATRICK, CELLA, HARPER & SCINTO
FARLICANT: New YORK
FALICANT: New YORK
FALICANT: New YORK
FALICANT: SHIMADA
FARLICANT: SHIMADA
FARLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: Other nucleic acid
DESCRIPTION: Synthetic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 47, Application US/09616990
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Best Local Similarity 81.2<sup>3</sup>
Matches 13; Conservative
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Best Local Similarity 76.5
Matches 13; Conservative
; TYPE: nucleic acid
; STRANDEDNESS: sing]
; TOPOLOGY: linear
US-08-967-727-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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US-08-606-505B-47
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US-08-967-727-28/C

i Sequence 28, Application US/08967727

i Patent No. 60254704;
GENERAL INFORMATION:
APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
APPLICANT: Van der Bruggen, Pierre; Boon-Falleur, Thierry
ITILE OF INVENTION: Tunor Rejection Antigen Precursor Mage-3 And Uses Thereof
NUMBER OF SEQUENCES:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
STATE: New York
CITY
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
COMPUTER: COMPUTER: IBM
COMPUTER: IBM
COMPUTER: COMPUTER: IBM
COMPUTER: COMPUTER: IBM
COMPUTER: COMPU
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CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/037,230

FILING DATE: 26-MARCH-1993
APPLICATION NUMBER: PCT/US92/04354

FILING DATE: 22-MAY-1992
APPLICATION NUMBER: 07/807,043

FILING DATE: 12-DECEMBER-1991

PRIOR APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,365
FILING DATE: 23-SEPTEMBER-1991

PRIOR APPLICATION NUMBER: 07/764,365
FILING DATE: 23-METHORS 1991

PRIOR APPLICATION DATA: 7728,838
FILING DATE: 23-MAY-1991

RELING DATE: 23-MAY-1991

APPLICATION NUMBER: 21-MAY-1991

RELING DATE: 23-MAY-1991

APPLICATION NUMBER: 21-MAY-1991

APPLICATION NUMBER: 21-MAY-1991

APPLICATION NUMBER: 21-MAY-1991

APPLICATION NUMBER: 21-MAY-1991

ATTORNEY/AGENT INFORMATION:
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                                                                 | TELEPHONE: (213) 489-1600
| TELERX: (213) 955-0440
| TELEX: 67-3510
| INFORMATION FOR SEQ ID NO: 1012:
| SEQUENCE CHRACTERISTICS:
| LENGTH: 17 base pairs
| TYPE: nucleic acid
| TYPE: nucleic acid
| TYPE: nucleic acid
| TOPOLOGY: linear
| US-08-435-628-1012
              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              913 TTTGGTCTTTGCCTTT 928
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Gaps
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; Sequence 1574, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION; Pamela
; APPLICANT: Pavco, Pamela
; APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS;
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Lyon & Ivero
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.3%; Score 11.2; DB 1;
81.2%; Pred. No. 1.1e+02;
tive 0; Mismatches 3;
                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/037,230D
FILING DATE: 26-MARCH-1993
CLASSIFICATION: 435
PRIOR APPLICATION JATA:
APPLICATION NUMBER: PCT/US92/04354
PLING DATE: 22-MAY-1992
PRIOR APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION NUMBER: 07/728,838
FILING DATE: 9-ULY-1991
PRIOR APPLICATION NUMBER: 07/728,838
FILING DATE: 9-ULY-1991
PRIOR APPLICATION NUMBER: 07/705,702
APPLICATION NUMBER: 07/705,702
PRIOR APPLICATION NUMBER: 07/705,702
PRIOR APPLICATION NUMBER: 07/705,702
APPLICATION NUMBER: 07/705,702
PRIOR APPLICATION NUMBER: 07/705,702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: IBM P.C. DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hanson, No. 6235525man D.
REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: LUD 5353
TELECOMMUTICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             927 TITAICCICCICTIC 942
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Best Local Similarity 81.27
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STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Suite 4700
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US-08-037~230D-28
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STREET:
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US-08-037-230D-28/c
; Sequence 28, Application US/08037230D
; Patent No. 6235525
; GENERAL INFORMATION:
    APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
    APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
    TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
    TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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COUNTRY: U.S.A.
ZIP: 10112-3801
COMPUTER REDABLE PORM:
MEDIUM TYPE: Diskette - 3.50 inch, 720 Kb storage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 15.3%; Score 11.2; DB 1; Length 17; Best Local Similarity 76.5%; Pred. No. 1.1e+02; Matches 13; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSER: FITZPATRICK, CELLA, HARPER & SCINTO STREET: 30 Rockefeller Plaza
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PS/V
OPERATING SYSTEM: MS-DOS Ver3.30
SOFTWARE: PATENT AID Ver1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/616,990
FILING DATE: 14-Jul-2000
PRIOR APPLICATION DATA:
FILING DATE: 0-Jul-2000
FILING DATE: 02-MAR-1992
                                                                                               SHIMADA, Yukihisa
CHBAYASHI, Masaya
SHIMADA, Ritsuko
CKINAKA, Yasushi
TITLE OF INVENTION: NOVEL PLANT GENES
NUMBER OF SEQUENCES: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DESCRIPTION: Synthetic DNA SEQUENCE DESCRIPTION: SEQ ID NO: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: Other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Perry, Lawrence S. REGISTRATION NUMBER: 31865
TELECOMMUNICATION INFORMATION:
, Patent No. 6232109
; GENERAL INFORMATION:
; APPLICANT: KIKUCHI, Yasuhiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 212-218-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          900 CCTGGTCATTTTCTTTG 916
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: CITY: STATE: New r
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RESULT 89

RESULT 89

RESULT 80

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Best Local Similarity 25.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 9; Mismatches 3;
                                                                                      TELEPHONE: (213) 489-1600
TELEFA: (213) 955-0440
TELEA: 67-3510
INFORMATION FOR SEQ ID NO: 2874:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                        FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  907 ATTTTCTTTGGTCTTT 922
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2 AUAUUCUCUGCUCUUU 17
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US-08-584-040-2874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INC. 034630

GENERAL INC. 034631

APPLICANT: Pavco, Pamela
APPLICANT: Berobedo, Jaime
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSES: Lyon & Lyon
STREET: 633 West Fith Street
STREET: Suite 4700
CITY: Los Angeles
STREET: California
CONDITY: U.S.A.
ZIP: 90701-2066
COMPUTER: LOS ANGELES
STATE: California
COMPUTER: STREET: STREET: STREET: STREET
COMPUTER: STREET: STREET: STREET
COMPUTER: STREET: STREET: STREET
COMPUTER: STREET: STREET: STREET
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COMPUTER: STREET: STREET
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COMPUTER: STREET
COMPUTER
COMPUTER: STREET
COMPUTER
COMP
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: 0ctober 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,32/
REFERENCE/DOCKET NUMBER: 218/064
TELEPHONE: (213) 489-1600
TELEFAX: (213) 489-1600
TELEFAX: (213) 955-0440
TELERX: 67-510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2874, Application US/08584040 Patent No. 6346398
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TOPOLOGY:
US-08-584-040-1574
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US-08-584-040-2874
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Patent No. 656587
GENERAL INFORMATION:
APPLICANT: GAUGLE, Barrice; Van den Eynde, Beno t;
APPLICANT: GAUGLE, Batrice; Van den Eynde, Beno t;
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof NUMBER OF SECURNCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                           ADDRESSE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
ZIP: New York
ZIP: New York
ZIP: Now York
COMPUTER READABLE FORM:
WEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IB
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRICE APPLICATION DATA:
APPLICATION NUMBER: US/08/037,230
FILING DATE: 26-MARCH-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/037,230
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA: 07/84,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION NUMBER: 07/764,364
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA: MAPLICATION NUMBER: 07/705,702
FILING DATE: 9-JULY-1991
PRIOR APPLICATION NUMBER: 07/705,702
FILING DATE: 12-MAY-1991
PRIOR APPLICATION NUMBER: 07/705,702
REGISTRATION NUMBER: 07/705,702
REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: 30,946
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US-09-311-772B-119/c
; Sequence 119, Application US/09371772B
; Patent No. 6566127
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   927 TITAICCCICCICITC 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09,
FILING DATE: US/23-SEPT-1999
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 17 nucleotides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                        RESULT 91
US-09-404-026-28/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
TOPOLOGY:
US-09-404-026-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gaugler, Beatrice; Van den Eynde, Benoit;
.van der Bruggen, Pierre; Boon-Falleur, Thierry
.tribe OF INVENTION: Isolated Nucleic Acid Molecules Coding
For Tumor Rejection Antigen Precursor Mage-3 And Uses There
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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15.3%; Score 11.2; DB 1; Length 17;
Best Local Similarity 81.2%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 3; Indels
                                                                                                                15.3%; Score 11.2; DB 1; Length 17; 81.2%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IEM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/579,197
FILING DATE: 26-May-2000
CLASSIFICATION: AUTHORM.
PRIOR APPLICATION NUMBER: 08/037,230
FILING DATE: CHEKNOWN.
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECRHER-1991
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SAPTEMBER-1991
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INNORMATION:
NAME: HARBON, NO. 655180man D.
REGISTRATION NUMBER: 100 5353
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION NUMBER: 100 5353
                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-579-197-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                               Sequence 28, Application US/09579197
Patent No. 6552180
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 17 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                 927 TTTATCCCTCCTCTTC 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 28: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                    Best Local Similarity
Matches 13; Conserva
                                             linear
                                                                                                                                                                                                                                                                                                                                                             US-09-579-197-28/c
                                           ;
TOPOLOGY:
US-09-583-850-28
                                                                                                                     Query Match
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APPLICANT: MCSWiggen, Jim
APPLICANT: MCSWiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Stoched, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REPERRORE: MBH00,876-J (237/198)
CURRENT FILING DATE: 1990-08-10
PRIOR PILING DATE: 1990-08-10
PRIOR PILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ. ID NOS: 14225
SOFTWARE: Patentin version 3.0
FEMALE. 17
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1 Sequence 621, Application US/09827998

2 Patent No. 6656700:

3 Patent No. 6656700:

4 APPLICANT: Gu, Xizhong

5 APPLICANT: Gu, Xizhong

7 TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E

7 TITLE OF INVENTION: NOVEL 1SOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E

7 TITLE OF INVENTION: NOVEL 1SOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E

7 TITLE OF TILNG DATE: 2000-05-26

7 PRIOR APPLICATION NUMBER: US 60/207,456

7 PRIOR APPLICATION NUMBER: US 60/207,456

7 PRIOR APPLICATION NUMBER: US 60/207,456

7 PRIOR APPLICATION NUMBER: US 60/236,359

7 PRIOR FILING DATE: 2000-05-27

7 NUMBER OF SEQ ID NOS: 1881

7 SEQ ID NOS: 1881

7 SEQ ID NOS: 1881
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Sequence 622, Application US/09827998

Factor No. 6656700

GENERAL INFORMATION:

APPLICANT: Shannon, Mark

TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E

FILE REFERENCE: MDHMORF-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Best Local Similarity 81.2%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 3;
      Ribozyme Pharmaceuticals, Inc.
Pavco, Pam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              914 TIGGICTITICCCTTT 929
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Best Local Similarity 81.2
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-5149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-09-827-998-621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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US-09-371-772B-1398
IS equence 1398, Application US/09371772B
Fatent No. 6566127
Fatent Ribozywe Pharmaceuticals, Inc.
FAPLICANT: Ribozywe Pharmaceuticals, Inc.
FAPLICANT: Roswiggen, Jim
APPLICANT: Stindfordb, Dan
FAPLICANT: Bit North No. Levels
FILE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBHB00, 876-J (227/198)
CURRENT FILING DATE: 1999-08-10
FRIOR FILING DATE: 1995-10-26
FRIOR PAPLICATION NUMBER: US 60/005, 974
FRIOR FILING DATE: 1995-01-08
FRIOR PILING DATE: 1995-01-08
FRIOR SEQ ID NOS: 14225
SEQ ID NO 1398
FRIOR PLING DATE: 1996-01-08
SEQ ID NO 1398
FRIOR PLING DATE: 1996-01-08
                           APPLICANT: Parcol Pam
APPLICANT: Barcol Pam
APPLICANT: Barcol Pam
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Scobedo, Jaime
ITTLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
ITTLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
ITTLE OF INVENTION: NUMBER: US/09/371,72B
CURRENT PILLIATION NUMBER: US 60/005,974
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR PILLING DATE: 1995-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
LENGTH: 17
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US-09-371-772B-5149/c
Sequence 5149, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          909 TTTCTTTGGTCTTTGC 924
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Best Local Similarity 81.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: RNA
ORGANISM: Homo sapiens
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CORGANISM: Homo sapiens
US-09-371-772B-1398
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-371-772B-119
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BIERMAN & MUSERLIAN
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                                      934 CICCICITCATIGGIT 949
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                                                                                                  17 crecrecreeringer
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APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , ORGANISM: Homo sapiens
US-09-866-108A-7084
                                                                                                                                                                                                                                            US-09-866-108A-7084/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-256-568B-34
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APPLICANT: O'. Y'ALDONG
APPLICANT: U'. Y'ALDONG
APPLICANT: U'. Y'ALDONG
APPLICANT: BERN', Sharron G.
APPLICANT: ERN', David R.
APPLICANT: ERN', David R.
APPLICANT: SHANKON, MARK
TITLE OP INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUWAN HEART AND MUSCLE
FILE REPERRENCE: ABOMICA-7
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US (0/20/456
PRIOR APPLICATION NUMBER: US (0/236,359
PRIOR APPLICATION NUMBER: US (0/236,359
PRIOR FILING DATE: 2000-09-36
PRIOR FILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-0
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CURRENT APPLICATION NUMBER: US/09/827,998
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 1881
SEQ ID NO 652
SEQ ID NO 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-866-108A-7083/c
; Sequence 7083, Application US/09866108A
; Patent No. 6686188
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15.3%;
Best Local Similarity 81.2%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 rescriciarectic 1
                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
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; ORGANISM: Homo E
US-09-866-108A-7083
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APPLICANT: PENN, SUBGREE
APPLICANT: PENN, SUBGREE
APPLICANT: PENN, BARKON G,
APPLICANT: PENN, BARKON G,
APPLICANT: CHEN, Wensheng
APPLICANT: GHEN, Wensheng
APPLICANT: GHEN, Wensheng
APPLICANT: GHEN, Wensheng
TITLE OF INVENTION: MYGSIN-IKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
TILE REPERBENCE: ABOMICA-7
CURRENT FILING DATE: 2001-05-25
FRIOR PEPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-04
PRIOR FILING DATE: 2001-01-30
PRIOR PELING 
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Best Local Similarity 81.2%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 34, Application US/08256568B
Patent No. 5846704
CENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT; STUTVER, LIEVEN;
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWIN, HUGO;
TITLE OF INVENTION: ISOLATES
NUMBER OF SEQUENCES: 97
CORRESPONDENCE 97
CORRESPONDENCE 197

Sequence 7084, Application US/09866108A Patent No. 6686188
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Gaps
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Best Local Similarity 100.0%; Pred. No. 1.18+02;
Matches 11; Conservative 0; Mismatches 0; Indels
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US-09-378-900A-34

i Sequence 34, Application US/09378900A

j Patent No. 6495670

GENERAL INFORMATION:
APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
TITLE OF INVENTION: ISOLATES
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
COUNTRY: USA
COMPUTER: ELERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
COMPUTER: ELERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
COMPUTER: STATE: NOIG
COMPUTER: ISON PC COMPAINE
SOFWWARE: ASCII
COMPUTER: ISON PC COMPAINE
SOFWWARE: ASCII
COMPUTER: ISON PC COMPAINE
SOFWWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/378,900A
FILING DATE:
CLASSIFICATION NUMBER: US/09/378,900A
FILING DATE: 18-UUL-1994
STILING DATE: 18-UUL-1994
SPRIOR APPLICATION NUMBER: 26-NOV-1993
FRING APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                   PRIORASPIFICATION:
PRIORA APPLICATION NUMBER:
APPLICATION NUMBER:
PRILING DATE: 18-JUL-1994
APPLICATION NUMBER: PCT/EP93/03325
FILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSEMILAN
REGISTRATION NUMBER: 19.683
ATTORNEY/AGENT INFORMATION:
TELEPOOMMUNCATION INFORMATION:
TELEPOOMMUNCATION INFORMATION:
TELEPAX: (212) 661-8002
INFORMATION FOR SED ID NO: 34:
SEQUENCE CHARACTERICICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL:
NO
                     APPLICATION NUMBER: US/09/038,369B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   900 CCTGGTCATTT 910
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15.1%; Score 11; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels
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US-09-038-369B-34
; Sequence 34, Application US/09038369B
; Batent No. 6171784
; GENERAL INFORMATION:
    APPLICANT: MARETENS, GERT; STUYVER, LIEVEN;
; APPLICANT: ROSSAU, RUD1; VAN HEUVERSHYN, HUGO
TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
; TITLE OF INVENTION: ISOLATES
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
    ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
COUNTRY: USA
CONPUTER: PLOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SOSTAMER: PC-DOS/MS-DOS
SOSTAMERS ASCII:
CURRENT APPLICATION DATA:
STREET: 600 THIRD AVENUE
CITY: NEW YORK
COUNTRY: USA
ZIP: 10016
COUNTRY: USA
ZIP: 10016
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppd disk
COMPUTER: IBM FC compatible
COMPUTER: IBM COMPUTER: US/08/256,568B
FILING DATE: 18-UUL-1994
CLASSIFICATION NUMBER: EP/93/402,129.6
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403,222.0
FILING DATE: 27-NOV-1992
ATTORNEY/AGENT INFORMATION:
FELEMANIC CHARACTER: 410.004
TELEPHONE: (212) 661-8000
INFORMATION FOR ERQ ID NO: 34:
SECUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYRRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: genomic DNA ANTI-SPACE. NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  900 CCTGGTCATTT 910
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US-08-256-568B-34
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Patent No. 5534631

GENERAL INFORMATION:
APPLICANT: Gaylor, Richard B.
APPLICANT: Li, Ching
TITLE OF INVENTION: DA ENCODING THE INTERLEUKIN BINDING
TITLE OF INVENTION: FACTOR (ILF)
NUMBER OF SEQUENCES: 33
CORRESPONDENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P. O. BOX 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 15;
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                                                                                                                                                                                                                                                                                                                                                  Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY:

STATE: Tex..

COUNTRY: USA

ZIP: 77210

COMPUTE: READABLE FORM:

MEDINM TYPE: Floppy disk

COMPUTE: IBM PC compatible

COMPUTE: BM PC compatible

COMPUTE: BM PC compatible

CORPTANCE: Patentin Release #1.0, Version #1.30

SOFTWARE: Patentin Nelease #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/906,930E

FILING DATE: 30-UN-1992

CLASSIFICATION 1992

ATTORNEY/AGENT INFORMATION:

NAME: Sertich, Gary J.

REGIGTRATION NUMBER: 34,430

REFERENCE/DOCKET NUMBER: 30,000

REFERENCE/DOCKET NUMBER: 30,000

REFERENCE/DOCKET NUMBER: 30,000

REFERENCE/DOCKET NUMBER: 30,000

REFERENCE/DOCKET NUMBER: 30
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Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 12; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                               15.1%; Score 11; DB 1; Le 100.0%; Pred. No. 1.1e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                               ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 34:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Arnold, White & Durkee STREET: P. O. Box 4433 CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DESCRIPTION: /desc = "DNA"
             TELEFAX: (212) 661-8002
                                   INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: NO
                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           934 CICCICITCATIGG 947
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INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHRACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     900 CCTGGTCATIT 910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-07-906-930E-8/c
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Pred. No. 1.1e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 34, Application US/09899044
Patent No. 6548244
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
ROSSAU, RUDI; VAN HEUVERSWIN, HUGO
TITLE OF INVANTION: PROCESS FOR TYPING OF HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: EF/93/402,129.6
FILING DATE: 31-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EF/92/403,222.0
FILING DATE: 27-NOV-1992
ATORNEY AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
FEFERENCE/DOCKET NUMBER: 410.004
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 661-8000
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: NULLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.1%; Scc...
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: genomic DNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              900 CCTGGTCATTT 910
                                                                                                                                                                                                                                                                                                                                                                                                                                       single
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ANTI-SENSE:
US-09-378-900A-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 102
US-09-899-044-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08317432A;
Sequence 2, Application US/08317432A;
Patent No. 5710028
GENERAL INFORMATION:
PAPLICANT. Nurit Eyal and Nir Navot
TITLE OF INVENTION:
CORRESPONDENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSE:
ADDRESSE:
ADDRESSE:
ALORESPONDENCE ADDRESS:
ADDRESSE:
ADDRESSE:
ALORESPONDENCE ADDRESS:
ADDRESSE:
AD
NUMBER OF SEQUENCES: 909
CORRESPONDENCE ADDRESS:
ADDRESSEB: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Diskette, 1.44 Mb
MEDIUM TYPE: 3.5 Diskette, 1.44 Mb
MEDIUM TYPE: 3.5 Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OORPOTER: IBM Compatible
OORPOTER: IBM Compatible
OORPOTER: IBM Compatible
OORPOTER: Nord Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/334,847
FILING DATE: No. 5633532ember 4, 1994
PRIOR APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard O.
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 209/032
TELEBPANE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (4.2.)
TELEX: 67-510
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    944 TIGGITIAAIGIAI 957
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Best Local Similarity 85.73
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 4-
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-317-432A-2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-334-847-46
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                                                                                                                                                                                                                                                    PAPELICANT: DESCRIPTION:
APPLICANT: MCSWiggen, James
APPLICANT: Draper, Kenneth
APPLICANT: Pavco, Pam
APPLICANT: Woolf, Tod
TITLE OF INVENTION: INHIBITING RESPIRATORY
TITLE OF INVENTION: INHIBITING RESPIRATORY
TITLE OF INVENTION: SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 909
CORRESCONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 631 West Fifth Street
COMPUTER REPARABLE FORM:
MEDIUM TYPE: Storage
COMPUTER REPARABLE FORM:
MEDIUM TYPE: Storage
COMPUTER: BEN Comparible OPERATION SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/334.847
FILING DATE: NO. 5693532ember 4, 1994
PRIOR APPLICATION NUMBER: 32,327
REGISTRATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LEERPAN: (213) 955-0440
TELLERA: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METHOD AND REAGENT FOR INHIBITING RESPIRATORY SYNCYTIAL VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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Patent No. 5693525
Patent No. 5693525
PAPLICANT: McSwiggen, James
APPLICANT: Draper, Kenneth
APPLICANT: Pavco, Pam
APPLICANT: Pavco, Pam
APPLICANT: Woolf, Tod
TITLE OF INVENTION: METHOD AND REAC
                                                                                                                                                                                             Sequence 45, Application US/08334847 Patent No. 5693532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 85.7%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    944 TIGGITIAAIGIAT 957
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           14 CTCTCCTTCATTGG
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US-08-334-847-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 105
US-08-334-847-46/c
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                                                                                                                                                       Query Match 14.8%; Score 10.8; DB 1; Length 15; Best Local Similarity 85.7%; Pred. No. 1.1e+02; Matches 12; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-585-684B-271

Sequence 271, Application US/08585684B

Sequence 271, Application US/08585684B

Sequence 271, Application US/08585684B

SENERAL INFORMATION:

APPLICANT: Stinchcomb, Daniel T.

APPLICANT: Stinchcomb, Daniel T.

APPLICANT: Maxwiggen, James

TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE

TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES

NUMBER OF SEQUENCES: 2751

CORRESPONDENCE ADDRESS:

ADDRESSE: Lyon & Lyon

STREET: 633 West Pifth Street

STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
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Local Similarity 42.9%; Pred. No. 1.1e+02;
nes 6; Conservative 6; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
CONTUTE READABLE FORM:
MEDIUW TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FESTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/585,684B
FILING DATE: January 16, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/000,951
FILING DATE: July 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERRNCE/DOCKET NUMBER: 32,327
REFERRNCE/DOCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHAR: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            924 CCTTTTATCCCTCC 937
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1 AUUUGCUUAAUGUA 14
                                                                                                                                                                                                                                                                                                                                                   15 ccirrirarccarrc 2
      STRANDEDNESS:
                                 ; TOPOLOGY: lir; MOLECULE TYPE: US-08-894-922A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
US-08-585-684B-271
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US-08-959-853-7/C
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: BERRY, Mark John
APPLICANT: BERRY, Mark John
APPLICANT: DAVIS, Paul James
APPLICANT: WAN DER LOGT, Cornelius P.E.
APPLICANT: WHITELAM, Garry Clark
ITLE OF INVENTION: PRODUCTION IN YEASTS OF STABLE ANTIBODY
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 14.8%; Score 10.8; DB 1; Length 15; Best Local Similarity 85.7%; Pred. No. 1.1e+02; Matches 12; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BARDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM FC compatible
OPERATING SYSTEM: PC-DGS/MS-DGS
SOFTWARE: BW WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,922A
FILING DATE: 03-KEP-1997
CLASSIPRICATION DATA:
APPLICATION NUMBER: GB 9504344,4
FILING DATE: 03-MAR-1995
FRICH APPLICATION DATA:
APPLICATION NUMBER: PCT/GB96/00468
FILING DATE: 01-MAR-1996
ATTOMES/AGGNT INFORMATION:
NAME: KOALLIS, PAUL K.
REGISTRATION NUMBER: 16,713
RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60113/241261
APPLICATION NUMBER: 08/919,872
FILING DATE: 27-Jul-92
APPLICATION NUMBER: 08/084,505
FILING DATE: 1-Jul-93
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 33,883
REGISTRATION NUMBER: 128/7
TELEPHONE: 972-3-5625553
TELEFRAK: 972-3-5625554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 107
US-08-894-922A-1/c
; Sequence 1, Application US/08894922A
; Patent No. 5863765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE DOCKET NUMBER: 6011
TELECOMMUNICATION INFORMATION:
TELEFRA: (202)-861-3503
TELEFRA: (202)-822-0944
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             911 TCTTTGGTCTTTGC 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 rcrrrddrgrrrcc 1
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                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 15
TYPE: nucleic acid
STRANDEDNESS: single
TYPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: Un
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; OTHER INFORMATION: Description of Artificial Sequence:probe sequence US-10-032-307-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 10.8; DB 1; Length 15;
Pred. No. 1.1e+02;
6; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 6683173
GENERAL INFORMATION
FAPELICANT: Democry, Robert O.
APPLICANT: Democry, Robert O.
APPLICANT: Dickov, Sergey G.
APPLICANT: Singer, Michael J.
APPLICANT: Epoch Biosciences, Inc.
TITLE OF INVENTION: T-m Leveling Methods
TITLE OF INVENTION: T-m Leveling Methods
CURRENT APPLICATION NUMBER: US/10/032,307
CURRENT FILING DATE: 1998-04-03
PRICR APPLICATION NUMBER: US 09/054,830
PRICR PILING DATE: 1998-04-03
PRICR APPLICATION NUMBER: US 09/054,832
PRICR PILING DATE: 1998-04-03
PRICR PILING DATE: 1999-11-01
PRICR APPLICATION NUMBER: US 09/054,959
PRICR PILING DATE: 1990-04-03
PRICR PILING DATE: 2000-08-16
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,073
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585,684
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Watburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORM: (213) 489-1600
TELEFORM: (213) 955-0440
TELEFO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 42.9%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            943 ATTGGTTTAATGTA 956
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1 AUUUGCUUAAUGUA 14
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US-09-038-073-271
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; Sequence 271. Application US/09038073
; Patent No. 6194150.
; GENERAL INFORMATION:
    APPLICANT: Stinchcomb, Daniel T.
    APPLICANT: Jarvis, Thale
    TITLE OF INVENTION: METHOD AND REAGENT FOR THE
    TITLE OF INVENTION: METHOD AND REAGENT TOLERANCE
    TITLE OF INVENTION: METHOD AND REAGENT TOLERANCE
    TITLE OF INVENTION: METHOD AND REAF
    TITLE OF INVENTION: METHOD AND REAF
    TITLE OF SEQUENCES: 2751
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Lyon & Lyon
    STREET: 633 West Fifth Street
    STREET: Suite 4700
    CITY: Los Angeles
    COUNTRY: U.S.A.
    ZIP: ANGELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
14.8%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 12; Conservative 0; Mismatches 2; Indels
                                                                                                            GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Robert S. Matson
TITLE OF INVENTION: USE OF URACIL-DNA GLYCOSYLASE
TITLE OF INVENTION: IN GENERIC ANALYSIS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Beckman Instruments, Inc.
STREET: 2500 Harbor Boulevard
CITY: Fulletron
STATE: California
ZIP: 9284-3100
COMPUTER: Edometic Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: Edometic Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: Edometic Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: EDAMETIC DISKETE, 1000 TEXT
OPERATING SYSTEM: WINDOWS 95 - WORDPERFECT 7.0
SOFTWARE: ASCII (DOS) TEXT
CHARATING SYSTEM: WINDOWS 95 983
FILING DATE: herewith
APPLICATION: 435
ATTORNEY AGENT INFORMATION:
REGISTRATION INFORMATION:
NAME: P. R. HARGER
REGISTRATION INFORMATION:
TELEPRAN: (714) 773-7936
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LEBRGTH: 15 base pairs
TYPE: INVOCATION INSER: SINGLE
TYPE: INACORACION: SINGLE
TYPE: TYPE: INACORACION: SINGLE
TYPE: TYPE: INACORACION: SINGLE
TYPE: TYPE: INACORACION: SINGLE
TYPE: TYP
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
SOFRAITING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FRAESEQ Version 1.5
                                    Sequence 7, Application US/08959853
Patent No. 6090553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         911 TCTTTGGTCTTTGC 924
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US-09-038-073-271
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; Sequence 286, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
, RELEVANT RESIDUES IN SEQ ID NO:
US-08-173-489C-85
                                                                                                                    Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                            934 CICCICITCAIT 945
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Best Local Similarity 91.7
Matches 11; Conservative
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ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-475-947A-286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-487-799-87
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                                                        Gaps
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CRIGINAL SOURCE:
ORGANISM: Homo sapiens
ORGANISM: Homo sapiens
CHROWSOME/SEGMENT: chromosome 13
MAP POSITION: 13414.2
PUBLICATION INFORMATION:
AUTHORS: Friend, S H, Horowitz, J M, Gerber, M R, AUTHORS: Wang X F, Bogenmann, E, Li, F P, Weinberg, M THORS: R A.
                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
DESCRIPTION: retinoblastoma gene (Accession #
DESCRIPTION: M33647, J02994) nucleotides 2236 to 2247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Deletions of a DNA sequence
in retinoblastomas and mesenchymal tumors:
Organization of the sequence and its encoded
                                                                                                                                                                                                                                                                                          RESULT 112
US-08-173-489C-85/c
US-08-173-489C-85/c
Sequence 85, Application US/08173489C
Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proceedings of the National Academy of Sciences, USA
               Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 12; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
F: 510 EAST 73RD STREET,
NEW YORK
NEW YORK
XY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPOTER: 1BM FOXT/AT
COMPOTER: 1BM FOXT/AT
CORERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 CCT 1992
ATTORNEY/AGENT: 189 CCT 1992
ATTORNEY/AGENT: 189 CCT 1992
REGISTRATION NUMBER: US518-6
FILING DATE: 26,179
REGISTRATION NUMBER: US518-6
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SECURIOR SECURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10021.

WEDIUM TYPE: 3.5 inch, 1.44MD storage COMPUTER: IBM PC/XI/AT
                                                                                                                        940 TICATIGGITIAAT 953
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DATE: 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: NI
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL:
JOURNAL:
VOLUME: 8
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Sequence 87, Application US/08487799C

Sequence 87, Application US/08487799C

Patent No. 6010908

GENERAL INFORMATION:
APPLICANT: Kunzelmann, Karl
TITLE OF INVENTION: GENEE THERAPY BY SMALL FRAGMENTS HOMOLOGOUS REPLACEMENT
FILER REPERENCE: 480.18 - 1(HV)
CURRENT APPLICATION NUMBER: US/08/487,799C

CURRENT FILING DATE: 1995-06-07

EARLIER APPLICATION NUMBER: 07/933,471

EARLIER FILING DATE: 1995-08-21

EARLIER FILING DATE: 1995-03-24

NUMBER OF SEQ ID NOS: 87

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 87
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; OTHER INFORMATION: Description of Unknown Organism: PCR product
US-08-487-799-87
Score 10.4; DB 1; Length 12;
Pred. No. 1e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 14.2%; Score 10.4; DB 1; Length 14; Best Local Similarity 91.7%; Pred. No. 1.2e+02; Matches 11; Conservative 0; Mismatches 1; Indels
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Pred. No. 1e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gener, Harold R.
APPLICANT: Wren, Jonathan D.
APPLICANT: Minna, John D.
TITLE OF INVENTION: Polymorphic Repeats in Human Genes
FILE REFERENCE: UTSD0667
CURRENT FILLING DATE: 1999-12-31
NUMBER OF SEQ ID NOS: 346
SOFTWARE Patentin Ver. 2.1
SEQ ID NO 286
LENGTH: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 117
US-08-319-492B-439
is Sequence 439, Application US/08319492B
is Patent No. S616488
is GENERAL INFORMATION:
APPLICANT: Sullivan, Sean M.
APPLICANT: Draper, Kenneth G.
APPLICANT: Manes
APPLICANT: Stinchcomb, Dan T.
TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF IL-5
NUMBER OF SEQUENCES: 751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
CITY: Los Angeles
STRATE: California
COUNTRY: U.S.A.
                                           CUUNTRIE O.S.T.

ZIPE 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 18 storage
COMPUTER: IEM COMPATIBLE
COMPUTER: NAVA PERFECT 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,492B
FILING DATE: October 7, 1994
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 09/08,895
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
NETERATION NOW SEQ ID NO: 438:
LENGHH: 15 base pairs
TYPE:
TYPE: Inneleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
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OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WOAT PERIFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,492B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                935 TCCTCTTCATTG 946
California : U.S.A.
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TOPOLOGY:
US-08-319-492B-438
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14.2%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 1.38+02;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 116
US-08-319-428-438

| Sequence 438, Application US/08319492B
| APPLICANT SUllivan, Sean M. APPLICANT Stinchcomb, Dan T. APPLICANT Stinchcomb, Dan T. ITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS INVENTE OF INVENTION: OF IL-5
| NUMBER OF SEQUENCES: 751
| CORRESPONDENCE ADDRESS: ADDRESSES Lyon & Lyon STREET: Stitch Street STREET: Stitch 4100
                                                                                                                           Sequence 245, Application US/08105483

Patent No. 5444807

GENERAL INFORMATION:
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
NUMBER OF SEQUENCES 462

CORRESPONDENCE ADDRESS:
ADDRESSE: c/o William S. Frommer
CITY: New York
STREET: 530 Fifth Avenue
CITY: New York
STATE: NEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONDITY: USA

CONDUTER READABLE FORM:

MEDIUM TYPE: Floppd disk

MEDIUM TYPE: TALENG DATA:

MEDIUM TYPE: MEDIUM TYPE: MEDIUM TYPE:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY:
US-08-105-483-245
                                                               RESULT 115
US-08-105-483-245
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                                                                                        Query Match 14.2%; Score 10.4; DB 1; Length 15; Best Local Similarity 91.7%; Pred. No. 1.3e+02; Matches 11; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19, Application US/08398945
Patent No. 5639872
GENERAL INFORMATION:
APPLICANT: Robinson, Gregory S.
TITLE OF INVENTION: Human VEGF-Specific
TITLE OF INVENTION: Oligonucleotides
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
SOFTWARE:
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REPERENCHOOR OF THE TELECOMMUNICATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19, Application US/08501779
Patent No. 5661135
GENERAL INFORMATION:
APPLICANT: RObinson, Gregory S.
TITLE OF INVENTION: Human VEGF-Specific
TITLE OF INVENTION: Oligonucleotides
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Lappin & Kusmer
STREET: 200 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 617-330-1311
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
                                                                                                                                                                                                                        934 CICCICITCATT 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       934 CTCCTCTTCATT 945
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Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                     3 Crccrcrrccrr 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANTOROLOGY: TOPOLOGY: CDN.
MOLECTLE TYPE: CDN.
TOTHETICAL: NO YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
; ANTI-SENSE:
US-08-502-185-19
                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-398-945-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-501-779-19
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Pred. No. 1.3e+02;
6; Mismatches 1; Indels
                                                                including application described below:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Second | Application US/08502185 | Patent No. 5639736 | Patent OF INVENTION: Uniquenclectides NUMBER OF SEQUENCES: 53 | CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESS: ADDRESSE: Lappin & Kusmer STREET: 200 State Street | CITY: Boston | CITY: Boston | Patent No. 5639736 | Patent No. 56
   FILING DATE: CLUCLE
PRIOR APPLICATION DATA: Including application DATA: Including application DATA: Including application DATA: Gescribed below APPLICATION NUMBER: G8/08,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,845
FILING DATE: December 7, 1992
APTORNEY, AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 209/276
REFERENCE/DOCKET NUMBER: 209/276
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 439:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: Innear
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APPLICATION NUMBER: US/08/502,185
FILING DATE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
NAME: Redistration Number: 33,523
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-O
TELECOMMUNICATION INFORMATION:
TELEPAX: 617-330-1311
INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
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41.7%;
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Best Local Similarity 41.7
Matches 5; Conservative
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COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
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TOPOLOGY: 1
US-08-319-492B-439
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US-08-502-185-19
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Pred. No. 1.3e+02;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,860
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: KENTEX, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-031
TELECHMONICATION INFORMATION:
                                                              HYZ-031DV2
                                                     REFERENCE DOCKET NUMBER: HYZ.
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-330-1310
TELEFAX: 617-330-1311
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                             REGISTRATION NUMBER: 33,523
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                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linea; MOLECULE TYPE: CE; HYPOTHETICAL: NO; ANTI-SENSE: YES US-08-501-713-19
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14.2%; Score 10.4; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 1.3e+02;
Matches 11; Conservative 0; Mismatches 1; Indels
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| Sequence | 19, Application US/08501713 |
| Patent No. 5710136 |
| GENERAL INFORMATION: APPLICANT: Robinson, Gregory S. APPLICANT: Smith, Lois B.H. |
| TITLE OF INVENTION: Inhibition of TITLE OF INVENTION: Used-Specific TITLE OF INVENTION: VEGF-Specific TITLE OF INVENTION: VEGF-Specific NUMBER OF SEQUENCES: 53 CORRESPONDENCE ADDRESS: 63 CORRESPONDENCE ADDRESS: 73 CORRESPONDENCE ADDRESS: 73 CORRESPONDENCE ADDRESS: 74 CORRESPONDENCE ADDRESS: 75 COUNTRY: USA STATE: Massachusetts COUNTRY: USA STATE: Massachusetts COUNTRY: USA STATE: 102109 |
| MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: 75 COUNTRY: IS MOSTUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OF COMPATIB
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APPLICATION NUMBER: US/08/501,779
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-031CPDV:
TELECOMMUNICATION INFORMATION:
TELEPAN: 617-330-1310
TELEPAN: 617-330-1311
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LEEPAN: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,713
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lappin & Kusmer STREET: 200 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE:
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; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-08-501-779-19
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Gaps
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Pred. No. 1.3e+02;
0; Mismatches 1; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: DEAD PY disk
COMPUTER: DEAD PY GONDALIDE
COMPUTER: DEAD PY GONDALIDE
COMPUTER: DATE: DOS/MS-DOS
SOFTWARE: PACHITIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,101
FILING DATE: 01-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: FROMMER: 25,506
REBERENCE/POCKET WHIBER: 25,506
REBERENCE/POCKET UNDER: 454310-2740
TELEFAK: (212) 840-3333
TELEFAK: (212) 840-3333
INFORMATION FOR SEO ID NO: 245:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
         APPLICANT: Limbach, Keith J.
APPLICANT: Johnson, Gerard P.
APPLICANT: Johnson, Gerard P.
APPLICANT: Cox, William I.
APPLICANT: Cox, William I.
APPLICANT: Audonnet, Jean-Christophe Francis
APPLICANT: Gettig, Russell Robert
TITLE OF INVENTION: STEATN
NUMBER OF SEQUENCES: 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19, Application US/08501626
Patent No. 5803156
GENERAL INFORMATION
APPLICANT: Robinson, Gregory S.
APPLICANT: Smith, Lois E.H.
TITLE OF INVENTION: Inhibition of
TITLE OF INVENTION: VEGF-Specific
TITLE OF INVENTION: VEGF-Specific
TITLE OF INVENTION: Oligonucleotides
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lappin & Kusmer
STREET: 200 State Street
CITY: BOSTON
                                                                                                                                                                                      SSEE: Curtis, Morris & Safford
SSEE: c/o William S. Frommer
7: 530 Fifth Avenue
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIF: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
Charles
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Best Local Similarity 91.7
Matches 11; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
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COUNTRY: USA
                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: C/o Willia
STREET: 530 Fifth Av
                                                                                                                                                                                                                                                                                                     ZIP: 10036
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                     USA
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US-08-501-626-19
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 1; Indels
                                                                                                                0; Mismatches
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No. 5765599ton, Elizabeth K.
Riviere, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Frommer, William S.
REGISTATION NUMBER: 25.506
REFERENCE/DOCKET NUMBER: 454310-2400
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 124
US-08-458-101-245
Sequence 245, Application US/08458101
Sequence 245, Application US/08458101
RENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: Perkus, Marion E.
APPLICANT: Taylor, Jill
APPLICANT: Tartaglia, Jämes
APPLICANT: Tartaglia, Jämes
APPLICANT: No. 5766599con, Elizabeth
APPLICANT: No. 5766599con,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 840-3333
TELEPAK: (212) 840-0712
INFORMATION FOR SEQ ID NO: 245:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   945 TGGTTTAATGTA 956
                                      934 CICCICITCATT 945
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Best Local Similarity 91.7
Matches 11; Conservative
   11; Conservative
                                                                        3 crccrcrrccrr 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY:
US-08-709-209-245
   Matches
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                                                                                                                                                                                     ;
0
                                                                                                                                       Query Match 14.2%; Score 10.4; DB 1; Length 15; Best Local Similarity 91.7%; Pred. No. 1.3e+02; Matches 11; Conservative 0; Mismatches 1; Indels
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Best Local Similarity 41.7%; Pred. No. 1.3e+02;
Matches 5; Conservative 6; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                      Sequence 8458, Application US/08584040
| Patent No. 6346398 |
| GENERAL INFORMATION: | GENERAL INFORMATION: | APPLICANT: Pavco, Pamela |
| APPLICANT: Barochomb, Dan T. |
| APPLICANT: Stinchcomb, Dan T. |
| APPLICANT: Stinchcomb, Dan T. |
| APPLICANT: Escobedo, Jaine |
| TITLE OF INVENTION: NETHOD AND REAGENT FOR THE |
| TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL |
| TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL |
| TITLE OF INVENTION: GROWTH FACTOR |
| NUMBER OF SEQUENCES: 8502 |
| ANDRESSEE: LYON & LYON |
| STREET: SIJ West Fifth Street |
| STREET: SIJ West Fifth Street |
| STREET: SILE 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM FC. DOS 5.0
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0/005,974
FILING DATE: OCTOBE 26, 1995
ATTORNEY/ACENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 218/064
TELEFONE: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: (7-5310
INPORMATION FOR SEQ ID NO: 8458:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                            934 CICCICITCAIT 945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Los Angeles
STATE: California
             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Californi
COUNTRY: U.S.A.
ZIP: 90071-2066
                           MOLECULE TYPE: C
HYPOTHETICAL: NC
ANTI-SENSE: YES
US-08-501-356-19
                                                                         YES
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             TOPOLOGY:
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Sequence 19, Application US/08501356

Patent No. 5814620

GENERAL INFORMATION:
APPLICANT: Robinson, Gregory S.
APPLICANT: Smith, Lois E.H.
TITLE OF INVENTION: Inhibition of
TITLE OF INVENTION: VEGF-Specific
TITLE OF INVENTION: VEGF-Specific
TITLE OF INVENTION: Oligonuclectides
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Lappin & Kusmer
STREET: 200 State Street
CITY: Boston
STATE: Massachusetts
COINTRY: USA
ZIP: 02109
COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEADABLE FORM:
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
RECESTRATION NUMBER: 33,523
RECESTRATION NUMBER: HYZ-031DV3
TELEFRONE; 617-330-1300
TELEFRONE: 617-330-1300
TELEFRONE: 617-330-1301
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,626
OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE:
                                                                    934 CICCICITCAIT 945
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US-928-465-9/C
IS-69-928-465-9/C
| Sequence 9, Application US/08928465
| Patent No. 6204024
| GENERAL INFORMATION:
| APPLICANT: Lee, Eum Mi
| TITLE OF INVENTION: Amplification Based
| TITLE OF INVENTION: Amplification Assay
| NUMBER OF SEQUENCES: 10
| CORRESPONDENCE ADDRESS:
| ADDRESSE: AACO NO. 6204024el Patent Department
| STREET: 1300 Piccard Drive
| CITY: Rockville
| STRATE: Maryland
| CONTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis B virus genome (subtype ayw) cloned in E coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RELEVANT RESIDUES IN SEQ ID NO: 167 :FROM 1 TO 16 US-08-173-489C-167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,465
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 10.4; DB 1;
Pred. No. 1.4e+02;
0; Mismatches 1;
                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
DESCRIPTION: heparitis B virus ayw isolate,
DESCRIPTION: nucleotides 2771 to 2786
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
(attorney) (212) 708-1880
                                                                                                                                                                                                                                                                                                                                                                                   PUBLICATION INFORMATION:
AUTHORS: Galibert, F, Mandart, E, AUTHORS: Tiollais, P, Charnay, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleotide sequence of the
                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double stranded
                                                                                                                                                                                                                                                                                                                                     ORGANISM: Hepatitis B virus INDIVIDUAL ISOLATE: ayw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gormley, Mary E.
REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
                      (212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
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                    TELEFAX: (attorney) (2
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                              LENGTH: 16 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL: Nature VOLUME: 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                646-650
  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                     APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: McSwiggen, Jim
APPLICANT: Bcobodo, Jam
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
APPLICANT: Stinchcomb, Dan
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REPERENCE: WBHB00, 876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
FILOR APPLICATION NUMBER: US 60/005,974
FRIOR APPLICATION NUMBER: US 60/005,974
FRIOR APPLICATION NUMBER: US 08/584,040
FRIOR APPLICATION NUMBER: US 08/584,040
FRIOR STUING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
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Pred. No. 1.3e+02;
6; Mismatches 1; Indels
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US-08-173-489C-167/C
US-08-173-489C-167/C
Sequence 167, Application US/08173489C
SEPLICANT: HEPBURN, A. G
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA TITLE OF INVENTION: TRIEBE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC., STREET: 510 EAST 73RD STREET;
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: 13M PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTATION NUMBER: 26,179
REFERRICE/DOCKET NUMBER: U9518-6
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
                                                                                                                            Sequence 4114, Application US/09371772B Patent No. 6566127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 41.7%;
Matches 5; Conservative
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          3 UUCCUUUUAUCC 14
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                                                                                                   US-09-371-772B-4114
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LENGTH: 15
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TITLE OF INVENTION: AND A SINGLE-CHAIN T-CELL RECEPTOR FILE REFERENCE: 46745(1758)
CURRENT APPLICATION SINGLE: US/09/813,781
CURRENT FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 130
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 57
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 47, Application US/08334847
Fatent No. 5693532
GENERAL INFORMATION:
FATENCE ATTON:
MCSWiggen, James
APPLICANT: Draper, Kenneth
APPLICANT: Pavco, Pam
APPLICANT: NOOLÉ, Tod
TITLE OF INVENTION: NHHBITING RESPIRATORY
TITLE OF INVENTION: SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 909
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STRRET: Suite 4700
STRRET: Suite 4700
                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              917 GICTITGCCTIT 928
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MEDIUM TYPE: 3.5" Di
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 134
US-08-334-847-47/c
                                                                                                                                                                                                                     FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Antisense nucleic Acids for the TITLE OF INVENTION: prevention and treatment of disorders in which expression TITLE OF INVENTION: of c-erbB plays a role NUMBER OF SEQUENCES: 106 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                   ö
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Patent No. 6405989
GENERAL INFORMATION:
APPLICANT: WEIDANT, JON A.
APPLICANT: CARD, KIMBERLYN F.
APPLICANT: WONG, HING C.
TITLE OF INVENTION: FUSION PROTEINS COMPRISING BACTERIOPHAGE COAT PROTEIN
                                                                                                                                                                                                                   ò
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ZIP: 20004

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disc

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/666,341A

FILING DATE: 15-AUG-1996

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

NRIOR APPLICATION DATA:

INFORMATION FOR SEQ ID NO: 101:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 base pairs

TYPE: nucleic acid

TYPE: nucleic acid

TYPE: nucleic acid
                                                                                                                                                                        Length 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 10.4; DB 1; Length 16;
Pred. No. 1.4e+02;
0; Mismatches 1; Indels
                                                                                                                                                                    Score 10.4; DB 1; Length 1
Pred. No. 1.4e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Jacobson, Price, Holman and Stern, PLLC STREET: 400 Seventh street, N.W. STREET: STATE: STATE: D.C. COUNTRY: USA
TYPE: nucleic acid
STRANDEDNESS: single
FOPOLOGY: not relevant
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA Oligonulceotide"
US-08-928-465-9
                                                                                                                                                                                                                                                                                                                                                          RESULT 131
US-08-666-341A-101/C
Sequence 101, Application US/08666341A
Patent No. 6365345
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                      Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                         948 TITAAIGIAICG 959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: DNA (gr
, ANTI-SENSE: YES
US-08-666-341A-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 132
US-09-813-781-57/c
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Gaps
) OTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: oligonucleotide
US-09-813-781-57
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TITLE OF INVENTION: PROCEDURES AND REGULATORY DNA SEQUENCES
FOR GENERICALLY ENGINEERING DISEASE RESISTANCE AND OTHER
FINDUCIBLE TRAITS IN PLANTS
NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/07/393,301
FILING DATE: 13-JUN-1989
SEQ ID NO:9:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5312912-9/c; Patent No. 5312912 | APPLICANT: HADWIGER, LEE A.; CHIANG, CHIN C.; HOROVITZ, CAPPLICANT: HADWIGER, LEE A.; CHIANG, CHIN C.; HOROVITZ, CAPPLICANT HADWIGER, LEE A.; CHIANG, CHIN C.; HOROVITZ, CAPPLICANT APPLICANT AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 10.4; DB 1;
Pred. No. 1.4e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                              Query Match
14.2%; Score 10.4; DB 1;
Best Local Similarity 91.7%; Pred. No. 1.4e+02;
Matches 11; Conservative 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
14.0%; Score 10.2; DB 1; Length 15
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPTRY: CALIFORIA
CONTRY: CALLED TO STATE:
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWAREN FORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,486C
FILING DATE: September 23, 1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/311,486C
FILING APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
TRING APPLICATION DATA:
APPLICATION NUMBER: 08/008,895
FILING DATE: December 7, 1992
ATTORNEY, ADENT INFORMATION:
NAME: WARDING, Richard J.
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 209/166
TELEDROWNURCATION INFORMATION:
TELEDROWNURCATION NUMBER: 209/166
TELEDROWNURCATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3.6 Application US/08311486C

Sequence 3.6 Application US/08311486C

SERERAL INFORMATION:

APPLICANT: Sean Sullivan
APPLICANT: Kenneth Draper
APPLICANT: Momes McSwiggen
TITLE OF INVENTION: BISASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: TNF.

NUMBER OF SEQUENCES: 1157
CORRESPONDENCE ADDRESS:
ADDRESSE:
ADDRESSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 36.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              944 TTGGTTTAATGTATC 958
                                               TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 rrgarrgrardrard 1
         (213) 955-0440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
EDNESS: single
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY:
US-08-334-847-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 136
US-08-311-486C-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 53, Application US/08334847
Patent No. 5693532
GENERAL INFORMATION:
APPLICANT: MCSWiggen, James
APPLICANT: Pavco, Pam
APPLICANT: Pavco, Pam
APPLICANT: Pavco, Pam
APPLICANT: Mcolf, Tod
TITLE OF INVENTION: INHIBITING RESPIRATORY
TITLE OF INVENTION: SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 909
CORRESPONDENCE ADDRESS:
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/334,847
FILING DATE: No. 569352ember 4, 1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 20,9/032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFACE: (7-3510
INFORMATION FOR SEQ ID NO: 47:
CELESCAR. (213) 955-0440
INFORMATION FOR SEQ ID NO: 47:
CELESCAR. (213) 955-0440
INFORMATION FOR SEQ ID NO: 47:
CENTRY IN SECURATE STREITSTICS:
CHARACTERISTICS:
CHAR
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ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 5.0 TORSE
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/334,847
PRICE DATE: NO. 5693532ember 4, 1994
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: Callfornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFRENCE/DOCKET NUMBER: 209/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     942 CATTGGTTTAATGTA 956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
US-08-334-847-47
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US-08-334-847-53/c
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Occurrent 14.01, Score 10.2, UB 1; Length 15;

Guert Local Similarity 46.71, Pred. No. 1.46.02;

Marches 7; Conservative 5; Mismatches 3; Indels 0; Gape 0;

Db 1 GCUCUTUCTCUUCC 15

ENSUIT 177

Marches 17; Conservative 5; Mismatches 3; Indels 0; Gape 0;

Marches 17; Conservative 5; Mismatches 3; Indels 0; Gape 0;

Marches 18; Marches 18; Marches 18; Mismatches 18;

MUTTIONS: Lifefram, B. P. Wonaco, A. P. Feener, C.C., ANTHOOS: Markel, L.M.

ITILES: Conservation of the Duckenne

TITLES: Mascular dystrophy gane in mice and humans

DOUGNALL: Sisteme dystrophy gane in mice and humans

SISTEME SISTEME CONTRIBETORS: A17-350

DATE: 1989

DATE: 1980

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US-09-479-770A-13
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                                                              Score 10.2; DB 1; Length 15;
Pred. No. 1.4e+02;
6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 10.2; DB 1; Length 15;
Pred. No. 1.4e+02;
6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
APPLICANT: McSwiggen, James
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
OPERATING SYSTEM: IBM P.C. DOS 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218/078
                                                                                                                                                                                                                                                   Sequence 272, Application US/09038073 Patent No. 6194150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585,684
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 216
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.0%;
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                                                   Query Match
Best Local Similarity 40.vv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 67.3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 40.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Los Angeles
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U.S.A.
                 ; TOPOLOGY: 1
US-08-585-684B-272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U
ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
US-09-038-073-272
                                                                                                                                                                                                                   RESULT 139
US-09-038-073-272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
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RESULT 1*1

US-09-479-770A-15

; Sequence 15, Application US/09479770A

; Sequence 15, Application US/09479770A

; Patent NO: 6391555

; GENERAL INFORMATION:

APPLICANT: Johnson, Eric S.

; APPLICANT: Johnson, Assay for the Detection of Avian Leukosis/Sarcoma

ITLE OF INVENTION: Assay for the Detection and Animal Biological Speci
Patent No. 6391555

GENERAL INFORMATION:
APPLICANT: Johnson, Eric S.
TITLE OF INVENTION: Assay for the Detection of Avian Leukosis/Sarcoma
TITLE OF INVENTION: Assay for the Detection of Avian Leukosis/Sarcoma
Viruses (ALSV) in DNA from Human and Animal Biological Speci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: GARVEY, SMITH, NEHRBASS & DOODY, L.L.C.
STREET: Three Lakeway Center, Suite 3290 3838 No. 6391555th Causeway
Boulevard
                                                                                                                                                 NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: GAVEY, SMITH, NEHRBASS & DOODY, L.L.C.
STREET: Three Lakeway Center, Suite 3290 3838 No. 6391555th Causeway
BOUlevard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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COMPUTEX: USA
COMPUTEX FEBDABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: Dell Diamension XPS D300
OPERATOR SYSTEM: Windows 98
SOFTWARE: Microsoft Word 2000
                                                                                                                                                                                                                                                                                                                                                         ZIP: 7002-1767
COMPUTER READABLE PORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: Dell Dimension XP5 D300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATION DATA DEMINISTRY AND OPERATION STREET WINDOWS 98
SOFTWARE: Microsoft Word 2000
CURRENT APPLICATION DATA: US/09/479,770A
APPLICATION NUMBER: US/09/479,770A
FILING DATE: 07-0ct-2000
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/115,087
FILING DATE: 07-JAN-1999
ATTORNEY AGENT INFORMATION:
NAME: Nehrbass, Seth M.
REGISTRATION NUMBER: 31,281
REFERENCE/DOCKET NUMBER: A98146US (88126.1)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 10.2; DB 1;
Pred. No. 1.4e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (504) 835-2000
TELEFAX: (504) 835-2070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGIH: 15 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (504) 835-2
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            930 ATCCCTCCTCTTCAT 944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 80.0 Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Metairie
                                                                                                                                                                                                                                                                                     CITY: Metairie
                                                                                                                                                                                                                                                                                                           STATE: LA
COUNTRY: USA
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Query Match 14.0%; Score 10.2; DB 1; Length 15; Best Local Similarity 80.0%; Pred. No. 1.4e+02; Matches 12; Conservative 0; Mismatches 3; Indels
                    PATENT NO. 6472154

GENERAL INFORMATION:

APPLICANT: Garner, Harold R.

APPLICANT: Wren, Jonathan D.

APPLICANT: Wren, John D.

ITILE OF INVENTION: Polymorphic Repeats in Human Genes

FILE REFERENCE: UPSD0667;

CURRENT APPLICATION NUMBER: US/09/475,947A

CURRENT FILING DATE: 1999-12-31

NUMBER OF SEQ ID NOS: 346

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 254
     Sequence 254, Application US/09475947A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                928 TTATCCCTCCTCT 942
                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-475-947A-254
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WS-09-031-952-8/c

Batent No. 639540*;

Patent No. 639540*;

Patent No. 639540*;

APPLICANT: Thomas, Howard C.

APPLICANT: Summerfield, John A.

APPLICANT: WINGERIER NEW STATEMENTION: METHODS OF PREDICTING THE OUTCOME OF INFECTION

FILE REPERENCE: Thomas

CURRENT APPLICATION NUMBER: US/09/031,952A

CURRENT FILING DATE: 1998-01-27

EARLIER APPLICATION NUMBER: 951803.8

EARLIER FILING DATE: 1995-07-27

EARLIER FILING DATE: 1995-07-27

EARLIER APPLICATION NUMBER: 961414.2

EARLIER FILING DATE: 1996-07-09

EARLIER PILING DATE: 1996-07-25

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIN Ver. 2.0

LENGTH: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
14.0%; Score 10.2; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 3; Indels
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/479,770A
FILING DATE: 07-Oct-2000
CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/115,087
FILING DATE: 07-JAN-1999
ATTORNY/AGENT INFORMATION:
NAME: Nehrbass, Seth M
REGISTRATION NUMBER: 31,281
REPERENCE/DOCACET NUMBER: A98146US (88126.1)
TELECOMUNICATION INFORMATION:
TELECHONE: (504) 835-2000
TELECHONE: (504) 835-2070
INFORMATION FOR SEQ. ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear ; SEQUENCE DESCRIPTION: SEQ ID NO: 15: US-09-479-770A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 15 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        930 ATCCCTCTTCAT 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
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Sequence 31, Application US/08192946
Patent No. 628688
GENERAL INFORMATION:
FAPLICATT: KENNETH G. DRAPER
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: INHIBITING INFLUENZA VIRUS
TITLE OF INVENTION: INHIBITING INFLUENZA VIRUS
TITLE OF INVENTION: MEDICATION
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER: 15 Diskette, 1.44 Mb storage
COMPUTER: 18M compatible
COMPUTER: 18M COMPATE: NOTGREFECT (Version 5.0)
CURRENT APPLICATION NUMBER: US/08/192,946
FILING DATE:
CONTROPTION NUMBER: US/08/192,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 197/294
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/882,713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-192-946-31
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Length 10;

DB 1;

13.7%; Score 10;

934 CICCICITCATIGGT 948

RESULT 143 US-09-475-947A-254/c

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APPLICANT: HEPBURN, A. G.

TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
NUMBER OF SEQUENCES: 365
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.7%; Score 10; DB 1; Length 14; 100.0%; Pred. No. 1.4e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Hepatitis B virus
INDIVIDUAL ISOLATE: adw2
INDIVIDUAL ISOLATE: adw2
PUBLICATION INFORMATION:
AUTHORS: Valenzuela, P, Quiroga, M, Zaldivar, J, AUTHORS: Gray, P, Ruter, W J.
TITLE: The nucleotide sequence of
TITLE: the Hepatitis B viral genome and the
TITLE: identification of the major viral genes
JONENAL: In "Animal Virus Genetics", Fields, B N, JONENAL: Jaenisch, R, Fox C P eds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quiroga, M, Zaldivar, J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; RELEVANT RESIDUES IN SEQ ID NO: 185 :FROM 1 TO 14 US-08-173-489C-185
                                                                                                                                                                                                                          ZIP: 10021.

COMPUTER READABLE FORM:
MEDIUW TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DGS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, JOSEPH H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOKERT NUMBER: 26,179
REFERENCE/DOKERT NUMBER: 26,179
REFERENCE/DOKERT NUMBER: 26,179
TELEPHONE: (attorney) (212) 708-1880
TELEPHONE: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 185:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
TYPE: genomic DNA
DESCRIPTION: nucleotides 1810 to 1823
HYPOTHETICAL: no
ANTI-SENSE: n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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les 10; Conserv
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ORIGINAL SOURCE:
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US-08-363-233B-13/c
US-08-363-233B-13/c
Sequence 13, Application US/08363233B
Patent No. 5714383
GENERAL INFORMATION:
APPLICAUT: Thompson, James D.
TITLE OF INVENTION: METHOD AND REAGENT FOR TREATING CHRONIC
TITLE OF INVENTION: MYELOGENOUS LEUKEMIA
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ALDERSS:
ADDRESSE: Lyon & Lyon
               Pred. No. 1e+02;
6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: December 23, 1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 07/882,822
FILING DATE: FEbruary 7, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 23,327

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 8.5" Diskette, 1.44 Mb MEDIUM TYPE: 8.5" Diskette, 1.44 Mb MEDIUM TYPE: 8.5" Diskette, 1.80 S.0 SOFTWARE: FastSEQ for Windows 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,233B FILING DATE: December 23, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/165
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3*:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700 CITY: Los Angeles CITY: Los Angeles COUNTRY: U.S.A. ZIPE: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                 Best Local Similarity 40.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
J TOPOLOGY: linear
US-08-363-2338-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 13.7
Best Local Similarity 100.
Matches 10; Conservative
                                                                                        902 TGGTCATTT 911
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1 UGGUCAUUUU 10
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Gaps

RESULT 147
US-08-173-489C-197
; Sequence 197, Application US/08173489C
; Parent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.

RESULT 146
US-08-173-468C-185
US-08-173-468C-185, Application US/08173489C
; Patent No. 586.1244
; GENERAL INFORMATION:
APPLICANT: WANG, C. -G.

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US-08-585-684B-2258
; Sequence 228, Application US/08585684B
; Sequence 228, Application US/08585684B
; Patent No. 5877021
; GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
APPLICANT: Jarvis, Thale
APPLICANT: McSwiggen, James
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 631 West Fifth Street
STREET: 63114 4700
                                                              TITLE OF INVENTION: METHOD AND REAGENT FOR THE TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES NUMBER OF SECURICES: 2751
CORRESPONDENCE ADDRESS: ADDRESSE: Lyon & Lyon STREET: Suite 4700
CITY: Los Angeles STREET: California COUNTRY: U.S.A.
ZIP: GONTRY: U.S.A.
ZIP: Solf Angeles STREET: Solf Angeles STREET: Solf Angeles STREET: Solf Angeles STREET: Gontre Broad Angeles STREET: California COUNTRY: U.S.A.
ZIP: 90071
COUNTRY: U.S.A.
ZIP: PROFES TEST SOL SOL OF 
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13.7%; Score 10; DB 1; I
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 5; Mismatches 0;
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COMPUTER READELE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 67-3510

INFORMATION FOR ESQ ID NO: 2257:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDENESS: single
;
TOPOLOGY: linear
US-08-585-6848-2257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             917 GICTITGCCT 926
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4 GUCUUUGCCU 13
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STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
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APPLICANT: HERBURN, A. G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
TITLE OF INVENTION: TAIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 3.65
CORRESPONDENCE ADDRESS:
CORPUTER: NEW YORK
CONTRY: USA
COMPUTER: READABLE FORM:
MEDIUMY TYPE: 3.5 Inch, 1.44Mb storage
COMPUTER: THA FOLYATA VESSION 5.1
COMPUTER: READABLE FORM:
MEDIUMY TYPE: 3.5 Inch, 1.44Mb storage
COMPUTER: THA FOLYATA VESSION 5.1
COMPUTER: TRAIL FOLYATION DATA:
COMPUTER: TRAIL FOLYATION DATA:
COMPUTER: TROUBARDITON:
NAME: 20 TOT 1992
FILING DATE: 20 TOT 1993
FILING DATE: 20 TOT 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DATE: 1983
; RELEVANT RESIDUES IN SEQ ID NO: 197 :FROM 1 TO 14
US-08-173-489C-197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 148
US-08-585-684B-2257
; Sequence 2257, Application US/08585684B
; Patent No. S877021;
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwiggen, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 13.7
Best Local Similarity 100.
Matches 10, Conservative
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                                                                                                                                                                                                             13.7%; Score 10; DB 1; Length 15; 50.0%; Pred. No. 1.5e+02; tive 5; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-038-073-2258

Sequence 2258, Application US/09038073

Sequence 2258, Application US/09038073

GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Stinchcomb, James
APPLICANT: OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 13.7%; Score 10; DB 1; I Best Local Similarity 50.0%; Pred. No. 1.5e+02; Matches 5; Conservative 5; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FastSEO Version 1.5 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/038,073 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: WATCHUEG, KICCHAEG
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELEPHONE: (213) 489-4600
TELEPHONE: (213) 955-0440
TELEPHONE: (213) 955-0440
TELERAX: (7-3510
TELERX: (7-3510
TELERX: (7-3510
TELERX: (7-3510
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TELERY: (7-3510
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APPLICATION NUMBER: 08/585,684
FILING DATE:
                                                                           LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                     Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 15 base pairs
nucleic acid
EDNESS: single
                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         917 GTCTTTGCCT 926
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4 GUCUUUGCCU 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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US-09-038-073-2257
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                                                                                                                                                                                                                     Query Match
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Sequence 2257, Application US/09038073

Batent No. 6194150

GENERAL INFORMATION:
APPLICANT: Jarvis, Thale
APPLICANT: Jarvis, Thale
APPLICANT: McSwiggen, James
ATTLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 631 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 13.7%; Score 10; DB 1; Length 15; Best Local Similarity 50.0%; Pred. No. 1.5e+02; Matches 5; Conservative 5; Mismatches 0; Indels
SOFTWARE: FASTEM: IEM P.C. DOS 5.0
SOFTWARE: FASTESD VESTEND 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/585,684B
FILING DATE: January 16, 1996
FILING DATE: January 16, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/000,951
FILING DATE: JULy 7, 1995
ATTORNEY/AGENT INTORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 218/078
TELECOMMUNICATION INFORMATION:
TELEFRAM: (213) 489-1600
TELEFRAM: (213) 489-1600
TELEFRAM: (213) 985-0440
ITELERA: 67-3510
INFORMATION FOR SEQ ID NO: 2258:
SEQUENCE CHARACTER/STICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
FILING APPLICATION NUMBER: US/09/038,073
FILING APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/595,684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,32
REFERENCE/DOCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELERAX: 67-3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    917 GTCTTTGCCT 926
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4 GUCUTUGCCU 13
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California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U.S.A.
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US-09-038-073-2257
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13.4%; Score 9.8; DB 1; Length 13; llarity 84.6%; Pred. No. 1.46+02; Conservative 0; Mismatches 2; Indels
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APPLICANT: Miyada, Charles Garrett
APPLICANT: Hubbell, Earl A.
APPLICANT: Hubbell, Earl A.
APPLICANT: Fodor, Stephen P.A.
APPLICANT: Hong, Xiachna C.
APPLICANT: Lobban, Peter E.
APPLICANT: Morris, Macdonald S.
APPLICANT: Morris, Detecting Cystic Fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from HER-2
DESCRIPTION: sequence region in Seq ID No. 586124455
HYPOTHETICAL: Yes
ANTI-SENSE: No
        GENETIC SEQUENCE ASSAY USING DNA TRIPLE-STRAND FORMATION.
365
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                                                                                                           DIAGNOSTIC SCIENCES, INC.,
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                                                                                                                                                                      STATE: NEW YORK
COUNTRY: USA
ZATE: 10021.
COMPUTER: EADABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
APPRICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REPERBNCE/DOCKET NUMBER: 26,179
REPERBNCE/DOCKET NUMBER: 26,179
TELEFPAN: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 bases
TYPE: Nucleic Acid
STRANDENBES: single stranded
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO:
TITLE OF INVENTION: GENETIC SEQUITILE OF INVENTION: TRIPLE-STRAN NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS: ADDRESSE: PROFILE DIAGNOSTIC STREET; 510 EAST 73RD STREET, CITY: NEW YORK STATE: NEW YORK COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            924 CCTTTTATCCCTC 936
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 11; Conserva
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                                                                                                                                       APPLICANT: Chee, Mark
APPLICANT: Choin, Maureen T.
APPLICANT: Fodor, Stephen P.A.
APPLICANT: Huang, Xiaohua X.
APPLICANT: Huang, Xiaohua X.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Lobban, Peter E.
APPLICANT: Sheldon, Edward L.
TILE OF INVENTION: Arrays of Nucleic Acid Probes on TITLE OF INVENTION: Biological Chips
NUMBER OF SOURDNESS: 360
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREES: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 13;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,887A
FILING DATE: 16-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/08/441,887A
TLING DATE: 26-OCT-1993
CLASSIFICATION NUMBER: US/08/143,312
FILING DATE: 26-OCT-1993
CLASSIFICATION NUMBER: US/08/082,937
FILING DATE: 25-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, JOSEPH O. REFERENCE/DOCKET NUMBER: 018547-004160US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 9.8; DB 1;
Pred. No. 1.4e+02;
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                                                                          Sequence 268, Application US/08441887A
Patent No. 5837832
GENERAL INFORMATION:
APPLICANT: Chee, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5861244
GENERAL INFORMATION
APPLICANT: HEPBURN, A. G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 650-326-2400
TELEFAX: 650-326-2422
INFORMATION FOR SEQ ID NO: 268:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 84.6%;
Matches 11; Conservative
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MOLECULE TYPE: DNA (probe)
US-08-441-887A-268
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                                                       US-08-441-887A-268/c
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US-08-173-489C-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
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13.4%; Score 9.8; DB 1; Length 13; 84.6%; Pred. No. 1.4e+02; tive 0; Mismatches 2; Indels
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US-08-25-664-15/C
US-08-25-664-15/C
US-08-25-664-15/C
US-08-264-15/C
US-08-264
                                                                                                                                                        MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEN for Windows Version 2.0
SOFTWARE: Value of the compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/143,312
FILING DATE: 26-OCT-1993
APPLICATION NUMBER: US 08/284,064
FILING DATE: 26-OCT-1994
APPLICATION NUMBER: WO PCT/US94/12305
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: US 08/510,521
FILING DATE: 02-AUG-1995
ATTORING DATE: 02-AUG-1995
ATTORING DATE: 02-AUG-1995
ATTORING DATE: 03-AUG-1995
ATTORING DATE: 01-OCT-1995
ATTORING DAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44Mb
COMPUTER: 1BM PC compacible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242,664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    915 TGGTCTTTGCCTT 927
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Best Local Similarity 84.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 13 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-778-794A-87
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US-08-794A-87
1S-08-794A-87
1 Sequent No. 670 Application US/08778794A
1 Partent No. 6309823
2 GENERAL INFORMATION:
APPLICANT: Miyada, Charles Garrett
APPLICANT: Chub, Earl A.
APPLICANT: Chub, Earl A.
APPLICANT: Choc, Mark
APPLICANT: Choc, Stephen P.A.
APPLICANT: Lipshuz, Kaohua C.
APPLICANT: Lipshuz, Robert J.
APPLICANT: Lipshuz, Robert J.
APPLICANT: Lipshuz, Robert J.
APPLICANT: Lipshuz, Robert J.
APPLICANT: MacDonald S.
APPLICANT: MacDonald S.
TITLE OF INVENTION: Arrays of Nucleic Acid Probes
TITLE OF INVENTION: Arrays of Nucleic Acid Probes
TITLE OF INVENTION: Arrays of Nucleic Acid Probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.4%; Score 9.8; DB 1; Length 13; 84.6%; Pred. No. 1.4e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/544,381B
FILING DATE: 10-OCT-1995
CLASSIPICATION: 435
PRIOR APPLICATION: A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/510,521
FILING DATE: 02-AUG-1995
FILING DATE: 26-OCT-1994
FILING DATE: 26-OCT-1994
FILING DATE: 26-OCT-1994
FILING DATE: 26-OCT-1994
FILING DATE: 12-OCT-1994
FILING DATE: 12-OCT-1994
FILING DATE: 12-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: US 08/143,312
FILING DATE: 26-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 018857-004130US
TELEPHONE: A15-576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Townsend and Townsend and Crew LLP Two Embarcadero Center, Eighth Floor
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear MOLECULE TYPE: DNA (oligonucleotide) US-08-544-3818-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                915 TGGTCTTTGCCTT 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 13.4
Best Local Similarity 84.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Two Embarca
CITY: San Francisco
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Sequence 29, Application US/08535249

Patent No. 645569

GENERAL INFORMATION:
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Managensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Managensiepen, APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,249
FILING DATE:
CLARROWERS PATENTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 9.8; DB 1; L. Pred. No. 1.6e+02; 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSITICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 30-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 649.7
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 11,409
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Patent No. 6632057
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E: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 84.6%;
Matches 11; Conservative
                 919 CTTTGCCTTTTAT 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (202) 393-5350
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                                                                              13 Crririccirrirr 1
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APPLICANT: LEWIN, ALFRED S.
APPLICANT: SHAW, LYNN C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: un
MOLECULE TYPE:
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                                                                                                                                                                              RESULT 158
US-08-535-249-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 13.4%; Score 9.8; DB 1; Length 14; Best Local Similarity 84.6%; Pred. No. 1.6e+02; Matches 11; Conservative 0; Mismatches 2; Indels
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84.6%; Pred. No. 1.6e+02;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KESULT 138-15/C

Sequence 15, Application US/08484138

Patent No. 565230

APPLICANT: Watanabe, Kyoichi A. APPLICANT: Watinabe, Kyoichi A. APPLICANT: Wail, Roger and Toxins TITLE OF INVENTION: Complementary DNA and Toxins NUMBER OF SEQUENCES: 43

CORRESPONDENCES: 43

CORRESPONDENCES: 6.3

STREET: 1185 Avenue of the Americas CORRESPENCE COOPEr & Dunham LLP STREET: 1185 Avenue of the Americas COUNTRY: U.S.A.

ZITY: New York

COUNTRY: U.S.A.

ZITE: 10036

COMPUTER READALE FORM: MEDIUM TYPE: 3.5 inch 1.44Mb

COMPUTER: IBM PC

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARR: Patentin Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,138

FILING BATE: Unne 7, 1995

FILING BATE: Unne 7, 1995

FILING BATE: Unne 7, 1995

FILING BATE: Unne 7, 1995
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                                                                                            NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFRENCE/COCKET NUMBER: 4468:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEPAX: 212-664-0525
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYRE: nucleic acid
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ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REPRENCE/DOCKET NUMBER: 4468
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 212-664-0525
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FILING DATE: May 12, 1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: DNA (genomic)
US-08-484-138-15
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Best Local Similarity 84.6
Matches 11; Conservative
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; Sequence 123, Application US/07744282C
; Patent No. 5521300
; GENERAL INFORMATION:
    APPLICANT: Shah, Jyotsna S.
    APPLICANT: Iiu, Jing
    TITLE OF INVENTION: Oligonuclectides Complementary to
    TITLE OF INVENTION: Mycobacterial Nucleic Acids
    NUMBER OF SEQUENCES: 127
    CORRESPONDENCE ADDRESS:
    STREET: P.O. Box 999
    CITY: York Harbor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 9.8; DB 1; Length 14;
Pred. No. 1.6e+02;
0; Mismatches 2; Indels
                          Sequence 15, Application PC/TUS9506379
GENERAL INFORMATION:
APPLICANT: Watanabe, Kyoichi A.
APPLICANT: Wen, Wu-Yun
APPLICANT: Well, Roger
TITLE OF INVENTION: Complementary DNA and Toxins
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPUTER: ISM PC COMPUTER: SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                   STREET: 1185 Avenue of the Americas CITY: New York STATE: New York COUNTRY: U.S.A. ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44Mb
COMPUTER: IBM PC
COMPUTER: IBM PC
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
RPLICATION NUMBER: PCT/US95/06379
FILING DATE: May 13, 1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/ACENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REPRENCE/DOCKET NUMBER: 4466:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 212-391-0526
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 84.6%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     919 CITIGCCTTTAT 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212-391-0526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 CTTTTCCTTTTT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                 PCT-US95-06379-15/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 162
US-07-744-282C-123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 03911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    임
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US-09-874-601-111/c

Sequence 111, Application US/09874601

Sequence 111, Application US/09874601

Sequence 111, Application US/09874601

GENERAL INFORMATION:

APPLICANT: LEWIN, ALFRED S.

APPLICANT: SHAW, LYNN C.

APPLICANT: SHAW, LYNN C.

APPLICANT: SHAW, LYNN C.

TILLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES

TILLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES

TILLE REFERENCE: 4300.014100

CURRENT APPLICATION NUMBER: 09/063,67

PRIOR APPLICATION NUMBER: 09/063,67

PRIOR PILING DATE: 1998-04-21

PRIOR PILING DATE: 1997-04-21

WHOBER OF SEQ ID NOS: 182

SOFTWARE: PATCHIN VERSION 3.0
TITLE OF INVENTION: ABBOOLASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES FILE REPERENCE: 4300.014100
CURRENT APPLICATION NUMBER: US/09/874,601
CURRENT FILING DATE: 2001-05-01
PRIOR APPLICATION NUMBER: 09/063,667
PRIOR APPLICATION NUMBER: 60/046,147
PRIOR APPLICATION NUMBER: 60/046,147
PRIOR FILING DATE: 1997-05-09
PRIOR FILING DATE: 1997-04-21
NUMBER OF SEQ ID NOS: 182
SEQ ID NO 110
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 9.8; DB 1; Length 14;
Pred. No. 1.6e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: ()...()
OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature

LOCATION: () ... ()

JOHER INVERNATION: SYNTHETIC OLIGONUCLEOTIDE

US-09-874-601-110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 13.4%;
Best Local Similarity 84.6%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 922 recentriatece 934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 111
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
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              Best Local Similarity 73.3%; Pred. No. 1.7e+02;
Matches 11; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sullivan, Sean M.
APPLICANT: Sullivan, Sean M.
APPLICANT: McSwiggen, James
APPLICANT: McSwiggen, James
APPLICANT: Stindhomb, Dan T.
TITLE OF INVENTION: RIBOZYNE TRRATMENT OF DISEASES
TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF IL-5
NUMBER OF SEQUENCES: 751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE AULAGES:
ADDRESSEE: Lyon & Lyon
STRRET: 633 West Fifth Street
STRRET: 631 West Fifth Street
STRRET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
ZIP: 9007
ZIP: 
                                                                                                                                                                                                                                                                                                                                              Sequence 64, Application US/08319492B; Patent No. 5616488; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 165
US-08-319-492B-73
; Sequence 73, Application US/08319492B
                                                                                                                920 TTTGCCTTTTATCCC 934
                                                                                                                                                              1 TTGGCMTTTCACCCC 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       943 ATTGGTTTAATGT 955
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Best Local Similarity 84.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 ATTGGTTTACTCT 3
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US-08-319-492B-64/C
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US-07-744-282C-125
i Sequence 125, Application US/07744282C
i Sequence 125, Application US/07744282C
i Patent No. 5521300
GENERAL INFORMATION:
APPLICANT: Shah, Jyotsna S.
APPLICANT: Liu, Jing
TITLE OF INVENTION: Oligonucleotides Complementary to TITLE OF INVENTION: Mycobacterial Nucleic Acids
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
CITY: York Harbor
STAIE: MB
COUNTRY: USA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
13.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 1.7e+02;
Matches 11; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER LIBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA;

APPLICATION NUMBER: US/07/744,282C

FILING DATE: August 13, 1991

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Kevin M. Farrell

REGISTRATION NUMBER: 35,505

REFERENCE/DOCKET NUMBER: 35,505

REFERENCE/DOCKET NUMBER: 35,505

REFERENCE/COCKET NUMBER: 35,505

TELEPAN: (207) 363-0528

INFORMATION FOR SEQ ID NO: 125:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 base pairs

TYPE: nucleic acid

STRANBEDNESS: double

TYPE: NOCHCURY TYPE: DNA (GENOMIC)

STRANBENESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (GENOMIC)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/744,282C
FILING DATE: Adgust 13, 1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kevin M. Farrall
REFERENCE/DOCKET NUMBER: 35.505
REFERENCE/DOCKET NUMBER: GTR90-05
TELEPHONE: (207) 363-0528
TELEPHONE: (207) 363-0528
TELEPHONE: (207) 363-0528
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTER/STICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDENESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-744-282C-123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  920 TITGCCTTTTATCCC 934
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DB 1; Length 15;

13.4%; Score 9.8;

Query Match

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Gaps
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Sequence 170
Sequence 170
Sequence 170
Sequence 170
Sequence 170
Set 49plication US/08319492B

Patent No. 561648B

GENERAL INFORMATION:
APPLICANT: Sullivan, Sean M.
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Galiferia
CONRIES: Califeria
COUNTRY: U.S.A.
ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.4%; Score 9.8; DB 1; Length 15; 30.8%; Pred. No. 1.7e+02; tive 7; Mismatches 2; Indels
                                                                                                  COUNTER TEADABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,492B
FILING DATE: October 7, 1994
PRIOR APPLICATION DATA:
APPLICATION DATA: including application
PRIOR APPLICATION DATA:
APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008/895
FILING DATE: December 7, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
RESERENCE-DOCKET NUMBER: 209/276
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
              Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 169
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 943 ATTGGTTTAATGT 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 30.83
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2 AUTUAUUUAAUGU 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
              STREET: 633 West Fi
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
            633 West F. Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
US-08-319-492B-169
ADDRESSEE:
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                                  APPLICANT: Sullivan, Sean M.
APPLICANT: Sullivan, Kenneth G.
APPLICANT: Draper, Kenneth G.
APPLICANT: Maswiggen, James
TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF IL-5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sullivan, Sean M.
APPLICANT: Draper, Kenneth G.
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
TITLE OF INVENTION: REBOZYME TREATMENT OF DISEASES
TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF IL-5
                                                                                                                                                                                                                                                                                                                    RESULT 166
US-08-319-492B-169
Sequence 169, Application US/08319492B
Parent No. 5616488
GENERAL INFORMATION:
                                                                                                                                                                                                          ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   944 TIGGITIAAIGIA 956
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Best Local Similarity 46.2
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
                                                                                                                                                                                                                                                                    CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                          U.S.A.
    Patent No. 5616488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ,
TOPOLOGY:
US-08-319-492B-73
                                                                                                                                                                                                                                                                                                          COUNTRY:
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; Sequence 437, Application US/08319492B
; Patent No. 561648B
; GENERAL INFORMATION:
APPLICANT: Sullivan, Sean M.
APPLICANT: Draper, Kenneth G.
APPLICANT: Draper, Kenneth G.
APPLICANT: Etinchcomb, Dan T.
ITILE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
TITLE OF INVENTION: OF LL-5
NUMBER OF SEQUENCES: 751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Los Augeles
STREET: Suite 4700
CITY: Los Angeles
COUNTRY: U.S.A.
ZIP. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 13.4%; Score 9.8; DB 1; Length 15; Best Local Similarity 61.5%; Pred. No. 1.7e+02; Matches 8; Conservative 3; Mismatches 2; Indels
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COMPUTER: IFE: SECTAGE
COMPUTER: IFE: SECTAGE
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/119,492B
FILING DATE: OCCODER 7, 1994
PRIOR APPLICATION DATA: including application
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Watburg, Richard
REGIETRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIF: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                           FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32, 327
REPERENCE/DOCKET NUMBER: 209/276
FELEPHONE: (213) 955-0440
FELEPAX: (213) 955-0440
FELEFAX: (213) 955-0440
FELEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        931 TCCCTCCTCTTCA 943
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
13.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 30.8%; Pred. No. 1.7e+02;
Matches 4; Conservative 7; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-319-492B-436

US-08-319-492B-436

Sequence 436, Application US/08319492B

Patent No. 5616488

APPLICANT: Sullivan, Sean M.
APPLICANT: Draper, Kenneth G.
APPLICANT: Stinchcomb, Dan T.
TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES

TITLE OF INVENTION: OF IL-5

TITLE OF INVENTION: OF IL-5

NUMBER OF SEQUENCES: 751

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: 633 West Fifth Street
STREET: California
COMPTRY: US.A.

COMPUTER: Storage

COMPUTER: IL-S.A.

COMPUTER: IS-C. DISEASE

COMPUTER: IBM P.C.

COMPUTER: IBM P.
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/19,492B
FILING DATE: Occober 7, 1994
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
RICHARTON NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
NEFERENCE/DOCKET NUMBER: 209/276
TELEFORWINICATION INFORMATION:
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFAX: (213) 555-0440
TELEFAX: 15 base pairs
TYPE: INCORMATION FOR SEQ ID NO: 170:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: Incleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/19,492B
FILING DATE: October 7, 1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: Gescribed below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         943 ATTGGTTTAATGT 955
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1 AUUUAUUUAAUGU 13
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US-08-319-492B-170
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GENERAL INFORMATION:
APPLICANT: Coutur
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                                         US-08-363-240A-228
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                                                                                                                          Length 15;
                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Couture, Larry
APPLICANT: McSwiggen, Charles
APPLICANT: Bisgaler, Charles
APPLICANT: Pape, Michael
ITILE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: PROGRESSION AND REGRESSION
TITLE OF INVENTION: OF VASCULAR DISEASES
NUMBER OF SEQUENCES: 1243
CORRESPONDENCE ADDRESS:
                                                                                                                      Query Match 13.4%; Score 9.8; DB 1; Best Local Similarity 61.5%; Pred. No. 1.7e+02; Matches 8; Conservative 3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PETECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,240A
FILING DATE: December 23, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage.
                                                                                                                                                                                                                                                                                                                                        Sequence 227, Application US/08363240A Patent No. 5705388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210/096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFRENCE/DOCKET NUMBER: 210/
TELECOMMUNICATION INFORMATION:
TELEPAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 227:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         915 TGGTCTTTGCCTT 927
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2 UGGACUUUGGCUU 14
) LENGTH: 15 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-319-492B-437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 13.4
Best Local Similarity 38.5
Matches 5; Conservative
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EDNESS: single
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US-08-363-240A-227
                                                                                                                                                                                                                                                                                                     RESULT 170
US-08-363-240A-227
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13.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 38.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 6; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 48, Application US/08294424
Patent No. 5800984
GENERAL INFORMATION
TITLE OF INVENTION: NUCLEIC ACID SEQUENCE DETECTION BY
TITLE OF INVENTION: TRIPLE HELIX FORMATION
TITLE OF INVENTION: TRIPLE HELIX FORMATION
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 255 Franklin Street
CITY: Boston
                                                                            APPLICANT: Gouture, Larry
APPLICANT: McSwiggen, James
APPLICANT: Biggalen, James
APPLICANT: Biggalen, James
APPLICANT: Pape, Michael
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: PROGRESSION AND REGRESSION
TITLE OF INVENTION: OF VASCULAR DISEASES
CORRESPONDENCE: 1243
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTY: 0.5.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: 1BM Compatible
OPERATING SYSTEM: 1BM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,240A
FILING DATE: December 23, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
TRING DATE:
APPLICATION NUMBER:
TRING DATE:
THING DATE:
; Sequence 228, Application US/08363240A; Patent No. 5705388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210/096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: WATDULE, RECHARD
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 210/C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 228:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    915 IGGICTITGCCTT 927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
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13.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 53.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 174
US-08-311-486C-75
US-08-311-486C-75
Sequence 75, Application US/08311486C
Patent No. 5811300
PAPLICANT: Sean Sullivan
APPLICANT: Kenneth Draper
APPLICANT: Kenneth Draper
APPLICANT: Memeth Draper
APPLICANT: Dan T. Stinchcomb
APPLICANT: Dan T. Stinchcomb
APPLICANT: Dan T. Stinchcomb
APPLICANT: Dan T. Stinchcomb
APPLICANT: NEWENTION: RELARD TO LEVELS OF
TITLE OF INVENTION: RELARD TO LEVELS OF
TITLE OF INVENTION: RELARD TO LEVELS OF
ANDRESSEE: Lyon & Lyon
STREET: 633 West Pifth Street
STREET: Galfornia
COUNTRY: LOS Angeles
STREET: Suite 4700
CITY: LOS Angeles
STREET: Suite 4700
CITY: LOS Angeles
COMPUTER READABLE FORM:
MEDIUM TYPE: Storage
MEDIUM TYPE: Storage
COMPUTER: BM Compatible
OPERATING SYSTEM:
MEDIUM TYPE: STORAGE
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION NUMBER: IN ANDRESSEE
APPLICATION NUMBER: IN ANDRESSEE
APPLICATION NUMBER: IN ANDRESSEE
APPLICANTON NUMBER: IN ANDRESSEE

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FILING DATE: September 23, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
                                                                                                                                                                              application
below:
FILING DATE: September 23, 120..
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/08,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/98,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/98,849
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/98,849
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/98,849
FILING DATE: January 19, 1993
ATOMER'S ANTONERRY 10, 1992
ATOMER'S ANTONERRY 10, 1992
ATOMER'S ANTONERRY 10, 1992
ATOMER'S ANTONERRY 10, 1993
ATOMER'S ANTONERY 10, 1993
ATOMER'S ANTONERRY 10, 1993
ATOMER'S ANTONERRY 10, 199
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13.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 1.7e+02;
Matches 11; Conservative 0; Mismatches 2; Indels
                   STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

CMEDTER: READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: 1BM PS/2 Model 502 or 55X
OCMPUTER: 1BM PS/2 Model 502 or 55X
OCMPUTER: WordPerfect (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294,424
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/000,922
FILING DATE: 16 JAN 1993
APPLICATION NUMBER: US/08/000,922
FILING DATE: 17-DEC-1990
ATTORNEY AGENT INFORMATION:
NAME: Freemen, John W.
RETERRATION NUMBER: 29,066
TELECOMMUNICATION NUMBER: 29,066
TELECOMMUNICATION NUMBER: 29,066
TELECOMMUNICATION NUMBER: 29,066
TELEFAX: (617) 542-8906
TELEFAX: (617) 542-8906
TELEFAX: (617) 542-8906
TELEFAX: (617) 542-8906
TELEFAX: 15
TENDER 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 173
US-08-311-486C-74

Sequence 74, Application US/08311486C
Sequence 74, Application US/08311486C
Sequence 74, Application US/08311486C
Sequence 74. Application
Sequence 74. Application
APPLICANT: Sean Sullivan
APPLICANT: Kenneth Draper
APPLICANT: Kenneth Draper
APPLICANT: Menneth Draper
APPLICANT: James McSwiggen
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DREASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: Applicant
STREET: Suite 4700
CITY: Los Angeles
STREET: Suite 4700
CITY: Los Angeles
STREET: Suite 4700
CITY: Los Angeles
STREET: Suite 4700
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATA: MACH Perfect 5.1
CURRENT APPLICATION NUMBER: US/08/311,486C
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TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear

US-08-294-424-48

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Gaps
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Best Local Similarity 84.6%; Pred. No. 1.7e+02;
Matches 11; Conservative 0; Mismatches 2; Indels
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US-08-292-620A-121/C
US-08-292-620A-121/C
Sequence 121, Application US/08292620A
FALCANT NO. 5837542
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James MCSWiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
ITLE OF INVENTION: RIBOZYME TREATMENT OF
ITLE OF INVENTION: DISEASES OR CONDITIONS
ITLE OF INVENTION: INTRACELULAR ADHESION
ITLE OF INVENTION: INTRACELLULAR ADHESION
ITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING UALE.
CLASSIFICATION: 415
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
FILING DATE: January 19, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: LYON & LYON
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
CITY: Los Angeles
COUNTY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: STORAGE
COMPUTER: IBM COMPATIBLE
OPERATION SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORT PREFECT 5.1
CURRENT APPLICATION DATA:
FILING DATE: AUGUST 17, 1994
CLASSIFICATION: 435
                       FILING DATE: 24-APR-1985
ATTORNEY/AGENT INFORMATION:
NAME: Rea, Teresa Stanck
REGISTRATION NUMBER: 30,427
REPERENCE/DOCKET NUMBER: 017753-061
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 836-620
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                          "oligonucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "oligonucle"
US-08-480-736-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: December 7, 1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    941 TCATTGGTTTAAT 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 rccrrccracarı
                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: LATTE, Richard
APPLICANT: LATTE, Marie-Paule
APPLICANT: KIRNY, Marie-Paule
APPLICANT: DRILLIEN, Roberte
APPLICANT: LOCOCO, Jean-Pierre
TITLE OF INVENTION: VACCINE AGAINST RABIES AND PROCESS FOR
TITLE OF INVENTION: PREPARATION THEREOF
CORRESPONDENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
13.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 53.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,736
FILING DATE: US/08/21,457
FILING DATE: 21-APR-1994
PRIOR APPLICATION NUMBER: US 08/231,457
FILING DATE: 29-MAR-1993
FILING DATE: 29-MAR-1993
FILING DATE: 29-MAR-1993
FILING DATE: 12-FP-1991
PRIOR APPLICATION NUMBER: US 07/759,138
FILING DATE: 11-SEP-1991
PRIOR APPLICATION NUMBER: US 07/378,801
FILING DATE: 11-JUL-1989
PRIOR APPLICATION NUMBER: US 06/829,144
FILING DATE: 24-DEC-1985
PRIOR APPLICATION NUMBER: FR 84/06499
FILING DATE: 25-AFR-1984
FILING DATE: 25-AFR-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandria
FILING DATE: December 7, 1992
ATTORNEY/AGENT IRFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/166
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAS: (213) 955-0440
TELEPAS: (7-3510
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: MUCleic acid
STRANDENNES: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08480736 Patent No. 5830477 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       935 TCCTCTTCATTGG 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 UCCUCUUCAAGGG 13
                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
US-08-311-486C-75
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US-08-480-736-4/c
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Score 9.8; DB 1; Length 15; Pred. No. 1.7e+02; O; Mismatches 2; Indels
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US-08-292-620A-289/A

US-08-292-620A-289/A

Patent No. 5837542

Fatent No. 5837542

Fatent No. 5837542

APPLICANT: Dan T. Stinchcomb

APPLICANT: James McSwiggen

APPLICANT: Senneth d. Draper

TITLE OF INVENTION: RELAFED TO LEVELS OF

TITLE OF INVENTION: RELAFED TO LEVELS OF

TITLE OF INVENTION: NOLECULE-1 (I-CAM-1)

NUMBER OF SEQUENCES: 339

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: Saite 4700

STREET: Saite 4700

CITY: Los Angeles

STREET: Saite 4700

STREET: Saite 4700

STREET: Saite 4700

STREET: Saite 6700

TELEPANDET

TELEPANDET: SAITE

TELEPANDET:
                                                                                                                                                    13.4%;
84.6%;
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                     959 GCTACCAACGGTG 971
                                                                                                                                             Query Match
Best Local Similarity 84.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                              15 gcraacaaagrg 3
; TYPE: nucleic acid
; STRANDEDNESS: singl
; TOPOLOGY: linear
US-08-292-620A-288
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Best Local Similarity
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US-08-292-620A-289
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                                                                                                                                                                                                                                                                                                                                                       Query Match
13.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 1.7e+02;
Matches 11; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESSE:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STRATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 18 Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: MACH PETECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/29,620A
FILING DATE: Angust 17, 1994
CLASSIFCATION DATA: including application
PRIOR APPLICATION DATA: 1994
FILING DATE: John TA: 1994
FILING DATE: John TA: 1992
APPLICATION NUMBER: 08/008,895
FILING DATE: December 7, 1992
ATTONEY/AGENT INFORMATION:
FRIEFRANCE/COCKET WINBER: 32,327
REGISTRATION NUMBER: 32,327
REBERENCE/COCKET WINBER: 208/149
TELEFRAN: (213) 955-0440
TELEFRANCE CHARACTERISTICS:
LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-292-620A-288/C

Sequence 288, Application US/08292620A

Sequence 288, Application US/08292620A

Sequence 288, Application US/08292620A

Patent No. 583784

APPLICANT: Susan Grimm

APPLICANT: Susan Grimm

APPLICANT: Sean Sullivan

APPLICANT: Sean Sullivan

APPLICANT: Sean Sullivan

APPLICANT: Remeth G. Draper

ITILE OF INVENTION: RIBOZNE TREATMENT OF

ITILE OF INVENTION: RELATED TO LEVELS OF

ITILE OF INVENTION: MOLECULE-1 (I-CAM-1)

NUMBER OF SEQUENCES: 2390

CORRESONDENCE 1005
                  TELEPANE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: TOPOLOGY: linear
US-08-292-620A-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               901 CTGGTCATTTTCT 913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 CTGGGAATTTTCT 1
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Length 15; Score 9.8; DB 1; Pred. No. 1.7e+02; 13.4%; 84.6%;

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TELECOMMUNICATION INFORMATION:

US-08-441-887A-16/c

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Gaps ö

2; Indels

Mismatches

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11; Conservative

Matches

Mon Oct 18 14:40:17 2004

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Gaps
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Best Local Similarity 78.6%; Pred. No. 1.76+02;
Matches 11; Conservative 0; Mismatches 3; Indels
                                                                     APPLICANT: Cronin, Maureen T.
APPLICANT: Cronin, Maureen T.
APPLICANT: Fodor, Stephen P.A.
APPLICANT: Hubbell, Earl A.
APPLICANT: Hubbell, Earl A.
APPLICANT: Hubbell, Earl A.
APPLICANT: Lipshurz, Robert J.
APPLICANT: Morris, Macdonald S.
APPLICANT: Morris, Macdonald S.
APPLICANT: Sheldon, Edward L.
TITLE OF INVENTION: Arrays of Nucleic Acid Probes on TITLE OF INVENTION: Biological Chips
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/41,887A
FILING DATE: 16-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION: A35
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: A35
PRIOR APPLICATION: DATA:
APPLICATION NUMBER: US 08/082,937
FILING DATE: 25-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Liebeschuerz, Joseph O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 018547-004160US
TELECOMMUNICATION INFORMATION:
TELECHONE: 650-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17, Application US/08441887A
Patent No. 5837832
GENERAL INFORMATION:
APPLICANT: Cronin, Marken T.
APPLICANT: Prodor, Stephen P.A.
APPLICANT: Prodor, Stephen P.A.
APPLICANT: Huang, Xiaohua X.
Application US/08441887A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 650-326-2422
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     911 TCTTTGGTCTTTGC 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (probe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 rcrrrngrgrrrcc 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 181
US-08-441-887A-17/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-441-887A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: CA
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Pred. No. 1.7e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                             APPLICANT: Chee, Mark
APPLICANT: Cronin, Maureen T.
APPLICANT: Fodor, Stephen P.A.
APPLICANT: Huang, Xiaohua X.
APPLICANT: Hubbell, Barl A.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Sheldon, Peter E.
APPLICANT: Sheldon, Edward L.
TITLE OF INVENTION: Arrays of Nucleic Acid Probes on TITLE OF INVENTION: Biological Chips
NUMBER OF SEQUENCES: 360
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,887A
FILING DATE: 16-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/143,312
FILING DATE: 26-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: US 08/082,937
FILING DATE: 25-UN-1993
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEE: Townsend and Townsend and Crew LLP: Two Embarcadero Center, 8th Floor Can Francisco California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Liebeschuetz, Joseph O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 018547-004160US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                      RESULT 179
US-08-441-887A-8/c
; Sequence 8, Application US/08441887A
; Patent No. 5837832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.4%;
84.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (probe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     938 TCTTCATTGGTTT 950
                                   959 GCTACCAACGGTG 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 84.6
Matches 11; Conservative
                                                                                 14 GCTAACAAAGGTG 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Chee, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-441-887A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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RESULT 180

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TYPE: nucleic acid STRANDEDNESS: single stranded STRANDEDNESS: single stranded TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: third strand derived from Hepatitis B DESCRIPTION: isolate adr sequence region in Seq ID No. 5861244141 HYPOTHETICAL: yes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 13.4%; Score 9.8; DB 1; Length 15; Best Local Similarity 84.6%; Pred. No. 1.7e+02; Matches 11; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-585-684B-1748/C

Sequence 1748, Application US/08585684B

Sequence 1748, Application US/08585684B

PARELL NO. S877021

GENERAL INCORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: MnD REPERSAL OF IMMUNE RESPONSES
TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: no'
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 142 :FROM 1 TO 15
US-08-173-489C-142
                                                         COMPUTER: IBM PC/XT/AT
COMPUTER: TBM SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordporfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATFORNEY/ABORT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REGISTRATION INFORMATION:
TELEPHONE: (attorney) (212) 708-1880
TELEPHONE: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 142:
SEQUENCE CHARACTERISTICS:
TENERY: 15 Dates
               MEDIUM TYPE: 3.5 inch, 1.44Mb storage COMPUTER: IBM PC/XT/AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          924 CCTTTTATCCCTC 936
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US-08-173-489C-142
i Sequence 142, Application US/08173489C
j Patent No. 5861244
j GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSEE: PROPILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
CITY: NEW YORK
STATE: NEW YORK
CITY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
13.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 78.6%; Pred. No. 1.7e+02;
Matches 11; Conservative 0; Mismatches 3; Indels
APPLICANT: Lipshutz, Robert J.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Lobban, Peter E.
APPLICANT: Sheldon, Edward L.
APPLICANT: Sheldon, Edward L.
TITLE OF INVENTION: Arrays of Nucleic Acid Probes on TITLE OF INVENTION: Biological Chips
NUMBER OF SEQUENCES: 360
CORRESPED TOWNSEND and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEDPPY disk
CURRENT APPLICATION NUMBER: US 08/143,312
FILING DATE: 28-0CT-1993
COMPUTER: IEDPPY disk
COMPUTER: IEDPPY disk
COMPUTER: IEDPPY disk
COMPUTER: IEDPPY disk
COMPUTER: IEDPPY DOCKET NUMBER: 37,505
FRIEDPHONE: 650-326-2400
TELEPPY SEQIENCE CHARACTERISTICS:
COMPUTER: IEDPPY DISK
COMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: DNA (probe)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-441-887A-17
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COMPUTER READABLE FORM:

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Gaps

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COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Varsion 1.5
CURRENT APPLICATION DATA:
FILING DATE: January 16, 1996 PRIOR APPLICATION DATA

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schultz1-899.rni

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Gaps
                                                       Score 9.8; DB 1; Length 15;
Pred. No. 1.7e+02;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lipshutz, Robert J.
APPLICANT: Lobban, Peter E.
APPLICANT: Morris, Macdonald S.
APPLICANT: Sheldon, Edward L.
TITLE OF INVENTION: Arrays of Nucleic Acid Probes for TITLE OF INVENTION: Detecting Cystic Fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER KEALABLE FORM:
COMPUTER KEALABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPANING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/544,381B
FILING DATE: UO-OCT-1995
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: US/08/510,521
PILING DATE: 02-AUG-1995
PRIOR APPLICATION NUMBER: US/08/12305
PILING DATE: 26-OCT-1994
PRIOR APPLICATION NUMBER: US/08/284,064
PILING DATE: 26-OCT-1994
PRIOR APPLICATION NUMBER: US/08/284,064
PILING DATE: 02-AUG-1994
PRIOR APPLICATION NUMBER: US/08/143,312
FILING DATE: 26-OCT-1993
ATTONREY/AGENT INPORMATION:
WAME: LA CANAGATION:
WATCH 

    Townsend and Townsend and Crew LLP
Two Embarcadero Center, 8th Floor

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                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 114, Application US/08544381B Patent No. 6027880 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cronin, Maureen T.
Miyada, Charles Garrett
Hubbell, Earl A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chee, Mark
Fodor, Stephen P.A.
Huang, Xiaohua C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE, DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                       13.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 250
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and
                                                                                                                                                                                       934 CTCCTCTTCATTG 946
                                                          Query Match
Best Local Similarity 46.23
Matches 6; Conservative
                                                                                                                                                                                                                                3 CUGCUCAUCAUG 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE:
US-08-544-381B-114
                                                                                                                                                                                                                                                                                                                                                                                           US-08-544-381B-114/c
US-08-585-684B-1811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                             ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
APPLICANT: Jarvis, Thale
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERRANCE
TITLE OF INVENTION: AND REVERSAL OF INMUNE RESPONSES
NUMBER OF SQUENCES: 2751
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: Suite 4700
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 13.4%; Score 9.8; DB 1; Best Local Similarity 84.6%; Pred. No. 1.7e+02; Matches 11; Conservative 0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFWARE: Feat-SEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/585,684B
FILING DATE: January 16, 1996,
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/000,951
FILING DATE: July 7, 1995
ATTORNEY/ACBNT INFORMATION:
NAME: Warburg Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEG 15 955-0440
TELEPRONE: (213) 955-0440
TELEPRONE: (213) 955-0440
TELEPRONE: (213) 955-0440
TELEPRONE: (213) 955-0440
TELEPRONE: (215) 955-0440
TELERA: (7-3510
TELERA: (7-3510
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                           FILING DATE: July 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (213) 955-0440
TELEFAX: (7-3510
INFORMATION FOR SEQ ID NO: 1748:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDENNES: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 184
2.08-58-688-1811
; Sequence 1811, Application US/08585684B
; Patent No. 5877021
   APPLICATION NUMBER: 60/000,951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             938 TCTTCATTGGTTT 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 rcrrcrradgiri 2
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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US-08-585-684B-1748
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Sequence 288/C
Sequence 289, Application US/09071845
Patent No. 613284
Patent No. 61284
Patent No
                                                                                                                  RESULT 187
US-09-071-845-288/c
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13.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 1.7e+02;
Matches 11; Conservative 0; Mismatches 2; Indels
Query Match
13.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 1.7e+02;
Matches 11; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 186
US-09-071-845-121/C
Sequence 121, Application US/09071845
Fatent No. 6132967
Fatent No. 6132967
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: James McSwiggen
APPLICANT: James McSwiggen
APPLICANT: Games McSwiggen
APPLICANT: James McSwiggen
APPLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE AUDGES.

ADDRESSEE: Lyon & Lyon & Lyon & STREET: Suite 4700
CITY: Los Angeles
STREET: Suite 4700
CITY: Los Angeles
STREET: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: BM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
PRICE APPLICATION NUMBER: US/09/071,845
FILING DATE: August 17, 1994
APPLICATION NUMBER: US/08/292,620
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: January 19, 1993
APPLICATION NUMBER: 208/149
FILING DATE: January 19, 1993
APPLICATION NUMBER: 208/149
FILING DATE: WARDATION: TELEPHONE: (213) 955-0440
TELEPHONE: (213) 955-0440
TELEFRANE (213) 955
                                                                                                                                                                                                                         938 TCTTCATTGGTTT 950
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US-09-071-845-121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-071-845-289/c
; Sequence 289, Application US/09071845
Patent No. 6132967
; GENERAL INFORMATION:
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 288:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPLOGY: linear
US-09-071-845-288
                                                                                                                                                                                                                                                                                                                                       959 GCTACCAACGGTG 971
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-038-073-1811

Sequence 1811, Application US/09038073

Patent No. 6194150

GENERAL INFORMATION:

APPLICANT: Stinchcomb, Daniel T.

APPLICANT: Jarvis, Thale

APPLICANT: MCSWIGGON, James

ITTLE OF INVENTION: METHOD AND REAGENT FOR THE

TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE

TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES

NUMBER OF SEQUENCES: 2751

CORRESPONDENCE ADDRESS:
                                                                                                                                                       CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: FastSEQ Version 1.5
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,073
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 8torage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,073
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585,684
FILING DATE: 100 NUMBER: 08/585,684
ATTORNEY/ACENT INFORMATION:
NAME: WAITDING, RICHARG, 32,327
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/078
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 1748:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 DASE PAIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218/078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                     Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.4%;
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Best Local Similarity 84.6
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                  EE: Lyon & Ly
633 West Fi
Suite 4700
                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-038-073-1748
                                                                                                  ADDRESSEE:
STREET: 63
STREET: Su
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METHOD AND REAGENT FOR THE INDUCTION OF GRAFT TOLERANCE AND REVERSAL OF IMMUNE RESPONSES 2751
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Sean Sullivan
APPLICANT: Renneth G. Draper
TITLE OF INVENTION: RELAZENE TRAIMENT OF
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lv~-
STREET: 633 W--
STRFET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: US/08/292,620
FILING DATE: August 17, 1994
APPLICATION NUMBER: 08/08,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REPERENCE/DOCKET NUMBER: 208/149
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 189
US-09-038-073-1748/c
| Sequence 1748, Application US/09038073
| Patent No. 6194150
| GENERAL INFORMATION:
| APPLICANT: Stinchcomb, Daniel T. APPLICANT: Jarvis, Thale
| APPLICANT: McSwiggen, James
| TITLE OF INVENTION: METHOD AND REAGEN TITLE OF INVENTION: AND REVERSAL OF INUMBER OF SEQUENCES: 2751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOPTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 289:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      959 GCTACCAACGGTG 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 84.6
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 GCTAACAAAGGTG 2
                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                 RY: U.S.A.
90071-2066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: nucleotide base recognition sequence substantially OTHER INFORMATION: complementary to SEQ ID No. 6361945. 1 and 3
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  CONDITIONS RELATED TO LEVELS
OF VASCULAR ENDOTHELIAL
GROWTH FACTOR
8502
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i Sequence 4, Application US/09346551B
; Sequence 4, Application US/09346551B
; Parent No. 6361945
; GENERAL INFORMATION:
; APPLICANT: BECKEN, Michael M.
; APPLICANT: SCHROTH, Gary P.
; TITLE OF INVENTION: MOLECULAR TORCHES
; TITLE REFERRACE: GP098-02.UT
; CURRENT APPLICATION NUMBER: US/09/346,551B
; CURRENT FILING DATE: 1999-07-01
; EARLIER FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 4
; SEQ ID NO 4
; LENGTH: 15
TITLE OF INVENTION: CONDITIONS RELATED TO TITLE OF INVENTION: OF VASCULAR ENDOTHEL.

TITLE OF INVENTION: GROWTH FACTOR NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS: 8502
CORRESPONDENCE ADDRESS: 8502
CORREST: 633 West Fifth Street STREET: 633 West Fifth Street STREET: Suite 4700
CITY: Los Angeles STATE: California COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTEN FRADABLE FORM: MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY, AGENT INPORMATION:
NAME: WARDING; Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,937
REFERENCE/DOCKET NUMBER: 32,937
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 8493:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: TIPMENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                916 GGTCTTTGCCTTT 928
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-584-040-8493
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Fatent No. 6333152

GENERAL INFORMATION:
APPLICANT: Kinzler, Kenneth
APPLICANT: Zhou, Lin
APPLICANT: Zhou, Lin
APPLICANT: Zhou, Wei
TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
TITLE OF INVENTION: Cancer Cells
TITLE OF INVENTION: Cancer Cells
FILE REFERENCE: 01107.74664
CURRENT APPLICATION NUMBER: 60/091,646

CURRENT FILING DATE: 1998-05-20

EARLIER FILING DATE: 1997-05-21

NUMBER OF SEQ ID NOS: 871

SOFTWARE: FREISE FREISE FREISE FAILNG WINDOWS Version 3.0

SEQ ID NO 3

LENGTH: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 13.4%; Score 9.8; DB 1; Length 15; Best Local Similarity 46.2%; Pred. No. 1.7e+02; Matches 6; Conservative 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.4%; Score 9.8; DB 1; Length 15; 84.6%; Pred. No. 1.7e+02; tive 0; Mismatches 2; Indels
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Patent No. 6346398
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: McSwiggen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE TITLE OF INVENTION: TREATMENT OF DISEASES OR
                                                                                                                                                                                       218/078
                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Warburgy Richard:
ROGISTRATION NUMBER: 32,327
REPERENCE/DOCKET NUMBER: 218/07
TELECOMUNICATION INFORMATION:
TELEFAN: (213) 489-160
                              PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/585,684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    934 CTCCTCTTCATTG 946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    922 TGCCTTTTATCCC 934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
US-09-038-073-1811
          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 192
US-08-584-040-8493
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US-09-081-646-3
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Sequence 4147, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
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84.6%;
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                                                                                                                                                                                         ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                              908 TTTTCTTTGGTCT 920
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Best Local Similarity 46.2.
Best Local Similarity 6.2.
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Best Local Similarity 84.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: RNA
; ORGANISM: Mus sp.
US-09-371-772B-4147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 196
US-09-371-772B-4147
                                                                                                                                                                                                                                                                                           US-10-001-344-4
                                                                                                                                                                        TYPE: DNA
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                                                                                                                                                                                                                                           Sequence 5, Application US/08461210;
Patent No. 6395475;
GENERAL INFORMATION:
APPLICANT: Leggett, Carol G.
TITLE OF INVENTION:
TITLE OF INVENTION: Semiautomated Method for Fingerprinting
TITLE OF INVENTION: Bacterial DNA
NUMBER OF SEQUENCES: 31
CORRESPONDENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell
STREET: 200 East Broward Boulevard
CITY: Port Lauderdale
STATE: Florida
                                                                           ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                 Score 9.8; DB 1; Length 15; Pred. No. 1.7e+02; 0; Mismatches 2; Indels
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Pred. No. 1.7e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,596
FILING DATE: 18-MAY-1993
ATTORNEY/AGENT INFORWATION:
NAME: MAINS. PETER J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: FL20979-20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32,264
ER: FL20979-20
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Patent No. 6534274
GENERAL INPORMATION:
APPLICANT: BECKER, Michael M.
APPLICANT: SCHROTH, Gary P.
TITLE OF INVENTION: MOLECULAR TORCHES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 84.6%;
Matches 11; Conservative
                                                                                                                908 TITICITIGGICT 920
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                                                                                                                                                      2 rrrrccrrccrcr 14
                                   Query Match
Best Local Similarity 84.6
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 Grcaarrccrrrg 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                RESULT 194
US-08-461-210-5/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-461-210-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-001-344-4
US-09-346-551-4
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APPLICANT: Rabozyme Pharmaceuticals, Inc.
APPLICANT: Rabozyme Pharmaceuticals, Inc.
APPLICANT: Rabozyme Pharmaceuticals, Inc.
APPLICANT: Bacco, Pam
APPLICANT: StinchComb, Jam
APPLICANT: StinchComb, Jam
APPLICANT: StinchComb, Jam
APPLICANT: Scobedo, Jaime
APPLICANT: Baccobedo, Jaime
APPLICANT: Baccobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
TITLE OF ILING DATE: 1999-08-10
CURRENT FILING DATE: 1999-08-10
PRIOR FILING DATE: 1995-10-26
PRIOR FILING DATE: 1996-01-08
PRIOR FILING DATE: 1996-01-08
RUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
SEQ ID NOS: 4147
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                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: nucleotide base recognition sequence substantially OTHER INFORMATION: complementary to SEQ ID No. 6534274. 1 and 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
FILE REFERENCE: GP098-02.UT
CURRENT APPLICATION NUMBER: US/10/001,344
CURRENT FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/346,551
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENT VET. 2.0
SEQ ID NO: 4
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 9.8; DB 1; Length 15; Pred. No. 1.7e+02; 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 9.8; DB 1; Length 15;
Pred. No. 1.7e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-US92-06821A-129
; Sequence 129, Application PC/TUS9206821A
; GENERAL INFORMATION:
APPLICANT: Shah, Jyotena S.
APPLICANT: Nietupski, Raymond M.
APPLICANT: Liu, Jing
TITLE OF INVENTION: Oligonuclectides Complementary to
; TITLE OF INVENTION: Mycobacterial Nucleic Acids
) NUMBER OF SEQUENCES: 133
; CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-UB-259-1480-199. Application US/08259148A
| Patent No. 5741490
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Reyes Gregory R. APPLICANT: Twu, Ur-Shin
| APPLICANT: Twu, Ur-Shin
| APPLICANT: Twu, Mchael A. APPLICANT: Twu, Albert W. APPLICANT: Twu, Albert W. APPLICANT: Krawczynski, Krzysztof Z. APPLICANT: Krawczynski, Krzysztof Z. APPLICANT: Warbough, Patrice D. Virus Vaccine and Method ITTLE OF INVENTION: Hepatitis E Virus Vaccine and Method NUMBER OF SEQUENCES:
| CORRESPONDENCE ADDRESS:
| CORRESPONDENCE ADDRESS:
| STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                       Query Match 13.4%; Score 9.8; DB 1; Length 15; Best Local Similarity 73.3%; Pred. No. 1.7e+02; Matches 11; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER REALABLE FORM:
COMPUTER REALABLE FORM:
COMPUTER: IBM PC Compatible
COMPRATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,148A
FILING DATE: 13-JUN 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
PRIOR APPLICATION NUMBER: US 505,888
FILING DATE: 05-APR-1990
PRIOR APPLICATION NUMBER: US 505,888
FILING DATE: 05-APR-1990
PRIOR APPLICATION NUMBER: US 505,888
FILING DATE: 13-OCT-1989
PRIOR APPLICATION NUMBER: US 367,486
FILING DATE: 14-JUN-1989
PRIOR APPLICATION NUMBER: US 356,672
FILING DATE: 1-APR-1989
PRIOR APPLICATION NUMBER: US 208,997
FILING DATE: 11-APR-1988
APPLICATION NUMBER: US 208,997
FILING DATE: 11-APR-1988
ATTOMENTAL AGENT INFORMATION:
ANDER APPLICATION NUMBER: US 208,997
FILING DATE: 17-DANATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0093.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        920 TITGCCTTTTATCCC 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TIGGCMITICACCCC 15
                                           312-856-7180
                                                                       TELEFAX: 312-856-4972
INFORMATION FOR SEQ ID NO;
SEQUENCE CHARACTERISTICS:
IENGTH: 15 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS; single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Sholtz, Charles K. REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                       linear
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CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                    ; TOPOLOGY: li
; MOLECULE TYPE:
PCT-US92-06821A-131
                                              TELEPHONE:
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FCT-US92-06821A-131

Sequence 131, Application PC/TUS9206821A

GENERAL INFORMATION:

APPLICANT: Nietupski, Raymond M.

APPLICANT: Liu, Jing

TITLE OF INVENTION: Mycobacterial Nucleic Acids

NUMBER OF SEQUENCES: 133

CORRESPONDENCE ADDRESS:

ADDRESSEE: Anacco Corporation

STREET: 200 East Randolph Drive, P.O. Box 87703

CITY: Chicago

STREET: 111inois

COUNTRY: U.S.A.

ZIP: 60680

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/WS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: BCT/US92/06621A

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/744,282

FILING DATE: 13-40G-1991

ATTORNEY/AGENT INFORMATION:

NAME: GALloway, Norval B.

REFERENCE/DOCKET NUMBER: CN 5851

FELECOMMUNICATION INFORMATION:

NEGRETRALEY NUMBER: CN 5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
13.4%; Score 9.8; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 1.7e+02;
Matches 11; Conservative 1; Mismatches 3; Indels
ADDRESSEE: Amoco Corporation
STREET: 200 East Randolph Drive, P.O. Box 87703
CITY: Clocago
STRATE: 111inois
COUNTRY: 111inois
COUNTRY: U.S.A.
ZIP: 60662
COMPUTER: READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: BEADABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: BEADABLE FORM:
COMPUTER: BEADABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: BEADABLE FORM:
COMPUTER: BEADABLE FORM:
APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06621A
APPLICATION NUMBER: US 07/744,282
FILING DATE: 13-AGG-1991
ATORNEY/AGENT INFORMATION:
APPLICATION NUMBER: GN 5851
ATORNEY/AGENT INFORMATION:
NAME: GALLOWAY: NORVAL B.
REGISTRATION NUMBER: 33,595
REFERENCE CHARACTERISTICS:
TELEPHONE: 312-856-7180
TELEPAONE: 312-856-7180
TELEPAONE: SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
COUNTY: 15 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    920 ITIGCCTTTTATCCC 934
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PCT-US92-06821A-129
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Gaps
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; Sequence 55, Application US/07876941A
; Patent No. 5883768
; GENERAL INFORMATION:
    APPLICANT: Bradley, Daniel W.
    APPLICANT: Tam, Albert W.
    APPLICANT: Antibodies
    NUMBER: OF INVENTION: Antibodies
    NUMBER: Dealinger & Associates
    STREET: 350 Cambridge Avenue, Suite 250
    CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                           Score 9.4; DB 1; Length 11;
Pred. No. 1.4e+02;
                                                         AUTHORS: Stahl, D.A., Urbance, J.W..
TITLE: The division between fast.
TITLE: and slow-growing species corresponds to natural
TITLE: relationships among the mycobacteria
JOURNAL: Journal of Bacteriology
VOLUME: 167
PAGES: 570-574
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDLING TYPE: FIOPPY disk
COMPUTER: READABLE FORM:
MEDLING TYPE: FIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM:
PC-DOS/MS-DOS
SOFTWARE: Patentin RC-Bos/MS-DOS
SOFTWARE: Patentin RC-Bos/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/876,941A
FILING DATE: U1-MAY-1992
PLION APPLICATION NUMBER: US/07/876,941A
FILING DATE: 17-JAN-1992
PRIOR APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
PRIOR APPLICATION NUMBER: US 36,7486
FILING DATE: 13-OCTOBER-1989
PRIOR APPLICATION NUMBER: US 36,7486
FILING DATE: 16-JUNE-1989
PRIOR APPLICATION NUMBER: US 36,7486
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION NUMBER: US 208,997
FILING DATE: 11-APRIL-1988
APPLICATION NUMBER: US 208,997
FILING DATE: 11-APRIL-1988
APPLICATION NUMBER: US 208,997
FILING DATE: NUMBER: US 208,997
                                                                                                                                                                                                                                             ) DATE: 1986 ... 

) RELEVANT RESIDUES IN SEQ ID NO: 307 :FROM 1 TO 11 US-08-173-489C-307
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4600-0093.33
ORGANISM: Corynebacterium renale PUBLICATION INFORMATION: AUTHORS: Stahl, D A, Urbance, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 460
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                              12.9%;
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Best Local Similarity 90.9
Matches 10; Conservative
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US-07-876-941A-55
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DESCRIPTION: 16s rRNA gene from Corynebacterium
DESCRIPTION: renale (Accession # M29553) nucleotides 997 to
DESCRIPTION: 1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 307, Application US/08173489C
Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG C. G.
APPLICANT: HEPBURN, A. G.
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
I: 510 EAST 73RD STREET,
NEW YORK
NEW YORK
                                                                                                                                                                                                                       TOPOLOGY: unknown
NOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: DNA sequence, Fig. 7
US-08-259-148A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: TBM FC/XT/AT
COMBUTER: TBM FC/XT/AT
CORRETING SYSTEM: Wo-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION NUMBER: US/08,436
FILING DATE: 29 OCT 1992
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: HAndelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: U9518-6
TELEPHONE: (attorney) (212,706,056)
TELEPHONE: (attorney) (212,706,056)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (atterney) (212) 708-1880
TELEFAX: (atterney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 307:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     double stranded
                            TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 39
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
            (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 90.9
Matches 10; Conservative
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US-08-173-489C-307
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STREET: 51
            TELEPHONE:
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FEATURE:
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Sequence 2, Application US/09593323

Patent No. 6265213

GENERAL INFORMATION:
APPLICANT: Severini, Alberto
TITLE OF INVENTION: Compositions and Methods for Determining the Activity
TITLE OF INVENTION: Of DNA-Binding Proteins and of Initiation of
TITLE OF INVENTION: Transcription
FILE REFERENCE: DNAB-02221
CURRENT APPLICATION NUMBER: US/09/593,323
CURRENT APPLICATION NUMBER: 09/344,300
FRIOR APPLICATION NUMBER: 09/344,300
FRIOR FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 72

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2
LENGTH: 11
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US-09-593-323-3/C
US-09-593-323-3/C
US-09-593-323-3/C
Sequence 3, Application US/09593323
Patent No. 6265213
GENERAL INPORMATION:
APPLICANT: Morgan, Antony-R.
TITLE OF INVENTION: Compositions and Methods for Determining the Activity
TITLE OF INVENTION: Of DNA-Binding Proteins and of Initiation of
TITLE OF INVENTION: Transcription
FILE REFERENCE: DNAB-02921
CURRENT APPLICATION NUMBER: US/09/593,323
CURRENT FILING DATE: 2000-06-13
FRIOR PRICATION NUMBER: 09/344,300
PRIOR FILING DATE: 1999-06-24
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-593-323-2
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                                                                                                                                                                                                                                                                                                                                                                                        Length 11
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
12.9%; Score 9.4; DB 1; Length 11
Best Local Similarity 90.9%; Pred. No. 1.4e+02;
Matches 10; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                             ORIGINAL SOURCE: INDIVIDUAL ISOLATE: DNA sequence, Fig. 7
(415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
                     TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 55
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          915 TGGTCTTTGCC 925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             924 CCTTTTATCCC 934
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                                                                                                                                                                           TOPOLOGY: unknown
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                        ANTI-SENSE: NO
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 202
US-09-593-323-2/c
                                                                                                                                                                                                                                                                                                                                    US-07-876-941A-55
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USSOURCE 3, Application US/09594108

Patent No. 6284468

FAENERAL INFORMATION:

APPLICANT: Morgan, Antony R.

APPLICANT: Severini, Alberto

TITLE OF INVENTION: Of DNA-Binding Proteins and of Initiation of

TITLE OF INVENTION: Of DNA-Binding Proteins and of Initiation of

TITLE OF INVENTION: Of DNA-Binding Proteins and of Initiation of

TITLE OF INVENTION: Of DNA-Binding Proteins and of Initiation of

TITLE OF INVENTION: UNRER: US/09/594,108

CURRENT FILING DATE: 2000-06-13

FRIOR APPLICATION NUMBER: US/09/344,300

PRIOR FILING DATE: 1999-06-24

NUMBER OF SEQ ID NOS: 72

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3

LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-594-108-2/c

| Sequence 2, Application US/09594108 |
| Pattent No. 62844108 |
| Pattent No. 62844108 |
| GENERAL INFORMATION |
| APPLICANT: Morgan, Antony R. |
| APPLICANT: Morgan, Antony R. |
| TILLE OF INVENTION: Compositions and Methods for Determining the Activity |
| TITLE OF INVENTION: Transcription |
| TITLE OF INVENTION: Transcription |
| TITLE OF INVENTION: Transcription |
| TITLE OF INVENTION: OF DNA-Binding Proteins and of Initiation of |
| TITLE OF INVENTION: Transcription |
| FILE REFERENCE: DNAB-029-21 |
| CURRENT APPLICATION NUMBER: US/09/594,108 |
| PRIOR APPLICATION NUMBER: 09/344,300 |
| PRIOR APPLICATION NUMBER: 09/344,300 |
| PRIOR FILING DATE: 1999-06-24 |
| NUMBER OF SEQ ID NOS: 72 |
| SEQ ID NO 2 |
| IBENGTH: 11 |
| ILENGTH: 11 |
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                                                                                                                                                                                 FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-593-323-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-594-108-2
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                                                                                                                                                                                                                                                                                                               Length 11;
                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                      Query Match 12.9%; Score 9.4; DB 1;
Best Local Similarity 90.9%; Pred. No. 1.4e+02;
Matches 10; Conservative 0; Mismatches 1
                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 11
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12.9%; Score 9.4; DB 1; 90.9%; Pred. No. 1.4e+02;
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                                                                                                                                    US-09-249-155A-59
Sequence 59, Application US/09249155A
Patent No. 6538173
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90.9%;
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Best Local Similarity 90.5
Best Local Similarity 90.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 90.5
Matches 10; Conservative
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      924 CCTTTTATCCC 934
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                                                   11 ccrrrrrrrcc 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-249-155A-279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 59
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Sequence 2, Application US/09344300B

Patent No. 6297013

GENERAL INFORMATION:

APPLICANT: Morgan, Antony R.

APPLICANT: Morgan, Antony R.

APPLICANT: Morgan, Alberto

TITLE OF INVENTION: Compositions and Methods for Determining the Activity

TITLE OF INVENTION: Transcription

FILE REFERENCE: DNAB-02921

CURRENT APPLICATION UNMERR: US/09/344,300B

CURRENT APPLICATION UNMERR: US/09/344,300B

CURRENT PILING DATE: 1999-06-24

NUMBER OF SEQ ID NOS: 72

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2

LENGTH: 11
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Sequence 3, Application US/09344300B

Patent No. 6297013

GENERAL INFORMATION:

APPLICANT: Morgan, Antony R.

APPLICANT: Morgan, Alberto

TITLE OF INVENTION: Compositions and Methods for Determining the Activity

TITLE OF INVENTION: Tomposition

TITLE OF INVENTION: Transcription

FILE REPERENCE: DNAB-0221

CURRENT APPLICATION UNMERR: US/09/344,300B

CURRENT FILING DATE: 1999-06-24

NUMBER OF SEQ ID NOS: 72

SEQ ID NOS: 72

LENGTH: 11
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                                                                                                                                                                  Gaps
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-594-108-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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                                                                                                                      12.9%; Score 9.4; DB 1; Length 11; 90.9%; Pred. No. 1.4e+02; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.9%; Score 9.4; DB 1; Length 11; 90.9%; Pred. No. 1.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                        Query Match
Best Local Similarity 90.9
Matches 10; Conservative
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Best Local Similarity 90.9
Matches 10; Conservative
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US-09-344-300-3/c
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US-09-344-300-2/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 11;
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| Sequence 279, Application US/09249155A |
| Patent No. 6538173 |
| GENERAL INFORMATION: |
| APPLICANT: HOBEL'RALZ, Ellen |
| TITLE OF INVENTION: Compositions and Methods for Wound |
| TITLE OF INVENTION: Healing |
| FILE REFERENCE: 00486, 78503 |
| CURRENT APPLICATION NUMBER: US/09/249,155A |
| CURRENT APPLICATION NUMBER: US 60/074,737 |
| PRIOR PRILING DATE: 1998-02-13 |
| PRIOR PLICATION NUMBER: US 60/097,937 |
| PRIOR PLICATION NUMBER: US 60/097,937 |
| PRIOR FILING DATE: 1998-09-28 |
| NUMBER OF SEQ ID NOS: 346 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEMINAL 11
FERENCE, NO. 02281/3.

GENERAL INFORMATION:
APPLICANT: Heber-Katz, Ellen
TITLE OF INVENTION: Compositions and Methods for Wound
TITLE OF INVENTION: Healing
TITLE OF INVENTION: Healing
FILE REFERENCE: 00486.78503
CURRENT FELING NUMBER: US/09/249,155A
CURRENT FILING DATE: 1999-02-13
FRIOR APPLICATION NUMBER: US 60/074,737
FRIOR FILING DATE: 1999-08-13
FRIOR FILING DATE: 1999-08-13
FRIOR FILING DATE: 1999-08-28
FRIOR FILING DATE: 1998-09-28
NUMBER OF SEQ IO D NOS: 346
SOUTHWARE FEATURE OF Windows Version 4.0
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TOPOLOGY: linear MOLECULE TYPE: other mucleic acid BESCRIPTION: third strand derived from superoxide BESCRIPTION: third strand derived from superoxide BESCRIPTION: third strand derived from superoxide HYPOTHETICAL: yes
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APPLICANT: Yagi, Sanjay
APPLICANT: Yagi, Sanjay
APPLICANT: Kramer, Fred R.
APPLICANT: Kramer, Fred R.
APPLICANT: Lizardi, DerecTably Labeled DUAL CONFORMATION
TITLE OF INVENTION: DETECTABLY LABELED DUAL CONFORMATION
TITLE OF INVENTION: OLIGONUCLEOTIDE PROBES, ASSAYS AND KITS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 45 Rockefeller Pl., Suite 2800
CITY: New York
STATE: N.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 9.4; DB 1; Length 14; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENBE: NO
PUBLICATION INFORMATION: 98 :FROM 1 TO 14
RELEVANT RESIDUES IN SEQ ID NO: 98 :FROM 1 TO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                          SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
RRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INPORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: US 07/9686
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 bases
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ZIP: 10111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Ver/
CURRENT APPLICATION DATA:
APPLICATION TOWNER: US/08/439,819
THING DATE: 12-MAY-1995
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 12-MAY-1995
CLASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/08439819
Patent No: 5925517
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
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US-08-439-819-9
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US-09-874-601-88
; Sequence 88, Application US/09874601
; Patent No. 6632057
; GENERAL INFORMATION;
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: CHANY, MARIA B.
; TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES
; TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES
; FILE REFERENCE: 4300.014100
; TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES
; FILE REFERENCE: 1900.014100
; CURRENT APPLICATION NUMBER: US/09/874,601
; CURRENT APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR FILING DATE: 1997-06-09
; PRIOR FILING DATE: 1997-04-21
; PRIOR FILING DATE: 1997-04-21
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOUPWARE: PATENTIN VERSION 3.0
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                                                                                                                            Score 9.4; DB 1; Length 12;
Pred. No. 1.6e+02;
0; Mismatches 1; Indels
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US-08-173-489C-98
US-08-173-489C-98
Sequence 98, Application US/08173489C
Patent No. 58-61244
GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANT: HERBURN, A. G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
                                                    216 : FROM 1 TO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROFILE DIAGNOSTIC SCIENCES, INC.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: ()...()
OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
     ; ANTI-SENSE: no
PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-173-489C-216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  510 EAST 73RD STREET
                                                                                                                                 Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
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Matches 4; Conserv
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NEW YORK
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STREET: 51
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                                                      Score 9.4; DB 1; Length 14; Pred. No. 1.8e+02; 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                              Sequence 147, Application US/08765340

Patent No. 6150092

GENERAL INFORMATION:

APPLICANT: UCHIDA, K.,

APPLICANT: TANAKA, Y.,

APPLICANT: KONDO, S.

TITLE OF INVENTION: AN ANTISENSE NUCLEIC ACID

TITLE OF INVENTION: COMPOUND

NUMBER OF SEQUENCES: 185

ADDRESSER: ANDRESS:

ADDRESSER: ANGRAN & FINNEGAN, L.L.P.

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

STATE: NEW YORK

STATE: NEW YORK

STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy albak
COMPUTER: IBM PC compatible
OPEARING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,340
FILING DATE: 23-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 145146/94
FILING DATE: 27-UUN-1994
PRIOR APPLICATION NUMBER: UP 311130/94
PRIOR APPLICATION NUMBER: UP 311130/94
PRIOR APPLICATION NUMBER: JP 31130/94
PRIOR APPLICATION NUMBER: JF 31130/94
PRIOR APPLICATION NUMBER: JF 35,353
REFERENCE/DOCKET NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 35,353
TELEPRAY: (212) 758-4800
TELEPRAX: (212) 758-4809
TELEPRAX: (214) 758-4809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
                                                         12.9%;
                                                         Query Match 12.9
Best Local Similarity 90.9
Matches 10; Conservative
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Best Local Similarity 90.9
Matches 10, Conservative
                                                                                                                                                                 910 TTCTTTGGTCT 920
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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US-08-765-340-147
     US-08-838-545-50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Shay, Jerry W.
APPLICANT: Widght, Woodring E.
APPLICANT: Wiright, Modeling E.
APPLICANT: Piatyszek, Miezyslaw A.
APPLICANT: Corey, David R.
APPLICANT: Corey, David R.
APPLICANT: No. 6046307ton, James C.
TITLE OF INVENTION: Modulation of Mammalian Telomerase by
TITLE OF INVENTION: Peptide Nucleic Acids
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                   Score 9.4; DB 1; Length 14;
Pred. No. 1.8e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPREX: USA3

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
CLASSIFICATION NUMBER: US 08/630,019
FILING DATE: 09-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REFERENCE/DOCKET NUMBER: 015389-001610US
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
REGISTRATION NUMBER: 26,739
FREFERENCE/DOCKET NUMBER: 07763/027001
TELECOMMUNICATION INFORMATION:
TELEFHONE: 212-765-5070
TELEFAX: 212-259-2291
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 bases
                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: DNA (oligonucleotide) US-08-439-819-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 215
US-08-838-545-50/c
; Sequence 50, Application US/08838545
; Parent No. 6046307
                                                                                                                                                                                                                                                                                                                                                                                      12.9%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                              Query Match 12.9
Best Local Similarity 90.9
Matches 10, Conservative
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                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
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908 TTTTCTTTGGTCTT 921
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 bases
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PUBLICATION INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: NEW STATE: NEW COUNTRY: US
                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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where (deoxy/ribose-phosphate linkages are replaced by
N-(2-aminoethyl)glycine units linked to nucleotide bases via
glycine amino N through a methylenecarbonyl linker"
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       Sequence 50, Application US/09349532;
Patent No. 6294660;
GENERAL INFORMATION:
APPLICANT: Wright, Woodring E.
APPLICANT: Piatyszek, Mieczyslaw A.
APPLICANT: Orey, David R.;
APPLICANT: No. 6294650ton, James C.
TITLE OF INVENTION: Modulation of Mammalian Telomerase by TITLE OF INVENTION: Peptide Nucleic Acids
NUMBER OF SEQUENCES:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 9.4; DB 1; Length 14; Pred. No. 1.8e+02;
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Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANT: HERBURN, A. G.
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/349,532
                                                                                                                                                                                                                                                                              ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRICR APPLICATION NUMBER: US 08/838,545
APPLICATION NUMBER: US 08/838,545
FILING DATE: 09-APR-1997
APPLICATION NUMBER: US 08/630,019
FILING DATE: 09-APR-1996
ATTORNEY/AGENT INFORWATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-0016
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 576-0200 TELEPAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 50: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 12.9
Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 TTTTTGGTCT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: lin
MOLECTLE TYPE:
DESCRIPTION:
DESCRIPTION:
DESCRIPTION:
DESCRIPTION:
US-09-349-532-50/c
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US-08-173-489C-78
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MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from
DESCRIPTION: retinoblastoma sequence region in Seq ID No. 586124477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.6%; Score 9.2; DB 1; Length 14; 78.6%; Pred. No. 2e+02; tive 0; Mismatches 3; Indels
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Sequence 97, Application US/08173489C

Sequence 97, Application US/08173489C

Sequence 97, Application US/08173489C

Sequence 97, Application

APPLICANT: WANG, C. -G.

APPLICANT: WANG, C. -G.

APPLICANT: WANG, C. -G.

APPLICANT: WEBURN, A. G.

APPLICANT: WEBURN, A. G.

TITLE OF INVENTION: TRIPLE-STRAND FORMATION.

TITLE OF SEQUENCES: 365

CORRESPONDENCES: 365

CORRESPONDENCE ADDRESS: ADDRESSE: PROFILE DIAGNOSTIC SCIENCES, INC., STREET, CITY: NEW YORK

STREET: SIO EAST 73RD STREET, CITY: NEW YORK

STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RELEVANT RESIDUES IN SEQ ID NO: 78 :FROM 1 TO 14 US-08-173-489C-78
PROFILE DIAGNOSTIC SCIENCES, INC.,
                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: 1BM FC/XT/AT
CORRATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURREMY APPLICATION DATA:
APPLICATION UNCHER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION NUMBER: US/08/173,489C
FILING DATE: 29 DEC 1993
CLASSIFICATION NUMBER: US/08/436
FILING DATE: 29 OCT 1992
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, JOSeph H.
REGISTRATICN NUMBER: 26,179
REFERENCE/DOCKET NUMBER: U9518-6
TELECOMMUNICATION INFORMATION:
TELEFHONE: (ALLCINEY) (212,70,001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: 3.5 inch, 1.44Mb storage COMPUTER: IBM PC/XT/AT OPERATING SYSTEM: MS-DOS version 6.2 SOFTWARE: Wordperfect Version 5.1 CURREMY APPLICATION DATA: APPLICATION NUMBER: US/08/173,489C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y) (212) 708-1880
(212) 246-8959
O: 78:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: Nucleic Acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
                      : 510 EAST 73RD STREET
NEW YORK
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APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: 05,179
REFERENCE/DOCKET NUMBER: 06,179
REFERENCE/DOCKET NUMBER: 06,179
RELEPHONE: (attorney) (212) 708-1880
TELEPHONE: (attorney) (212) 708-1880
TELEPHONE: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 318:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 bases
TYPE: nucleic acid
STRANDEDNESS: single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 931 TCCCTCCTCTTCAT 944
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ORGANISM: Homo sapiens
FEATURE:
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FILING DATE: 22 DEC 1993
CCASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: 26,179
REFERENCE/DOCKET NUMBER: 26,179
REFERENCE/DOCKET NUMBER: 09518-6
TELECOMMUNICATION NUMBER: 097: 246-8959
INFORMATION FOR SEQ IN 00: 97: 246-8959
INFORMATION FOR SEQ IN 00: 97: 246-8959
INFORMATION FOR SEQ IN 00: 97: 246-8959
INFORMATION: prealbumin gene exons 1 and 2
DESCRIPTION: prealbumin gene exo
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Patent No. 5861244

GENERAL INFORMATION:

APPLICANT: HEPBURN, A. G.

TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
TITLE OF INVENTION: TRIPLE-STRAND FORMATION:

NUMBER OF SEQUENCES: 365

CORRESPONDENCE ADDRESS:

ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
CITY: NEW YORK

COUNTRY: USA
STATE: NEW YORK

COMPUTER READABLE FORM:

MEDIJM TYPE: 3.5 inch, 1.44Mb storage

COMPUTER: IBM PC/XT/AT

COMPUTER: SYSTEM: MS-DOS Version 6.2

SOFTWARE: WORDGEFECT VERSION 5.1

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE: Structure and expression of TITLE: the mutant prealbumin gene associated with TITLE: Eautial amyloidotic polyneuropathy JOURNAL: Molecular Biological Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VOLUME: 3
PACES: 329-338
DATE: 1986
RELEVANT RESIDUES IN SEQ ID NO: 97 :FROM 1 TO 14
US-08-173-489C-97
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Best Local Similarity 78.6%
Matches 11; Conservative
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ö Sequence 2, Application US/09458481B
Sequence 2, Application US/09458481B
Setent No. 631048
GENERAL INFORMATION:
APPLICANT: KUMAR, Vijaya B.
TITLE OF INVENTION: ANTISENSE MODULATION OF AMYLOID BETA PROTEIN EXPRESSION
TITLE OF INVENTION: AND SETENSE OF SEQUENCE TO CURRENT APPLICATION NUMBER: US/09/458,481B
CURRENT FILING DATE: 1999-12-09
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2
LENGTH: 14 Gaps ; OTHER INFORMATION: Description of Artificial Sequence: Antisense; OTHER INFORMATION: Oligonucleotide US-09-458-481B-2 ö ; 0 MOLECULE TYPE: other nucleic acid DESCRIPTION: third strand derived from H. DESCRIPTION: influenzae 16s region in Seq ID No. 5861244317 Query Match
12.6%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 2e+02;
Matches 11; Conservative 0; Mismatches 3; Indels Query Match
12.6%; Score 9.2; DB 1; Length 14;
Best Local Similarity 78.6%; Pred. No. 2e+02;
Matches 11; Conservative 0; Mismatches 3; Indels HYPOTHETICAL: yes

ANTI-SENSE: no

PUBLICATION INFORMATION:

RELEVANT RESIDUES IN SEQ ID NO: 318 :FROM 1 TO 14
US-08-173-489C-318 US-08-535-249-118
; Sequence 118, Application US/08535249
; Patent No. 6455899; GENERAL INFORMATION;
GAPPLICANT: Schlingensiepen, Georg-Ferdinand

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                                        FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target
OTHER INFORMATION: sequences
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Pred. No. 2e+02;
0; Mismatches 3; Indels
                                                                                                                                        Score 9.2; DB 1; Length 14;
Pred. No. 2e+02;
                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: TRESCO, Jacques R.
APPLICANT: FRESCO, Jacques R.
TITLE OP INVENTION: TRIPLEX IN-SITU HYBRIDIZATION
FILE REPERENCE: 2448-103
CURRENT FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: PCT/US98/23765
PRIOR FILING DATE: 1998-11-10
PRIOR FILING DATE: 1998-11-10
PRIOR FILING DATE: 1997-11-10
NUMBER OF SEQ ID NOS: 77
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO. 48
LENGTH: 14
                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                           US-09-531-000-48/c; Sequence 48, Application US/09531000 Patent No. 6461810; GENERAL INFORMATION:
    TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                               Query Match
Best Local Similarity 78.6%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 78.6%;
Matches 11; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                920 TITGCCTTTTATCC 933
                                                                                                                                                                                                                                  921 TIGCCTITITATCCC 934
                                                                                                                                                                                                                                                                      14 rrccrrrrrcracc 1
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United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Garden City
STATE: New York
COUNTRY: United St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-388-353-182/c
                                                                                                       US-09-531-000-14
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APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Schlingensiepen, Reimar
APPLICANT: Schlingensiepen, APPLICANT: Schlingensiepen, TITLE OF INVENTION: Antisense-oligonuclectides for the treatment of
TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
TOWBER OF SEQUENCES: 137
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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US-09-511-000-14/c

Sequence 14, Application US/09531000
Patent No. 6461810
GENERAL INFORMATION:
APPLICANT: DANNSON, Marion D.
TITLE OF INVENTION: TRIPLEX IN-SITU HYBRIDIZATION
FILE REFERENCE: 2448-103
CURRENT APPLICATION NUMBER: US/09/531,000
CURRENT PILING DATE: 2000-09-08
PRIOR PLICATION NUMBER: PCT/US98/23765
PRIOR FILING DATE: 1998-11-10
PRIOR FILING DATE: 1998-11-10
PRIOR FILING DATE: 1998-11-10
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRAIT APPLICATION DATA:
APPLICATION NUMBER: US/08/535,249
                                                                                                                                               3: Jacobson, Price, Holman & Stern
400 Seventh St. N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93 107 089.0
FILING DATE: 30-APR-1993
PRIOR APPLICATION UNMBER: EP 93 107 849.7
APPLICATION WUMBER: EP 93 107 849.7
APTICRNEY/AGENT INFORMATION:
NAME: Player, William E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10577/P58418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-6666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (202) 393-5350
TELETS: RCA 248939 IDEA UR
INFORMATION FOR SEQ ID NO: 118:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    945 TGGTTTAATGTATC 958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 78.69
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
                                                                                                                                                               STREET: 400 Seven... CITY: Washington D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGI.
MOLECULE TYPE: D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-535-249-118
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; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-183
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Best Local Similarity 100.0%;
Matches 9; Conservative 0
                single
                                                                                                                                                                                                                                                         933 CCTCCTCTT 941
                STRANDEDNESS:
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US-08-388-35-183/C
Sequence 183, Application US/0838353
Sequence 183, Application US/0838353
Sequence 183, Application US/0838353
Sequence 183, Application US/0838353
Sequence 183, Application, Nicholas J.
APPLICANT: Learmont, Jennifer C.
APPLICANT: Crowe, Suzane
APPLICANT: Crowe, Suzane
APPLICANT: Crowe, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBES OF SEQUENCES: 800
CORRESCE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City Plaza
CITY: Garden City Plaza
COUNTRY: United States
ZIP: 11530
COMPUTER: Elempth Release #1.0, Version #1.25
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PROPAMARE: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIFICATION NUMBER: 31,346
STELEXY: Galdillo, Frank S.
RECISTRATION NUMBER: 31,346
TELEXCOMMUNICATION INPORMATION:
MAME: Didigillo, Frank S.
RECISTRATION NUMBER: 31,346
TELEXCOMMUNICATION INPORMATION:
TELEXERE (16) 742-4343
TTELEXX: 230 901 SANS UR
TELEXIS 200 FARENCE PROPER PROPER PAIRS
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TTPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 12.3%; Score 9; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 1.5e+02; Matches 9; Conservative 0; Mismatches 0; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTAARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
ATTORNEY AGENT INFORMATION:
NAME: Didiglio, Frank S.
REGISTRATION NUMBER: 9606
TELESPHONE: (516) 742-4343
TELEPHONE: (516) 742-4346
TELEFAX: (516) 742-4366
TELEFAX: (516) 742-4366
TELEFAX: (516) 742-4366
TELEFAX: (516) 742-4366
TELEFAX: (516) DOS SANS UR
INFORMATION FOR SEQ ID NO: 182:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  933 CCTCCTCTT 941
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Gaps
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JUS-08-488-551B-182/c

Sequence 182, Application US/08488551B

Sequence 182, Application US/08488551B

Patent No. 6015661

APPLICANT: Nicholas J. Deacon

APPLICANT: David Cooper

IILLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1

NUMBER OF SEQUENCES: 841

CORRESPONDENCE ADDRESS:

ADDRESSE: SCULLY, SCOTT, MURPHY & PRESSER

STREET: 400 GARDEN CITY PLAZA

STREET: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: ORACION CONTRY: U.S.A.

COUNTRY: U.S.A.

ZIP: 11530-0299

COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PACOMPACIBLE
APPLICATION NUMBER: PACOMPACIBLE
CALING DATE: 12-FEB-1995
APPLICATION NUMBER: DASCHING
APPLICATION NUMBER: PACOMPACIBLE
CALING DATE: 17-MAX-1995
ATTORNEY PACOMPACIBLE
CALING DATE: 17-MAX-1995
APPLICATIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          933 CCTCCTCTT 941
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MOLECULE TYPE: DNA
US-08-488-5518-182
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Gaps

0; Indels

Score 9; DB 1; Length 10; Pred. No. 1.5e+02; 0; Mismatches 0; Indels

MOII OCC TO T#:#0:1/ Z00;

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Gaps
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i Sequence 80, Application US/09508753B

patent No. 6544736

GENERAL INFORMATION:
APPLICANT: Akira SHIRAMOTO
APPLICANT: Yuko SHIRAM
APPLICANT: Yuko FUNUICHI
APPLICANT: Hiroko FUNAKI
APPLICANT: Masanori WATAHIKI
TITLE OF INVENTION: Method for Synthesizing cDNA from mENA sample
FILE REPERENCE: 0016-62/HG
CURRENT APPLICATION NUMBER: US/09/508,753B
CURRENT FILING DATE: 2000-06-16
PRIOR FILING DATE: 1997-09-18
NUMBER OF SEQ ID NOS: 472
SEQ ID NO 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 60, Application US/09508753B
Fatent No. 6544736
FARENTEL INFORMATION
APPLICANT: Akira SHIMAMOTO
APPLICANT: Yasuhiro FURUICHI
APPLICANT: Wick SHIBATA
APPLICANT: Hiroko FUNAKI
APPLICANT: Masanori WATAHIKI
APPLICANT: Masanori WATAHIKI
APPLICANT: Hiroko FUNAKI
APPLICANT: Masanori WATAHIKI
APPLICANT: Horoko FUNAKI
APPLICANT: HORARA
APPLICANT: HORARA
APPLICANT:
ANDRER: 1910-06-16
CURRENT APPLICATION NUMBER: UP 9/270324
FRIOR FILING DATE: 1997-09-18
NUMBER: OF SEQ ID NOS: 472
BENCH APPLICANT: NOS: 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: Primer US-09-508-753B-60
                                                                                                                                                                                                                                                                                                                                                       Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.3%; Score 9; DB 1; Length 10; 100.0%; Pred. No. 1.5e+02; tive 0; Mismatches 0; Indels
                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
FRATURE:
OTHER INFORMATION: Majority consequences sequence.
US-09-445-388A-5
                                                                                                                                                                                                                                                                                                                                                    Query Match
12.3%; Score 9; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 0;
NUMBER OF SEQ ID NOS: 11
SOFWARE: Patentin version 3.1
SEQ ID NO 5
LENCTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  939 CTTCATTGG 947
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US-09-445-38A-5/c
is equence 5, Application US/09445388A
Patent No. 6534259
GENERAL INFORMATION:
TITLE OF INVENTION: PALE ON Andrew J.
FILE REFERENCE: ABPLICATION NUMBER: US/09/445,388A
CURRENT PAPLICATION NUMBER: US/09/445,388A
CURRENT FILING DATE: 2000-03-23
PRIOR FILING DATE: 1998-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONDITY: 0.5.A.

CONDITY: 0.5.A.

CIP: 11530-0239

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-JUN 1995
PRIOR APPLICATION DATA: PM364 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM024 (AU)
FILING DATE: 12-FEB-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PM321/95
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: PM321/95
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: 9606Z
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: 9606Z
TELEPHONE: G160 742-4366
INPORMATION FOR SEQ ID NO: 183:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
                                                                                             Sequence 183, Application US/08488551B
Patent No. 6015661
GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhee
APPLICANT: Dale A. McPhee
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESSE:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
                                                                                                                                                                                                                                                                                               JALESSEE: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 GARDEN CITY PLAZA CITY: GARDEN CITY STATE: NEW YORK COUNTRY: II COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.3%; Score 9; DB 1
100.0%; Pred. No. 1.5
tive 0; Mismatches
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12.3
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 933 CCTCCTCTT 941
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                                                                              -08-488-551B-183/c
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: storage
COMPUTER: BKOTAGE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PATFACTS: 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/0245,466
FILING DATE: MAY 18, 1994
APPLICATION NUMBER: 08/245,466
FILING DATE: MAY 18, 1994
                  APPLICATION NUMBER: US/07/854,596B
FILING DATE: 03-JUN-1992
CLASSIFCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McDonnell, John J
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,337
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION ON: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 925 CTTTTATCC 933
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US-09-508-753B-143

is Sequence 143, Application US/0950B753B

is Sequence 143, Application US/0950B753B

is GENERL INFORMATION:
is APPLICANT: Attra SHIMAMOTO
is APPLICANT: Yake SHIBATA
is APPLICANT: Histor CHARA
is APPLICANT: Histor CHARA
is APPLICANT: Histor CHARA
is APPLICANT: Histor CHARA
is APPLICANT: Massnori WATAHIKI
is APPLICANT: Massnori WATAHIKI
is APPLICANT: Massnori WATAHIKI
is APPLICANT: NUMBER: US/09/50B, 753B
is TILE OF INVENTION: Whethod for Synthesizing CDNA from mRNA sample
is TILE REFERENCE: 00162/HG
is TILE OF INVENTION: NUMBER: US/09/50B, 753B
is PRIOR FILING DATE: 1997-09-18
is SEQ ID NO 143
is SEQ ID NO 143
is LENTH: 10
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; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-7538-143
                                                                           FEATURE:
, OTHER INFORMATION: Description of Artificial Sequence: Primer US-09-508-753B-80
                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 0; Mismatches 0; Indels
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Sequence 6, Application US/07854596B

Patent No. 5434073

Patent No. 5434073

Patent No. 5434073

APPLICANT: Dawson, Keith M
APPLICANT: Dawson, Keith M
APPLICANT: Caplewski, Lloyd G

TITLE OF INVENTION: Proteins and nucleic acids

NUMBER OF SEQUENCES: 73

CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. John J. McDonnell

STREET: Ten South Wacker Drive, Suite 3000

CITY: Chicago

STATE: IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 60606
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IB Floppy disk
COMPUTER: PROPERTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
LENGTH: 10
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                             911 TCTTTGGTC 919
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ö NAMENTY KEY: misc\_feature | IOCATION: 1..11 | OTHER INFORMATION: /note= "bottom strand of adapter to | OTHER INFORMATION: fuse c-terminal end of the a-factor pro-peptide to | OTHER INFORMATION: synthetic hirudin gene" | US-07-854-596B-6 ö Query Match 12.3%; Score 9; DB 1; Length 11; Best Local Similarity 100.0%; Pred. No. 1.7e+02; Matches 9; Conservative 0; Mismatches 0; Indels RESULT 234
US-08-373-124A-46/C

Sequence 46, Application US/08373124A

Patent No. 5646042

GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Dayls, Thale
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: STILE 4700

STREET: STILE 4700

STREET: California

COUNTRY: US-A.

0; Gaps

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DB 1, Length 11;
0. 1.7e+02;
ches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SITE: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 07/982,759
FILING DATE: 08-MAR.1993
PRICH APPLICATION NUMBER: GB 9127319.3
FILING DATE: 14-0CT.1991
FILING DATE: 14-0CT.1992
APPLICATION NUMBER: GB 9221587.0
FILING DATE: 14-0CT.1992
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 102.378.120DV-2
TELEPROME: 617-526-6110
TELEPROME: 617-526-610
INFORMATION FOR SEO ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
TITLE OF INVENTION: Stem Cell Inhibiting Proteins
NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE and DORR
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
| LOCATION: 1.11
| COTHER LINFORMATION: /product= "BOTTOM STRAND OF OTHER INFORMATION: OLIGONUCLEOTIDE ADAPTOR"
| US-08-450-9058-33
                                                                                                                                                                                                                                                                                                                                      Query Match 12.3%; Score 9; DB :
Best Local Similarity 100.0%; Pred. No. 1.7
Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S-08-450-905B-33
Sequence 33, Application US/08450905B
Patent No. 5856301
GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     906 CATTITCTT 914
                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boston
                                                                                                                                                                                                                                                                                    US-08-435-628-46
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Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 46, Application US/08435628
Fatent No. 5817796
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Brayer, Kenneth
APPLICANT: Jarvis, Thales
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
TITLE OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTES: Dayon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
CITY: Los Angeles
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER: READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: STORME
COMPUTER: NORTH PROMATION
MEDIUM TYPE: 10.5" OR 5.0
SOFTWARE: WORD Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,628
FILING DATE: D-AX-1995
APPLICATION NUMBER: 08/245,466
FILING DATE: MAY 18, 1994
APPLICATION NUMBER: 08/245,466
FILING DATE: MAY 18, 1994
APPLICATION NUMBER: 07/931,132
FILING DATE: PEDRUARY 7, 1994
APPLICATION NUMBER: 07/931,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/931,132
FILING DATE: PEDRUARY 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: PEDRUARY 26, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: PEDRUARY 7, 1992
  APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
TELEPAX: (213) 955-0440
TELEPAX: (213) 955-0460
TELERAX: (213) 955-0460
TELERAX: (213) 955-0460
TELERY: 67-3510
NPORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        906 CATTTTCTT 914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 235
US-08-435-628-46/c
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COUNTRY:
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                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single stranded
STRANDENNESS: single stranded
MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from Hepatitis B
DESCRIPTION: isolate adr sequence region in Seq ID No. 5861244133
                        ;
0
                                                                                                            12.3%; Score 9; DB 1; Length 11; 100.0%; Pred. No. 1.7e+02; trive 0; Mismatches 0; Indels
Query Match 12.3%; Score 9; DB 1; Length 11; Best Local Similarity 100.0%; Pred. No. 1.7e+02; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: no
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 134 :FROM 1 TO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 238
2.08-173-489C-160
3. Sequence 160, Application US/08173489C
5. Patent No. 5861244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 12.3
Best Local Similarity 100.
Matches 9; Conservative
                                        925 CTTTTATCC 933
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2 CTTTTATCC 10
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US-08-173-489C-134
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Patent No. 6682930
GENERAL INFORMATION:
APPLICANT: LU, CHANODE
TITLE OF INVENTION: NEW TRIPLEX FORMING OLIGONUCLEOTIDES AND THEIR USE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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| Sequence 222, Application US/09249155A
| Sequence 222, Application US/09249155A
| Patent No. 6538173
| GENERAL INFORMATION:
| TITLE OF INVENTION: Compositions and Methods for Wound:
| TITLE OF INVENTION: Compositions and Methods for Wound:
| TITLE OF INVENTION: Compositions and Methods for Wound:
| TITLE OF INVENTION: Compositions and Methods for Wound:
| TITLE OF INVENTION: Compositions and Methods for Wound:
| TITLE OF INVENTION: 1996-09-12
| FILE REPERENCE: 1996-02-12
| PRIOR FILING DATE: 1996-02-13
| PRIOR FILING DATE: 1996-09-28
| PRIOR FILING DATE: 1996-09-28
| PRIOR FILING DATE: 1996-09-28
| WINDER OF SEQ IN NOS: 346
| SEQ ID NOS: 2346
| SEQ ID NO 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.3%; Score 9; DB 1; Length 11; 100.0%; Pred. No. 1.7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 1..1
OTHER INFORMATION: /product= "BOTTOM STEAND OF
OTHER INFORMATION: OLIGONUCLEOTIDE ADAPTOR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 12.3%; Score 9; DB 1
Best Local Similarity 100.0%; Pred. No. 1.7
Matches 9; Conservative 0; Mismatches
                                                                                                                           102378.120
GB 9221587.0
                  FILING DATE: 14-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, HOLLIE L.
REGISTRATION NUMBER: 31,321
REFERENCE/OCCET VUMBER: 1023
TELEPHONE: 617-526-600
INFORMATION FOR SEQ ID NO: 35EQUENCE CHARACTERISTICS: LENGHAL SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGHH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
Lag 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  910 TICTITGGT 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         925 CTTTTATCC 933
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-249-155A-222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-07-982-759F-33
                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: third strand derived from Hepatitis B DESCRIPTION: third strand derived from Hepatitis B DESCRIPTION: isolate adw2 sequence region in Seq ID No. 5861244195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 12.3%; Score 9; DB 1; Length 11; Best Local Similarity 100.0%; Pred. No. 1.7e+02; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: CRAIG, Stewart
APPLICANT: GRONGE, Michael
APPLICANT: EDWARDS, Richard Mark
APPLICANT: CZAPLEWSKI, Lloyd George
APPLICANT: CZAPLEWSKI, Lloyd George
APPLICANT: GIBERY: Richard
TITLE OF INVENTION: Stem Cell Inhibiting Proteins
NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE and DORR LLP
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , RELEVANT RESIDUES IN SEQ ID NO: 196 :FROM 1 TO 11 US-08-173-489C-196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                  COMPUTER: 18M PC/XT/AT
COMPUTER: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/05/968,436
FILING DATE: 29 OCT 1992
ATPONEY/AGENT INFORMATION:
NAME: HANGEIMEN, JOSEPH H.
REGISTRATION NUMBER: 26,179
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 196:
ENDTH: 11 Dases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/07/982,759F
FILING DATE: 08-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9127319.3
FILING DATE: 23-DEC-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 33, Application US/07982759F Patent No. 6057123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
EDNESS: single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: no PUBLICATION:
  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    932 CCCTCCTCT 940
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STREET: 60
CITY: Boston
STATE: MA
TP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic
STRANDEDNESS:
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US-09-231-303-88

US-09-231-303-88

Sequence 88 Application US/09231303

Patent No. 6395478

GENERAL INFORMATION:
APPLICANT: Nandabalan, Krishnan
APPLICANT: Nandabalan, Krishnan
TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-
TITLE OF INVENTION: IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS
TITLE OF INVENTION: IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS
TITLE OF INVENTION: UMBER: US/09/231,303
CURRENT APPLICATION NUMBER: US/09/231,303
CURRENT APPLICATION NUMBER: 08/663,824
EARLIER PILING DATE: 1996-06-14
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 88
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 244
US-08-663-824-88

i Squence 88, Application US/08663824

i Sequence 88, Application US/08663824

i Saturner 89, Application US/08663824

i SATURNER INFORMATION:

APPLICANT: Nandabalan, Krishnan

APPLICANT: Rothberg, Jonathan

ITILE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN

ITILE OF INVENTION: IDENTIFICATION THAT OCCUR IN POPULATIONS

ITILE OF INVENTION: 1108

CURRENT FILING DATE: 1996 06-14

NUMBER OF SEQ ID NOS: 118

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 88

LENGTH: 12

TYPE: DNA

ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: linker US-09-231-303-88
                                                                                                                                                                                                              12.3%; Score 9; DB 1; Length 12; ilarity 100.0%; Pred. No. 1.9e+02; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.3%; Score 9; DB 1; Length 12;
100.0%; Pred. No. 1.9e+02;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100...
Thes 9; Conservative
             ; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-874-825-88
                                                                                                                                                                                                                                                                                                                                               936 CCTCTTCAT 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  936 CCTCTTCAT 944
                                                                                                                                                                                                                                                                                                                                                                                                          3 CCTCTTCAT 11
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Best Local Similarity
Matches 9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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Sequence 88, Application US/08874825

PARENT No. 6057101

GENERAL INFORMATION:

APPLICANT: Nandabalan, Krishnan

APPLICANT: Raibfiled, Jonathan

APPLICANT: Knight, James

APPLICANT: Knight, James

APPLICANT: Knight, James

APPLICANT: Knight, James

APPLICANT: Malbfleisch, The General String 
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CTHER INFORMATION: Description of Artificial Sequence: Triplex

CTHER INFORMATION: forming oligonuclectide

CTHER INFORMATION: This oligo may or may not be 3'-monophosphorylated
US-09-529-812A-6
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FILE OF INVENTION: ANTI-HBV
CURRENT APPLICATION NUMBER: US/09/529,812A
CURRENT FILING DATE: 2000-07-24
FRIOR APPLICATION NUMBER: PCT/CN98/00248
FRIOR FILING DATE: 1998-10-19
FRIOR FILING DATE: 1997-10-21
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
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ZIP: 10036/271
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPACIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/874,825
FILING DATE: 13-UN-1997
CLASSIFICATION NUMBER: 08/663,824
FILING DATE: 14-UN-1996
ATTORNEY/AGBNT INFORMATION:
NAME: MISIOCK, S. DESLIE
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 7934-045
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEX: 66141 PENNIE
INFORMATION FOR SEG ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 DASE PAILS
                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          932 CCCTCCTCT 940
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US-08-410-116B-24
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                                                                                                                                                                                                                                                                                                                                            Sequent No. 555278
Sequent No. 555278
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: DNA Sequencing by Stepwise Ligation and Cleavage NUMBER OF SEQUENCES:
ADDRESSEE: Stephen C. Macevicz
STREET: 21890 Rucker Drive
CITY: Cupertino
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 247
US-08-410-116B-24
Sequence 24, Application US/08410116B
Sequence 24, Application US/08410116B
Patent No. 5599675
GENERAL INFORMATION:
APPLICANT: Sydney Brenner, Glenn Albrecht, Andrew J. Blasband
TITLE OF INVENTION: DNA Sequencing by Stepwise Ligation and Cleavage
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 95014
COMPUTER READABLE FORM:
MEDIUM TUPE: 3.5 inch diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 3.1/DOS 5.0
SOFTWARE: Microsoft Word for Windows, vers. 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/280,441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; L
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Best Local Similarity 100.0%; Pred. No. 2e+
Matches 9; Conservative 0; Mismatches
    Mismatches
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222,300
FILING DATE: 04-APR-94
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 30,285
REFERENCE/DOCKET UNBER: S1
TELECOMMUNICATION:
TELEPHONE: (415) 638-5552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Stephen C. Macevicz
REGISTRATION NUMBER: 30,2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (510)670-9302
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 13 nucleotides
TYPE: nucleic acid
STRANDEDNESS: double
        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 935 TCCTCTTCA 943
                                                                                      936 CCTCTTCAT 944
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                                                                                                                                                                    3 CCTCTTCAT 11
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        9
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                                                                                                                                                                                                                                                                                                                                        US-08-280-441-7
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        Matches
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US-OB-667-689A-24

US-OB-667-689A-24

Sequence 24, Application US/08667689A

Patent No. 574330

GENERAL INFORMATION:

APPLICART: Sydney Brenner, Robert B. DuBridge
TITLE OF INVENTION:

APPLICART: Sydney Brenner, Robert B. DuBridge
TITLE OF INVENTION:

MUMBERS OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics, Inc.

STREE: California

COUNTER: Galifornia

COMPUTER: Galifornia

COMPUTER: BADABLE FORM:

MEDIUM TYPE: 3.5 inch diskette

COMPUTER: BADABLE FORM:

MEDIUM TYPE: 3.5 inch diskette

COMPUTER: 1.5 inch diskette

COMPUTER: 2.5 inch diskette

COMPUTER: APPLICATION NATA:

APPLICATION NUMBER: 08/10,116

FILING DATE: 2.5 inch diskette

FILING DATE: 2.5 inch d
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: 11m compatible
COMPUTER: 11m compatible
COMPUTER: 11m compatible
COMPUTER: 12m compatible
COMPUTER: 12m compatible
COMPUTER: Windows 3.1/DOS 5.0
SOFTWARE: Microsoft Word for Windows, vers. 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,116B
FILING DATE: 04-ARA-95
RIGHOR APPLICATION NUMBER: 08/222,300
FILING DATE: 04-APR-94
PRIOR APPLICATION NUMBER: 08/220,411
FILING DATE: 25-JUL-94
ATTONEY/AGENT INFORMATION:
AMPLICATION NUMBER: 08/280,441
FILING DATE: 25-JUL-94
ATTONEY/AGENT INFORMATION:
AMPLICATION COMPATION:
AMPLICATION NUMBER: 08/280,441
FILING DATE: 25-JUL-94
ATTONEY/AGENT INFORMATION:
AMPLICATION COMPATION:
AMPLICATION COMPATION:
AMPLICATION COMPATION:
AMPLICATION COMPATION:
AMPLICATION NUMBER: 08/280,441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 670-9365
TELEFAX: (510)670-9302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (510) 670-9365
TELEFAX: (510) 670-9302
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERRETICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Stephen C. Macevicz
REGISTRATION NUMBER: 30,28
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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US-09-516-667-87/c

Sequence 87, Application US/09516667

Sequence 87, Application US/09516667

Sequence 87, Application US/09516667

APPLICANT: Incuye, Masayori

APPLICANT: Mang, Nan

APPLICANT: Yamanaka, Kunitoshi

TITLE OF INVENTION: COLD-SHOCK REGULATORY ELEMENTS, CONSTRUCTS THEREOF, AND
                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                 0
                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 3.1/DOS 5.0
SOFTWARE: Microsoft Word for Windows, vers. 2.0
RAPLICATION DATA: 07-JUN-95
FILING DATE: 07-JUN-95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/22,300
FILING DATE: 24-MAR-95
PRIOR APPLICATION NUMBER: 08/28,441
FILING DATE: 25-JUL-94
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 310:361
FILING DATE: 55-JUL-94
ATTORNEY/AGENT INFORMATION:
REFERENCE/COCKET NUMBER: 310:361
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
TENANTH: 13 nucleotides
                                                                                                                                                                                            US-08-478-239A-24

) Sequence 24, Application US/08478239A

) Sequence 24, Application US/08478239A

) PAREAL INFORMATION:

APPLICANT: Sydney Brenner

ITILE OF INVENTION:

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:

ADDRESSEE: Stephen C. Macevicz, Spectragen, Inc.

STREET: 3832 Bay Center Place

CITY: Hayward

STREET: 2812 Center Place

CITY: Hayward

STREET: 2816cnia

SCOUNTRY: USA
                 ..
0
                 Mismatches
                 .;
0
                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                             935 TCCTCTTCA 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            935 TCCTCTTCA 943
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US-08-478-239A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 9; Conserv
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                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Sydney Brenner
TITLE OF INVENTION: Kits for DNA Sequencing by Stepwise Ligation and Cleavage
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen C. Macevicz, Spectragen, Inc.
STREET: 3832 Bay Center Place
                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                     12.3%; Score 9; DB 1; Length 13; 100.0%; Pred. No. 2e+02; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 3824 BBY CELLER COLUMENT: Hayward STATE: California COUNTRY: USA ZIP: 94545
ZIP: 94545
ZIP: 94545
COUNTRY: USA SIPCHING GENERALE COMPUTER. READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette COMPUTER: IBM compatible OPERATING SYSTEM: Windows 3.1/DOS 5.0 SOFTWARE: Microsoft Word for Windows, vers. 2.0 CURRENT APPLICATION NUMBER: US/08/712,011
RILING DATE: 11-SEP-96
CLASSIPICATION HARN-95
PRIOR APPLICATION NUMBER: 08/410,116
FILING DATE: 24-WAR-95
PRIOR APPLICATION NUMBER: 08/222,300
FILING DATE: 04-APR-94
PRIOR APPLICATION NUMBER: 08/280,441
FILING DATE: 04-APR-94
FRICK APPLICATION NUMBER: 08/286
FILING DATE: 04-APR-94
FRICK APPLICATION NUMBER: 08/286
FRIEFRANCE CHARACTERISTICS: 10.050-9365
TELECOMMUNICATION INFORMATION: TELEFAM: (510) 670-9365
TELEFAM: (510) 670-9365
TELEFAM: MICLOSIDES
SEQUENCE CHARACTERISTICS: MICLOSIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24, Application US/08712011
Patent No. 5831065
NAME: Stephen C. Macevicz
REGISTRATION NUMBER: 30,285
REPRENCE/POCKET NUMBER: 801-0
TELECOMUNICATION INFORMATION:
TELEPHONE: (510) 670-9362
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 nucleotides
TYPE: nucleic acid
STRANDEDRESS: single
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100."
Matches 9; Conservative
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STRANDEDNESS: sing
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Best Local Similarity
                                                                                                                                                                                                                                                                     ; TOPOLOGY:
US-08-667-689A-24
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US-08-712-011-24
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9.08-412-913-2/c
| Sequence 2, Application US/08412913
| Sequence 2, Application US/08412913
| Patent No. 5652103
| GENERAL INFORMATION:
| APPLICANT: Tang Jin-Yan TITLE OF INVENTION: Method of Sequencing Synthetic TITLE OF INVENTION: Oligonucleotides Containing No. 5652103-Phosphodiester TITLE OF INVENTION: Internucleotide Linkages
| NUMBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ÷.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3: Banner & Allegretti, Ltd.
10 South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/412,913
FILING DATE: March 29, 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Greenfield, Michael S.
REGISTRATION NUMBER: 37,142
REFERENCE/DOCKET NUMBER: 92,620-R
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)715-100
TELEPAX: (312)715-1234
TELEX: No. 5652103e
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 254
US-08-441-887A-30/C
US-08-441-887A-30/C
US-08-441-887A-30/C
US-08-441-887A-30/C
US-08-441-08-7A-30/C
US
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HYPOTHETICAL: NO
ANTI-SENSE: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.1%;
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   933 CCTCCTCTTCAT 944
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Banner
STREET: 10 South
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-412-913-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2. Application US/07958133
Patent No. 5403709
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Agrawal, Sudhir
APPLICANT: Tang, Jin-Yan
TITLE OF INVENTION: Oligonuclectides Containing No. 5403709-Phosphodiester
TITLE OF INVENTION: Internuclectide Linkages
NUMBER OF SEQUENCES: SCORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
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                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: primer US-09-516-667-87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 12.3%; Score 9; DB 1; Length 13; Best Local Similarity 100.0%; Pred. No. 2e+02; Matches 9; Conservative 0; Mismatches 0; Indels
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CUCNITAL: USD.

CUCNITAL: USD.

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: USD.

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/958,133

FLING DATE: 19921006

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Keown, Wayne 33,923

REGISTRATION NUMBER: 33,923

REGISTRATION NUMBER: 33,923

REGISTRATION NUMBER: 32,620

TELEPHONE: 617/345-911

TELEPHONE: 617/345-911
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Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches
TITLE OF INVENTION: METHODS OF USE
FILE REPERENCE: 10.53-00
CURRENT APPLICATION NUMBER: US/09/516,667
CURRENT FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 75 State Street, Suite 2300
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA (genomic)
                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELERAX: 617/345-9111
TELEX: No. 5403709e
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Massachusetts
: USA
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US-07-958-133-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: 1ii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 252
US-07-958-133-2/c
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Pred. No. 2e+02;
0; Mismatches 2; Indels
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| Sequence 165, Application US/08173489C
| Sequence 165, Application US/08173489C
| Patent No. 5861244
| GENERAL INPORMATION:
| APPLICANT: WANG, C. -G. APPLICANT: HEPBURN, A. G. |
| TITLE OF INVENTION: GENERIC SEQUENCE ASSAY USING DNA TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
| NUMBER OF SEQUENCES: 365 |
| CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: ROFFLED INAGNOSTIC SCIENCES, INC., CITY: NEW YORK STATE: NEW YORK STATE: NEW YORK STATE: NEW YORK
                                                                         COMPUTER 1 USA

ZIP: 94111

COMPUTER REDDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIDE
COMPUTER: IBM PC COMPATIDE
COMPUTER: DEATHOR FELGES #1.0, Version #1.25
SOFWTARE: PETENTN DATA:
APPLICATION NUMBER: US/08/441,887A
FILING DATE: 16-MAY-1995
CLASSIFICATION NUMBER: US 08/143,312
FILING DATE: 26-CCT-1993
CLASSIFICATION NUMBER: US 08/082,937
FILING DATE: 26-CCT-1993
CLASSIFICATION NUMBER: US 08/082,937
FILING DATE: 25-JUN-1993
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 08/082,937
FILING DATE: 25-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschum CONCET NUMBER: 37,505
REGISTRATION NUMBE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONTINUED TO THE TOTAL T
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Best Local Similarity 83.3%;
Matches 10; Conservative
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MOLECULE TYPE: DNA (probe)

US-08-441-887A-197
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               California
: USA
                     STATE: C
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Pred. No. 2e+02;
0; Mismatches 2; Indels
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US-08-441-887A-197/C
; Sequence 197, Application US/08441887A
; Sequence 197, Application US/08441887A
; Setent No. 5837832
; GENERAL INFORMATION:
    APPLICANT: Chee, Mark
    APPLICANT: Fodor, Stephen P.A.
    APPLICANT: Hubbell, Earl A.
    APPLICANT: Lipshutz, Robert J.
    APPLICANT: Lipshutz, Robert J.
    APPLICANT: Lipshutz, Robert J.
    APPLICANT: Morris, Macdonald S.
    APPLICANT: Arrays of Nucleic Acid Probes on TITLE OF INVENTION: Biological Chips
    NUMBER OF SEQUENCES: 360
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Townsend and Townsend and Crew LLP
    STREET: Two Embarcadero Center, 8th Floor
    CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 94111
COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/441,887A
FILING DATE: 16-MAY-1995
CLASSIPICATION NUMBER: US 08/143,312
FILING DATE: 26-OCT-1993
CLASSIPICATION NUMBER: US 08/082,937
FILING DATE: 26-OCT-1993
ATPORTED APPLICATION NUMBER: US 08/082,937
FILING DATE: 25-UN-1993
ATPORTED APPLICATION NUMBER: 37,505
REGISTRATION NUMBER: 37,505
REQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: mucleic acid
APPLICANT: Sheldon, Edward L.
TITLE OF INVENTION: Arrays of Nucleic Acid Probes on
TITLE OF INVENTION: Biological Chips
NUMBER OF SEQUENCES: 360
CORRESPONDENCES: 360
CORRESPONDENCES: Townsend and Cowniend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                915 TGGTCTTTGCCT 926
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Gaps
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Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 258
US-08-173-489C-227/c
is Sequence 227, Application US/08173489C
is Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANT: WANG, C. -G.
TITLE OF INVENTION: TRIELE-STRAND FORMATION:
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Hepatitis B virus
INDIVIDUAL ISOLATE: adw2
INDIVIDUAL ISOLATE: adw2
AUTHORS: Valenzuela, P, Quiroga, M, Zaldivar, J,
AUTHORS: Gray, P, Ruter, W J.
ITLE: The nucleotide sequence of
TITLE: the Hepatitis B viral genome and the
TITLE: identification of the major viral genes
JOURNAL: In "Animal Virus Genetics", Fields, B N,
JOURNAL: Jaenisch, R, Fox C F eds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DATE: 1980
RELEVANT RESIDUES IN SEQ ID NO: 187 :FROM 1 TO 12
US-08-173-489C-187
                                                                                                     TELEPHONE: (attorney) (212) 708-1880
TELEPACH (attorney) (212) 708-1880
TELEPACH (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 187:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
DESCRIPTION: hepatitis B virus adw2 isolate,
DESCRIPTION: nucleotides 1833 to 1844
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPES: 3.5 inch, 1.44Mb storage
COMPUTER: 1BM PC/XT/AT
COMPUTER: 1BM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfact Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
                 NAME: Handelman, Joseph H. REGISTRATION NUMBER: 26,179 REFERENCE/DOCKET NUMBER: U9518-6 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F: 510 EAST 73RD STREET,
NEW YORK
NEW YORK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Hepa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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COUNTRY:
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US-08-173-489C-187
US-08-173-489C-187
; Sequence 187, Application US/08173489C
; Batcht No. 5861244
; GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: ....ork
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 8.8; DB 1; Length 12;
Pred. No. 2e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Hepatitis B virus
INDIVIDUAL ISOLATE: ayw
INDIVIDUAL ISOLATE: ayw
PUBLICATION INFORMATION:
AUTHORS: Galibert, F, Mandart, E, Fitoussi, F,
AUTHORS: Tiollais, P, Charmay, P.
TITLE: Nucleotide sequence of the
ITILE: Hepatitis B virus genome (subtype ayw) cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; RELEVANT RESIDUES IN SEQ ID NO: 165 :FROM 1 TO 12 US-08-173-489C-165
NAME: Handelman, Joseph H.

REGISTRATION NUMBER: 26,179
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: 0518-6
TELEPHONE: (attorney) (212) 708-1880
TELEPAX: (attorney) (212) 708-1880
TELEFAX: (attorney) (212) 246-8959
INPORMATION FOR SEQ ID NO: 165:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYRE: nucleic acid
TYRE: nucleic acid
TYRE: nucleic acid
TYRE: nucleic acid
TYRE: product acid
TYRE: nucleic acid
TYRE: nucleic acid
DESCRIPTION: hepatitis B virus ayw isolate,
DESCRIPTION: nucleotides 2750 to 2761
HYPOTHERICAL: no
ANTI-SENSE: no
ORGANISM: DESCRIPTION: nucleotides 2750 to 2761
CORGANISM: DESCRIPTION: nuc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTY:

COUNTY:

COUNTY:

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44Mb storage

COMPUTER: 18M FC/XT/AT

OPERATING SYSTEM: MS-DOS version 6.2

SOFTWARE: Wordperfect Version 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/173,489C

FILING DATE: 2 DEC 1993

CLASSIFTCATION 5435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/968,436

FILING DATE: 29 OCT 1992

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
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DATE: 1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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TOPOLOGY: linear MOLECULE TYPE: genomic DNA DESCRIPTION: 23s TXNA gene from Leptospira DESCRIPTION: interrogans (Accession # X14249) nucleotides DESCRIPTION: http://doi.org/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/10.1001/1
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MYTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Leptospira interrogans serovar canicola
STRAIN: moulton
PUBLICATION INFORMATION:
AUTHORS: Publication of a 23s
TITLE: Nucleotide sequence of a 23s
TITLE: ribosomal RNA gene for Leptospira interrogans
TITLE: serovar canicola strain moulton
JOURNAL: Nucleic Acids Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 8.8; DB 1; Length 12;
Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WESOUR 260
US-08-173-489C-249/C

Sequence 249 Application US/08173489C

Sequence 249 Application US/08173489C

Sequence 249 Application US/08173489C

SEGUENCE NO. SE61244

TIPLE OF INVENTION: TRIPLE-STRAND FORMATION.

TITLE OF INVENTION: TRIPLE-STRAND FORMATION.

TITLE OF INVENTION: TRIPLE-STRAND FORMATION.

TITLE OF SEQUENCES: 365

CORRESPONDENCES: 365

CORRESPONDENCES: 365

COURTEY: USA TARD STREET,

CITY: NEW YORK

STATE: NEW YORK

COUNTY: USA

ZIP: 10021.

COMPUTER: ISH PC/XT/AT

COMPUTER: ISH PC/XT/AT

COMPUTER: ISH PC/XT/AT

COMPUTER: SOFTWARE: WCGDERfect Version 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/173,489C

FILING DATE: 22 DEC 1993

CLASSITCATION NUMBER: US/08/173,489C

FILING BATEL SPOCT 1992

ATTORNEY APPLICATION DATA:

APPLICATION NUMBER: US/08/173,489C

FILING DATE: 29 OCT 1992

FILING DATE: 29 OCT 1992

ATTORNEY APPLICATION NUMBER: US/08/173,480C

FILING DATE: 29 OCT 1992

ATTORNEY APPLICATION NUMBER: US/08/173,480C

FILING DATE: 29 OCT 1993

FILING DATE: 29 OCT 1992

ATTORNEY APPLICATION NUMBER: US/08/173,480C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAGES: 2123-2123
DATE: 1989
RELEVANT RESIDUES IN SEQ ID NO: 237 :FROM 1 TO 12
US-08-173-489C-237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
    REGISTRATION NUMBER: 26,179
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: U9518-6
TELECHONE: (attorney) (212) 706-1880
TELEPHONE: (attorney) (212) 706-1880
INFORMATION FOR SEQ ID NO: 237:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                   LENGIR: 12 TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear Stranded
TOPOLOGY: linear Persistence of the Molecule TYPE: genomic DNA
DESCRIPTION: 23s rRNA gene from Halococcus morrhuae
DESCRIPTION: (Accession # X05481) nucleotides 880 to 891
HYPOTHETICAL: no
ANTI-SENSE: no
ORAGINEM: HALOCOCCUS morrhuae
ORAGINEM: HALOCOCCUS morrhuae
PUBLICATION INFORMATION: Kjems, J, Ostergaard, L, AUTHORS: Leffers, H, Kjems, J, Ostergaard, L, AUTHORS: Leffers, H, Kjems, J, Ostergaard, L, TILLE: Evolutionary Relationship
TITLE: Amongst Archaebacteria: A Comparative Study of
TITLE: Amongst Archaebacteria: A Comparative Study of
TITLE: Extreme Thermophile, an Extreme Halophile and a TITLE: Thermophilic Methanogen
JUURNAL: Lournal of Molecular Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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12.1%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 10; Conservative 0; Mismatches 2; Indels
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; Sequence 237, Application US/08173489C
; Sequence 237, Application US/08173489C
; GENERAL INFORMATION:
; PAPLICANT: WANG, C. -G.
; APPLICANT: WANG, C. -G.
; APPLICANT: WANG, C. -G.
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; TITLE OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; STREET: NEW YORK
; STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DATE: 1987
; RELEVANT RESIDUES IN SEQ ID NO: 227 :FROM 1 TO 12
US-08-173-489C-227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTY: USA.

ZIP: 10021.

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XT/AT

OPERATING SYSTEM: MS-DOS version 6.2

SOFTWARE: WORDER: CV (08/173, 489C

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/173, 489C

FILING DATE: 22 DEC 1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/968,436

FILING DATE: 29 OCT 1992

ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.

REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: 10518-6
TELECOMMUNICATION INFORMATION:
TELEPAX: (attorney) (212) 708-1880
INFORMATION FOR SEQ ID NO: 227:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDENESS: double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     924 CCTTTTATCCCT 935
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TELECOMOUNICATION INFORMATION:
TELEPHONE: (attorney) (212) 708-1880
TELEFAX: (attorney) (212) 246-8959
INFORMATION FOR EQU ID NO: 259:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: uncleic acid
STRANDEDNES: double stranded
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (attorney) (212) 708-1880
attorney) (212) 246-8959
SEQ ID NO: 263:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RELEVANT RESIDUES IN SEQ ID NO:
US-08-173-489C-259
                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Frankia sp.
PUBLICATION INFORMATION:
AUTHORS: No. 5861244mand, P.
TITLE: unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       924 CCTTTTATCCCT 935
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 510 EAST
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
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                                                                                                                                                                                                                                                                                             HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
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0
                                                                                                                                                                                                                                                    MOLECULE TYPE: genomic DNA
DESCRIPTION: 23s rRNA gene from Micrococcus luteus
DESCRIPTION: (Accession # X06484) nucleotides 859 to 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 261
US-08-173-489C-259/C

Sequence 259, Application US/08173489C

Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANT: HEBBURN, A. G.
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
ITTLE OF INVENTION: TRIPLE-STRAND FORMATION.
CORRESPONDENCE ADDRESS:
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 12.1%; Score 8.8; DB 1; Length 12; Best Local Similarity 83.3%; Pred. No. 2e+02; Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Micrococcus luteus
STRAIN: dsm 20030
PUBLICATION INFORMATION:
AUTHORS: Regensburger, A, Ludwig, W, Frank, R,
AUTHORS: Bloecker, H, Schleifer, K H.
TITLE: Complete nuclectide sequence
TITLE: Complete nuclectide sequence
TITLE: luteus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; RELEVANT FEIDUES IN SEQ ID NO: 249 :FROM 1 TO 12 US-08-173-489C-249
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ZIP: 10021.

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
  REGISTRATION NUMBER: 26,179
REPERBENCE/DOCTET NUMBER: U5518-6
TELECHONE: (attorney) (212) 708-1880
FELEPA: (attorney) (212) 246-8559
INFORMATION FOR SEQ ID NO: 249:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 00T 1992
ATTORNEY/AGENT INFORMATION:
NAME: HANGELMAN, JOSEPH H.
REGISTRATION NUMBER: 26,179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL: Nucleic Acids Research
VOLUME: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       924 CCTTTTATCCCT 935
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                                                                                                                                                                                                                                 TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: no
ORIGINAL SOURCE:
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MOLECULE TYPE: genomic DNA
DESCRIPTION: 23s rRNA gene from Frankia sp
DESCRIPTION: (Accession # M55343) nucleotides 3314 to 3325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 262
US-08-173-489C-263/C
US-08-173-489C-263/C
Sequence 263, Application US/08173489C
Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANT: HEPBURN, A. G.
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESSE:
ADDRESSEE: PROFILED DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 8.8; DB 1; Length 12;
Pred. No. 2e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                     259 :FROM 1 TO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: USA
ZIP: 10021.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44MD storage
COMPUTER: 18M PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 2 DEC 1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, JOSEPH H.
REGISTRATION NUMBER: U9518-6
REFERENCE/DOCKET NUMBER: U9518-6
TELECOMMUNICATION INFORMATION:
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Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                        | INFORMATION FOR SEQ ID NO: 1 | SEQUENCE CHARACTERISTICS: | LENGTH: 12 base pairs | TYPE: nucleic acid | STRANDEDNESS: single | TOPOLLGY: linear US-08-927-165A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 83.33,
...nhes 10; Conservative
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                TELEFAX: 215-504-4545 TELEX:
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US-07-715-183C-9
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SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
DESCRIPTION: 23s FRNA gene from Rhodobacter
DESCRIPTION: capsulatus (Accession # X06485) nucleotides 842
HYPOTHETICAL: no
ANTI-SENSE: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Rhodobacter capsulatus
STRAIN: AGM 348
PUBLICATION INPORMATION:
AUTHORS: Regensburger, A, Ludwig, W, Frank, R,
AUTHORS: Bloecker, H, Schlaifer, K H.
TITLE: Complete nucleotide sequence
TITLE: of a 235 ribosomal RNA gene from Rhodobacter
TITLE: Of a 235 ribosomal RNA gene from COURMAL: NUCLUME: 16
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PAGES: 2243-2343

PAGES: 2243-2343

PAGES: 1988

RELEVANT RESIDUES IN SEQ ID NO: 263 :FROM 1 TO 12
US-08-173-489C-263
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Sequence 17, Application US/08927165A

Patent No. 6410226

GENERAL INFORMATION:
APPLICANT: Kmiec, Eric B.
APPLICANT: Holloman, William K.
APPLICANT: Rice, Michael C.
APPLICANT: Smith, Sheryl T.
APPLICANT: Smith, Sheryl T.
APPLICANT: Shu, Zhigang
ITILE OF INVENTION: Mammalian and Human Rec2
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
NAME: Hansburg, Daniel
REGISTRATION NUMBER: 36156
REFERENCE/DOCKET NUMBER: 799:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-504-4444
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COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDLUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: 18M PC/XY/AT
COPERATING SYSTEM: MS-DOS version 6.2
SOFFWARE: 18M PC/SPATON 6.2
SUFFWARE: WORDER: 2 DEC 1993
CLASSIFICATION NUMBER: US/08/173,489C
FILLING DATE: 2 DEC 1993
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, JOSEPh H.
REFERENCE/DOCKET NUMBER: US-179
REFERENCE/DOCKET NUMBER: US-179
REFERENCE/DOCKET NUMBER: US-189
                                                                                      FILING DATE: 21-MAY-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA: 33-MAR-1995
RIOR APPLICATION DATA: 08/409,852
PRIOR APPLICATION DATA: 08/220,604
ATTORNEY, GENT INFORMATION:
NAME: JACKSON, DAVIG A.
REGISTRATION NUMBER: 26,742
TELECHOME: (201) 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 267
20.08-173-489C-334
; Sequence 334, Application US/08173489C
; Patent No. 5861244
PC-DOS/MS-DOS
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Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 133521
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 13 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inear
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HYPOTHËTICAL:
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                                           GENERAL INFORMATION:

APPLICANT: Belagaje, Rama M
APPLICANT: DIMArchi, Richard D
APPLICANT: Long, Harlan F
APPLICANT: Long, Harlan B
TITLE OF INVENTION: A-C-B PROINSULIN, METHOD OF
TITLE OF INVENTION: MANUPACTURING AND USING SAME, AND INTERMEDIATES IN
TITLE OF INVENTION: INSULIN PRODUCTION
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bli Lilly and Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NESULT 266
US-08-651-835A-9
Squence 9, Application US/08651835A
Squence 9, Application US/08651835A
Space No. 570786
STREAL INFORMATION:
APPLICANT: DELANT: MAICA MAICA APPLICANT: Carberine
TITLE OF INVENTION: USE OF DNA OLIGOMERS FOR INHIBITION OF
TITLE OF INVENTION: USE OF DNA SPECREASING RIBOSOMAL FRAMESHIFTING
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USAN
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/715,183C
ILING DATE: 19910611
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: CORTEA( WILLiam A
NAME: CORTEA( WILliam A
REGISTRATION NUMBER: X-7866
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION CONTROLLE AINGLE
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Continental Plaza, 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                ADDRESSEE. Eli Lilly and Company STREET: Lilly Corporate Center CITY: Indianapolis STATE: Indiana
Sequence 9, Application US/07715183C
Patent No. 5304473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
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Matches 10; Conservative
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STATE: N.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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Gaps
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APPLICANT: WANG, C. -G.
APPLICANT: HERBIRAN, A. G.
TITLE OF INVENTION: GENERIC SEQUENCE ASSAY USING DNA
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/651,835A
FILING DATE: 21-MAY-1996
CLASSIFICATION: 514
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Pred. No. 2.2e+02;
0; Mismatches 2;
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12.1%;
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                                                                              923 GCCTTTTATCCC 934
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Best Local Similarity 83.3
Matches 10; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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US-08-930-798-4
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10-08-761-243C-18/c
15-08-761-243C-18/c
15-08-761-243C-18/c
15-08-761-243C-18/c
15-08-761-243C-18/c
17-08-761-243C-18/c
18-08-761-243C-18/c
18-08-761-243C-18/c
18-08-761-243C-18/c
18-08-761-243C-18/c
18-08-761-243C-
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12.1%; Score 8.8; DB 1; Length 13
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 10; Conservative 0; Mismatches 2; Indels
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PUBLICATION INFORMATION:
HOBLICATION INFORMATION:
HOSTORY ASSET OF THE SELECT OF THE
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ADDRESSE:
ATTORNEY/ADDRESSE:
ADDRESSE:
ADD
TELEPHONE: (attorney) (212) 708-1880
TELEFAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 334:
SEQUENCE CHARACTERISTICS:
LENGHH: 13 bases
TYPE: nucleic acid
STRANDEDNESS: single stranded
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LENGTH: 13 bp
LENGTH: 13 bp
STYPE: nucleic acid
STYPE: nucleic acid
STYPE: linear
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US-08-761-243C-18
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MOLECULE TYPE:
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ANTI-SENSE: N
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WESTLY 269

US-8607-018-2/6

1 Sequence 2, Application US/08607078

PARENT NO. 600947

PARENT NO. 600947

PARENT CALIFORNIA INSTITUTE OF TRANSMISS OF Pyrrole

FILLS OF INVESTION NAMED OF Extraction, L.L.C.

PARENT SALES Season's Extraction, L.L.C.

FILLS OF INVESTION NAMED OF Extraction, L.L.C.

STREET 8400 E Frantice Avenue, Silte 200

GTY: Englewood Frantice Avenue, Silter 200

GTY: Englewood Franti
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September of September

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TYPE: DNA ORGANISM: Artificial Sequence
                                                                                     918 TCTTTGCCTTTT 929
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Best Local Similarity 83.3
Matches 10; Conservative
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STATE: Massachusetts
COUNTRY: U.S.A.
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US-09-360-344-2/c
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TITLE OF INVENTION: A METHOD FOR ANALYSING A POLYNUCLECTIDE CONTAINING A TITLE OF INVENTION: OMAIGABLE SEQUENCE AND A SET OR ARRAY OF TITLE OF INVENTION: OLIGONUCLECTIDES THEREFOR (AS AMENDED)
FILE REFERENCE: 97-1173*/wmc/263
CURRENT APPLICATION NUMBER: US/09/502,778A
CURRENT FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 4
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Sequence 2, Application US/09359921
| Patent No. 6645162
| GENERAL INFORMATION:
| APPLICANT: DERVAN, PETER B.
| APPLICANT: BAIRD, ELDON E.
| TITLE OF INVENTION: METHOD FOR THE SYNTHESIS OF PYRROLE AND IMIDAZOLE
| TITLE OF INVENTION: CARBOXAMIDES ON A SOLID SUPPORT
| TITLE OF INVENTION: CARBOXAMIDES ON A SOLID SUPPORT
| CURRENT APPLICATION NUMBER: US/09/359,921
| CURRENT FILING DATE: 1999-07-22
| NUMBER OF SEQ ID NOS: 31
| SOFTWARE: PatentIn Ver. 2.1
| SEQ ID NO 2
| LENGTH: 13
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                                                                                       FEATURE:
OTHER INFORMATION: Description of Unknown Organism:synthetic - other COTHER INFORMATION: dna
US-08-930-798-4
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US-09-502-778A-4
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Pred. No. 2.2e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09502778A; Patent No. 6307039; GENERAL INFORMATION: APPLICANT: SOUTHERN, EDWIN
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Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                 925 CTTTTATCCCTC 936
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Best Local Similarity 83.3
Matches 10; Conservative
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                                          TYPE: DNA
ORGANISM: Unknown
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US-09-359-921-2/c
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US-09-502-778A-4
SEQ ID NO 4
LENGTH: 13
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                                                                        Gaps
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APPLICANT: DERVAN, PETER B.
APPLICANT: DERVAN, PETER B.
APPLICANT: DERVAN, PETER B.
APPLICANT: BAIRD, ELDON E.
TITLE OF INVENTION: METHOD FOR THE SYNTHESIS OF PYRROLE AND IMIDAZOLE
TITLE OF INVENTION: CARBOXAMIDES ON A SOLID SUPPORT
FILE REFERENCE: 025098-1664
CURRENT APPLICATION NUMBER: US/09/360,344
CURRENT FILING DAIE: 1999-07-22
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIN VAY: 2.1
SEQ ID NO.2
LENGTH: 13
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US-09-360-344-2
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Score 8.8; DB 1; Length 13
Pred. No. 2.2e+02;
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APPLICANT: Alexander T. Young
TILLE OF INVENTION:
TILLE OF INVENTION: VIRAL VECTORS
NUMBER. OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIN: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 558X
OPERATING SYSTEM: IBM P.C. DOS (Version 5.00)
SOFTWARE: WordPerfect (Version 5.1)
APPLICATION DATA: PST/US93/02957
FILING DATE: 19930331
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/862,795
FILING DATE: April 3, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 05140/002002
TELECOMMUNICATION INFORMATION:
                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09360344
Patent No: 6683189
GENERAL INFORMATION:
                         12.1%;
                         Query Match 12.1
Best Local Similarity 83.3
Matches 10; Conservative
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Patent No. 6277571
GENERAL INFORMATION:
APPLICANT: FILLWORE, WILLIAM:
APPLICANT: GILLIES, GEORGE
TITLE OF INVENTION: SEQUENTIAL CONSENSUS REGION-DIRECTED AMPLIFICATION OF
TITLE OF INVENTION: KNOWN AND NOVEL MEMBERS OF GENE FAMILIES
FILE REFERENCE: VCUIP4B
CURRENT APPLICATION NUMBER: US/09/163,485
CURRENT FILING DATE: 1998-08-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                      Length 13;
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Sequence 5, Application US/07651710A

Sequence 5, Application US/07651710A

FENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Trans-Activating Factor-1
TITLE OF INVENTION: Trans-Activating Factor-1
TITLE OF INVENTION: Trans-Activating Factor-1
TITLE OF INVENTION: Tans-Activating Factor-1
TITLE OF INVENTION: Tans-Activating Factor-1
TITLE OF INVENTION: Tans-Activating Factor-1
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: USA.
ZIP: New York
COMPUTER: New York
MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC COMPATION
COMPUTER: LEM PC COMP
                                                                                                                                  Score 8.8; DB 1; L
Pred. No. 2.2e+02;
0; Mismatches 2;
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APPLICATION NUMBER: US/07/651,710A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                  Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                 919 CTTTGCCTTTTA 930
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                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 277
US-09-163-485-25/c
                                     ; LENGTH: 13
5514646-34
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LENGTH: 12
          SEQ ID NO:34:
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; Patent No. 5514646
; Patent No. 5514646
; Patent No. 5514646
; RRUGE H.; SHIELDS, JAMES E.
    TITLE OF INVENTION: INSULIN ANALOGS MODIFIED AT POSITION
; 29 OF THE B CHAIN
; WUMBER OF SEQUENCES: 52
; CURRENT APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US/08/57,201
; FILING DATE: OS-MAY-1993
; APPLICATION NUMBER: 886,632
; APPLICATION NUMBER: 388,201
; FILING DATE: O4-A0G-1989
; FILING DATE: O9-FEB-1989
; FILING DATE: 09-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MARIACATION THREADEN JACOB R., OPPENHEIM, AMOS B., GORECKI,
MARIAN, ATU, HAMM, OREN, RACHEL
JAMAIN, PATURE OF INVENTION: THERAPEUTIC COMPOSITIONS COMPRISING
JAMAINTURE OF HUMAN CUZN SUPEROXIDE DISMUTASE ANALOGS
NUMBER OF SEQUENCES: 30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 449,125
FILING DATE: 21-A0G-1992
FILING DATE: 08-DG-1989
FILING DATE: 03-DW-1988
FILING DATE: 03-DW-1988
FILING DATE: 19-A0G-1985
FILING DATE: 27-AUG-1984
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                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                              Score 8.8; DB 1;
Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
; TELEPHONE: (617) 542-5070; TELEPAX: (617) 542-8906; TELEX: 200154; INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 13 TYPE: NUCLEIC ACID; TYPE: NUCLEIC ACID; TYPE: NUCLEIC ACID; TYPE: TOPOLOGY: linear PCT-US93-02957-3
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 908 TTTTCTTTGGTC 919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Patent No. 5455029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 13
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5455029-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from esterase D
DESCRIPTION: sequence region in Seq ID No. 586124467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: WANG, C. -G.
APPLICANT: HERBURN, A. G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER: OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSEE: PROFILE DISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RELEVANT RESIDUES IN SEQ ID NO: 68 :FROM 1 TO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:

COUNTRY:

COUNTRY:

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: 10 inch, 1.44Mb storage
COMPUTER: 10 inch, 1.44Mb storage
COMPUTER: MS-DOS version 6.2
SOSTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 2 DEC 1993
CLASSIFICATION NUMBER: US 07/966,436
FILING DATE: 29 OCT 1992
ATTORNEY AGENT INFORMATION:
NAME: Handelman, Joseph H.
REFERENCE/DOCKET NUMBER: US-179
REFERENCE/DOCKET NUMBER: US-180
TELEPHONE: (attorney) (212) 708-180
TELEPHONE: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 280
US-08-173-489C-68
Sequence 68, Application US/08173489C
Patent No: 5861244
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 10 bases
TYPE: Nucleic Acid
STRANDEDNESS: single stranded
                                                                                                                                                                                                      Query Match
Best Local Similarity 90.0°
SEQUENCE CHARACTERISTICS:
LENGTH: 10
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PUBLICATION INFORMATION:
                                                              TYPE; nucleic acid
STRANDEDNESS: single
TOPOLOGY:
US-08-060-952C-11
                                                                                                                                                                                                                                                                                                                                                               941 TCATTGGTTT 950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEW YORK
: NEW YORK
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HYPOTHETICAL:
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Batent No. 569532

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Jerry W. Shay
APPLICANT: Jerry W. Shay

TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
TITLE OF INVENTION: TELOMERASE ACTIVITY
TITLE OF INVENTION: TELOMERASE ACTIVITY

NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSES: Lyon & Lyon
STREET: 633 West Pifth Street
STREET: 634 West Pifth Street
STREET: California
COUNTRY: U.S.A.

SEDIUM TYPE: Storage
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 8.4; DB 1; Length 10;
Pred. No. 2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/060,952C
FILING DATE: May 13, 1993
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/882,438
FILING DATE: May 13, 1992
APPLICATION NUMBER: 08/038,766
FILING DATE: March 24, 1993
ATTORNEY/AGENT INFORMATION:
MATCHER AND ACCOUNTY OF THE 
                 TILLING UALD: ASSACE CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 3288-014
TELECOMMUNICATION INFORMATION:
TELEFAN: 212 8698864/9741
TELERA: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: NUCLEIC ACID
SITAMBENNES: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown MOLECULE TYPE: TAF-1 binding motif US-07-651-710A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3110
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative
      19910206
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US-08-060-952C-11
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GENERAL INFORMATION:

APPLICANT: Walling, Linda L.
APPLICANT: Pautot, Veronique
APPLICANT: Caronique
APPLICANT: Caronique
APPLICANT: Chao, Wun Shaw
TITLE OF INVENTION: Productivity
NUMBER OF SEQUENCES: 13
CORRESPONDENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTY: USA
ZIP: 9411-384
COMPUTER REABABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PetentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,770
FILING DATE: 15-JUL-1997
CLASSIFICATION NUMBER: US-41,261
REGISTRATION NUMBER: 0-41,261
REFERENCE/DOCKET NUMBER: 0-23070-072100US
TELEFRAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LEMOTH: 10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 11.5%; Score 8.4; DB 1; Length 10; Best Local Similarity 90.0%; Pred. No. 2e+02; Matches 9; Conservative 0; Mismatches 1; Indels
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APPLICANT: Deacon, Jennifer C.
APPLICANT: Learmont, Jennifer C.
APPLICANT: Morbhee, Dale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Coper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                Sequence 13, Application US/08892770; Patent No. 5962670; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-388-353-49/c
; Sequence 49, Application US/08388353
; Patent No. 6010895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  905 TCATTTTCTT 914
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10 TCTTTCCCTT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-892-770-13
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                                                                                                                                                                                   APPLICANT: NAWA, C. G. G.
APPLICANT: MANG, C. G. G.
APPLICANT: HANG, C. G. G.
APPLICANT: HANG, C. G. G.
APPLICANT: HANG, C. G.
APPLICANT: HANG, C. G.
TITLE OF INVENTION: TRIPLE-STRAND FORWATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSER: FORTILE DIAGNOSTIC SCIENCES, INC.,
CITY: NEW YORK
COUNTRY: USA
STRATE: NEW YORK
COUNTRY: USA
ZIP: 10021.
COMPUTER: INDW TOPR: 3.5 inch, 1.44Mb storage
COUNTRY: USA
ZIP: 10021.
COMPUTER: SEADABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: SEADABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: SEADABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: SEADABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: SEADABLE FORM:
MEDIUM TYPE: 2.5 EC 1993
CLASSIFICATION NUMBER: 1.0508/173,489C
FILING DATE: 2.9 CCT 1992
TELECOMMUTICATION NUMBER: 26,178
REFERENCE/DOCKET NUMBER: 1.0518-6
FELECOMMUTICATION NUMBER: 26,178
REFERENCE/DOCKET NUMBER: 26,178
REFERENCE/DOCKET NUMBER: 1.0518-6
FELECOMMUTICATION NUMBER: 26,178
REFERENCE/DOCKET NUMBER: 26,178
REFERENCE/DOCKET NUMBER: 26,178
REFERENCE/DOCKET NUMBER: 26,178
SEQUENCE CHARACTERISTICS:
FELECOMMUTICATION NUMBER: 26,178
REFERENCE/DOCKET NUMBER: 27,188
REFERENCE/DOCKET NUMBER: 27,188
REFERENCE/DOCKET N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE: human esterase D gene, a genetic marker of TITLE: retinoblastoma JOURNAL: Proceedings of the National Academy of JOURNAL: Sciences, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 :FROM 1 TO 10
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US-08-173-489C-71
                                                                                                               US-08-173-489C-71/c
; Sequence 71, Application US/08173489C
; Patent No. 5861244
1 TCCTTTTCTT 10
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Best Local Similarity
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ADDRESSEE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City

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Gaps

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918 TCTTTGCCTT 927

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Gaps
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                                                                                                                                                                                                                        DB 1; Length 10;
                                                                                                                                                                                                                                                                  1: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Learmont, Jennifer C.
APPLICANT: Methee, Dale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Crowe, Suzanne
APPLICANT: Cooper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM FO COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City STATE: New York COUNTRY: United States
                                                                                                                                                                                                                        11.5%; Score 8.4; DB 1; 90.0%; Pred. No. 2e+02; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 136, Application US/08388353
Patent No. 6010895
GENERAL INFORMATION:
APPLICANT: Deacon, Nicholas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: D161910, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9606
TELECOMMUICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
                         135:
                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPLOGY: linear
MOLECTLE TYPE: DNA (genomic)
US-08-388-353-135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                      Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 90.0
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                                                                   10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QUENCTH: 10 Dasc. TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                            954 GTATCGCTAC 963
                                                                                                                                                                                                                                                                                                                                      10 GTATTGCTAC 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 11530
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Best Local S
Matches 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 135, Application US/08388353
Patent No. 6010895
GENERAL INFORMATION:
APPLICANT: Learmont, Jennifer C.
APPLICANT: Crowe, Suzane
APPLICANT: Crowe, Suzane
APPLICANT: Crowe, Suzane
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
                                                                                                                                                CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB.1995
CLASSIPICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Didiglio, Frank S.
REGISTRICATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9606
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (516) 742-4343
TELEFEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPIET INTEGRATED STATES

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CONFURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIFICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIFICATION NUMBER: 31,346
ATTORNEY/AGENT INFORMATION:
NAME: Did3alio, Frank S.
REGISTRATION NUMBER: 9606
TELECOMMUNICATION INFORMATION:
TELEPRAK: (516) 742-4343
TELEFRAK: (516) 742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Scully, Scott, Murphy & Presser
400 Garden City Plaza
                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                       COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy dis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      918 TCTTTGCCTT 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 400 cc.
CITY: Garden City
CHATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 284
US-08-388-353-135/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 192, Application US/08388353
Patent No. 610895
GENERAL INFORMATION
APPLICANT: Deacon, Nicholas J.
APPLICANT: Learmont, Jennifer C.
APPLICANT: Crowe, Suzanne
APPLICANT: Cooper, David
ITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
ADDRESSEE: Soully, Scott, Murphy & Presser
COMPUTER READABLE FORM:

MEDIUM TYEE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SUSTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/383,353
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DidStallo, Frank S.
REGISTRATION NUMBER: 9606
TELECOMMUNICATION INFORMATION:
TELERENCE/DOCKET NUMBER: 9606
TELECOMMUNICATION INFORMATION:
TELERENCE (516) 742-4336
TELERENCE (516) 742-4336
TELEREX: 230 901 SANS UR
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNES: single
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CARESPONDENCE ADDRESSE

STREET: 400 Garden City Plaza

STREET: 400 Garden City Plaza

STREET: 400 Garden City Plaza

STATE: New York

COUNTRY: United States

CANDUTER: New York

COMPUTER: New York

COMPUTER: DEADELE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/388,353

FLING DATE: 14-FEB 1995

CLASSIFICATION: 424

ATTORNEY/AGENT INPORMATION:

NAME: DIGIGIO, Frank S.

REGISTRATION NUMBER: 31,346

REGISTRATION NUMBER: 31,346

REBERRICE/DOCKET NUMBER: 3606

TELEPAX: (516) 742-4366

TELEPAX: (516) 742-4366

TELEPAX: (516) 742-4366

TELEPAX: (516) 742-4366

TELERAX: (516) 742-4365

TELERAX: SOU 10 NO: 192:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
11.5%; Score 8.4; DB 1;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           933 CCTCCTCTTC 942
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US-08-388-353-192/c
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                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Deacon, Nicholas J.
APPLICANT: Deacon, Nicholas J.
APPLICANT: Deacon, Nicholas J.
APPLICANT: Crowe, Suzanne
APPLICANT: Crowe, Suzanne
APPLICANT: Crowe, Suzanne
APPLICANT: Crowe, Suzanne
APPLICANT: Crower, Suzanne
APPLICANT: Crower, Suzanne
APPLICANT: Crower, Suzanne
APPLICANT: Crower, Non-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESCONDERS: Scully, Scott, Murphy & Presser
CITY: Garden City Plaza
CONTENT: Deacen City Plaza
COUNTRY: United States
SIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Diciglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/POCKET NUMBER: 3606
TELECPHONE: (516) 742-4366
TELEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S-08-388-353-184/c
Sequence 184, Application US/08388353
Patent No. 6010895
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic) US-08-388-353-184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Garden City
STATE: New York
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                931 TCCCTCCTCT 940
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Query Match
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11.5%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.5%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 2e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 229 Application US/08388353
Fatent No. 6010895
GENERAL INFORMATION:
APPLICANT: Deacon, Nicholas J.
APPLICANT: Learmont, Jennifer C.
APPLICANT: Crowe, Suzanne
APPLICANT: Cooper, David
ITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN RE-BESS #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIFGATION: 424
ATTORNEY/AGRAT INFORMATION:
NAME: Didiglio, FRANCE, 9606
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 229:
SEQUENCE CHARACTERISTICS:
FWACTH: 10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 290
US-08-388-353-230/c
; Sequence 230, Application US/08388353
           TYPE: nucleic acid
STRANDENNES: single
FOOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-388-353-192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New York
: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 90.0
Matches 9; Conservative
10 base pairs
                                                                                                                                                                                                                                              932 CCCTCCTCTT 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               912 CTTTGGTCTT 921
                                                                                                                                                                                                                                                                                           10 CCCACCTCTT 1
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                                                                                                                                                                                                                                                                                                                                                           RESULT 289
US-08-388-353-229/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Ne
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Gaps
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APPLICANT: Deacon, Nicholas J.
APPLICANT: Learmont, Jennifer C.
APPLICANT: McDee, Dale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Crower, David
TITLE OF TOWNITION: NON-PATHOGENIC STRAINS OF HIV-1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Deacon, Nicholas J.
APPLICANT: Learmont, Jennifer C.
APPLICANT: More, Bule A.
APPLICANT: Crowe, Suzanne
APPLICANT: Coper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
WUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                        COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14 FEB-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Scully, Scott, Murphy & Presser
400 Garden City Plaza
                                                                                                                                                                            ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.5%; Score 8.4; 90.0%; Pred. No. 2
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; Sequence 275, Application US/08388353
Partent No. 6010895
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELERA: (516) 742-4346
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 230:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                              New York
: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         United States
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 911 TCTTTGGTCT 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
STREET: 40
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Gaps
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Sequence 49, Application US/08488551B
Sequence 49, Application US/08488551B
Sequence 49, Application US/08488551B
SERECANT: Nicholas J. Deacon
APPLICANT: Dale A. Morbee
APPLICANT: DAIG Cooper
STREET: 400 GRADEN CITY PLAZA
CITY: GANDEN CITY PLAZA
CITY: GANDEN CITY
STATE: NEW YORK
COMPUTER: BARDEN CITY PLAZA
ZIP: 11530-0298
COMPUTER: PLOPPY disk
STATEL APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PN402 (AU)
FILING DATE: 12-FEB-1994
APPLICATION NUMBER: PN4021
FILING DATE: 12-FEB-1994
APPLICATION NUMBER: PN3021/95
FILING DATE: 17-PMAY-1995
APTOLICATION NUMBER: PN3021/95
FILING DATE: 17-PMAY-1995
APPLICATION NUMBER: PN3021/95
APPLICATION NUMBER: PN3021/95
FILING DATE: 17-PMAY-1995
APPLICATION NUMBER: PN3021/95
FILING DATE: 17-PMAY-1995
APPLICATION NUMBER: PN3021/95
AP
                                                                                                                                                                                                    Query Match 11.5%; Score 8.4; DB 1; Length 10; Best Local Similarity 90.0%; Pred. No. 2e+02; Matches '9; Conservative 0; Mismatches 1; Indels
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Pred. No. 2e+02;
0; Mismatches 1; Indels
                                                          ; MOLECULE TYPE: DNA (genomic) US-08-388-353-310
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TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                         908 TTTTCTTTGG 917
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          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE:
US-08-488-551B-49
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11.5%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 310, Application US/08388353
Fatent No. 6010895
FALL INFORMATION, Nicholas J.
APPLICANT: Learmont, Jennifer C.
APPLICANT: Crowe, Suzane
APPLICANT: Crowe, Suzane
APPLICANT: Crowe, Suzane
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SECURNCES: 800
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSE:
SCULLY, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
COMPUTER: New York
COMPUTER: Disponting Compatible
COMPUTER: ISBN PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BM PC compatible
COMPUTER: BM PC compatible
COMPUTER: BM PC compatible
COMPUTER: BM PC compatible
COMPUTER: Disponting Compatible
COMPUTER: Disponting Compatible
COMPUTER: Data FFEB-1995
CLEASTRICATION NUMBER: 9606
TELESPICATION NUMBER: 9606
TELERPHONE: Gisl 742-4343
TELERPHONE: Gisl 742-4343
TELERRY: CISL 742-4366
TELERRY: CISL 742-4368
TELERRY: CISL 7
                               GETWALE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FILNG DATE: 14-FEB.1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Didiglio, Frank S.
REGISTRATION NUMBER: 31,346
REGISTRATION NUMBER: 31,346
REGISTRATION NUMBER: 31,346
REGISTRATION NUMBER: 31,346
RELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-436
TELEPH
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            906 CATTITITY 915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-388-353-310/c
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Gaps
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Pred. No. 2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-06-488-551B-184/C
US-08-488-551B-184/C
Sequence 184, Application US/08488551B
Sequence 187, Application US/08488551B
Sequence 10. 6015661
Sequence 10. 6015661
Set 10. 6015
                                                                                                               CUMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-010-1995
PRICH APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PN0284 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PN3021/95
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: PN3021/95
APPLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-005/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-UN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (516) 742-4343
TELEPRX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.5%;
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Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE, nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     953 TGTATCGCTA 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 rGrArrdcrA 1
GARDEN CITY
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                                                                                    XY: U.S.A.
11530-0299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-488-551B-136
                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: GARDEN CLII
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
TELEFAX: (516) 742-4366
INFORMATION FOR EQ ID NO: 135:
SEQUENCE CRAAACTERISTICS:
LENGTH: 10 base pairs
TTELEFAX: (516) 742-4366
INFORMATION FOR EQ ID NO: 135:
SEQUENCE CLARAACTERISTICS:
LENGTH: 10 base pairs
TTELEFAX: (100 base pairs
TTELEFAX: (100 base pairs
TTELEFAX: 110 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Darle A. McPhee
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Nicholas J. Deacon
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESSE:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 295
US-08-488-551B-136/c
; Sequence 136, Application US/08488551B
; Patent No. 6015661
                                                                           Sequence 135, Application US/08488551B Patent No. 6015661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.5%;
90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               954 GIATCGCTAC 963
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             RESULT 294
US-08-488-551B-135/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-488-551B-135
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US-08-488-551B-192/C
US-08-488-551B-192/C
Sequence 192, Application US/08488551B
Setenn No. 60156A
SERVERAL INFORMATION:
APPLICANT: Dale A. Mochee
APPLICANT: NEW YORK
COMPTR: NEW YORK
COMPTR: NEW YORK
COMPTR: READABLE FORM:
APPLICANTON NUMBER: DALE A. MOCHEE A. MOCHEE A. MOCHEE B. MO
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
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         TELECOMMUNICATION INFORMATION:
TELEPRONE: (516) 742-4343
TELEPRAX: (516) 742-4363
INFORMATION FOR SEQ ID NO: 191:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  933 CCTCCTCTTC 942
                                                                                                                                                                                                                                                                                                                           US-08-488-551B-191
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11.5%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 297

US-08-488-551B-191/C

Sequence 191, Application US/08488551B

Sequence 191, Application US/08488551B

Sequence 191, Natholise

MEDICANT: Natholise J. Deacon

APPLICANT: Dale A. McPhee

APPLICANT: CARABER CITY

STATE: NEW YORK

COUNTRY: U. S.A.

ZIPE TISSOURCES: Flopy disk

COMPUTER REABALE FORM:

MEDIUM TYPE: Flopy disk

COMPUTER REABALE FORM:

MEDIUM TYPE: PC-DOS/MS-DOS

SOFTWARE: PRABALE FORM:

MEDIUM TYPE: PC-DOS/MS-DOS

SOFTWARE: PRABALE FORM:

MEDIUM TYPE: APPLICATION DATA:

APPLICATION NUMBER: WH002 (AU)

FILING DATE: 07-JUN 1995

PRILING DATE: 21-FEB-1994

APPLICATION NUMBER: PN0284 (AU)

FILING DATE: 21-FEB-1995

APPLICATION NUMBER: PN301/95

FILING DATE: 14-FEB-1995

APPLICATION NUMBER: PN301/95

FILING DATE: 14-FEB-1995

APPLICATION NUMBER: PN301/95

FILING DATE: 17-MAY-1995

ATTORNEY/AGENT INFORMATION:

NAME: FRANK S. DIGIGILO

SEFERENCE/DOCKET NUMBER: 9606Z
APPLICATION ...

RILING DATE: 14-FEB-1994
APPLICATION NUMBER: PH002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PN0284 (AU)
FILING DATE: 22-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PN3021/95
RILING DATE: 17-MAY-1995
ATTORNEY AGENT INFORMATION:
NAME: FRANK S. DIGIGLIO
REFERENCE/DOCKET NUMBER: 96062
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4366
INFORMATION FOR SEQ ID NO: 184:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-488-551B-184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          931 TCCCTCCTCT 940
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: NE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
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                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: 0.5.4.

ZIP: 11530-0239

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ELBM PC Compatible
COMPUTER: PIEM PC Compatible
COMPUTER: PERMIT SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: BM364 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PN0284 (AU)
FILING DATE: 12-FEB-1994
APPLICATION NUMBER: BN0284 (AU)
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PN021/95
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PN3021/95
FILING DATE: 14-FEB-1995
ATTORNEY/AGENT INFORMATION:
RAME: FRAMK S. DIGIGILO:
REFERENCE/DOCKET NUMBER: 9606Z
TELECOMMUNICATION INFORMATION:
TELEPRONE: (516) 742-4343
TELEPRONE: (516) 742-4343
TELEFAX: (516) 742-4343
TELEFAX: (516) 742-4343
TELEFAX: CSTONENTICS:
                                                                                                                                                                                                                                        APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhee
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                           SSEE: SCULLY, SCOTT, MURPHY & PRESSER
T: 400 GARDEN CITY PLAZA
GARDEN CITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 8.4; DB 1;
Pred. No. 2e+02;
0; Mismatches
Pred. No. 2e+02;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 300
US-08-488-551B-230/c
'S equence 230, Application US/08488551B
'Patent No. 6015661
'GENERAL INFORMATION:
                                                                                                                                                                       US-08-488-551B-229/c
; Sequence 229, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.5%;
Best Local Similarity 90.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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                                                        932 CCCTCCTCT 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 CATTGGTCTT 1
                                                                                            10 CCCACCTCTT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                        NEW YORK
U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: NE COUNTRY:
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APPLICANT: HAN, YE SUN
APPLICANT: HAN, YE SUN
APPLICANT: KIM, SUNG HOU
APPLICANT: LIM, JAE HWAN
APPLICANT: LIM, JAE HWAN
APPLICANT: LIM, JAE HWAN
APPLICANT: CHOI, IN GENE SEQUENCE OF AQUIFEX PYROPHILUS
TITLE OF INVENTION: SUPERCYIED DISMUTASE AND PROTEIN EXPRESSED IN ESCHERICHIA
TITLE OF INVENTION: COLI
TITLE OF INVENTION: COLI
TITLE OF INVENTION: COLI
TITLE OF INVENTION: COLI
TITLE OF INVENTION: SUPERCYIED DISMUTASE AND PROTEIN EXPRESSED IN ESCHERICHIA
TITLE OF INVENTION: COLI
TITLE OF INVENTION: COLI
TITLE OF INVENTION: COLI
STRESSER: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSER: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
STREET: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Pred. No. 2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: F102Py disk
MEDIUM TYPE: F102Py disk
COMPUTER: ISM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,303
FILING DATE: 16-JAN-1998
CLASSIPICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: J97-1140
FILING DATE: 16-JAN-1997
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 2901-0109-0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: BN3021/95
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGILO
REFERENCE/DOCKET NUMBER: 9606Z
TELECOMONINICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEPAX: (516) 742-4343
TELEPAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 310:
SEQUENCE CHARACTERISTICS:
LENGRICE CHARACTERISTICS:
LENGRICE CHARACTERISTICS:
LENGRICE CHARACTERISTICS:
LENGRICE CHARACTERISTICS:
TELEPAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 310:
SEQUENCE CHARACTERISTICS:
TYPE: NUCLEIC acid
STRANDENES: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NS-09-008-303-3/c

Sequence 3, Application US/09008303

Patent No. 6033889

FRENREL INFORMATION:

APPLICANT: HAN, YE SUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.5%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             908 TITICITIES 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 refrerred 1
                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: DNA US-08-488-5518-310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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Pred. No. 2e+02;
0; Mismatches 1; Indels
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Sequence 310, Application US/08488551B

Patent No. 6015661

Patent No. 6015661

PAPLICANT: Nicholas J. Deacon

APPLICANT: Dale A. McPhee

APPLICANT: Dale A. McPhee

APPLICANT: David Cooper

ITILE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1

NUMBER OF SEQUENCES: 841

CORRESPONDENCE ADDRESS:
ADDRESSE: SCULLY, SCOTT, MURPHY & PRESSER

STREET: 400 GARREN CITY PLAZA

CITY: GARDEN CITY

STATE: NEW YORK

COUNTY: COOPER CITY

STATE: NEW YORK

COMPUTER READABLE PORM:
MEDIUM TYPE: PLOSY MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: DAY-008/488,551B

FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA: PRES-1994

PRILICADION NUMBER: PM4002 (AU)

FILING DATE: 21-FEB-1994

APPLICATION NUMBER: PN0284 (AU)
                                    COMPUTER: A.E., L. COMPUTER: A.E., L. COMPUTER: A.E., L. COMPUTER: A.E., L. C. COMPUTER: A.E., L. C. COMPUTER: PACEDIA RELEASE #1.0, Version #1.25
CURRENT A.PLICATION DATA:
A.PPLICATION NUMBER: US/08/488,551B
FILING A.E. OT-UN-1995
PRIOR A.PPLICATION NUMBER: PM3864 (AU)
FILING DATE: 12-FEB-1994
A.PPLICATION NUMBER: PM022 (AU)
FILING DATE: 21-FEB-1994
A.PPLICATION NUMBER: BN3021/95
FILING DATE: 12-FEB-1995
A.PPLICATION NUMBER: US 08/388,353
FILING DATE: 17-MAY-1995
A.PPLICATION NUMBER: PN3021/95
FILING DATE: 17-MAY-1995
ATTORNEY AGENT INFORMATION:
NAME: FRANK S. DIGIGIO
REFERENCE/DOCKET UNBER: 9606Z
TELEPHONE: (516) 742-4366
INFORMATION FOR SEQ ID NO: 275:
SEQUENCE CHARACTERISTICS:
LEMGTH: 10 base pairs
LEMGTH: 10 base pairs
TTYPE: nucleic acid
TTORNING TINGAL
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.5%;
90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
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Sequence 15, Application US/08675816
Patent No. 6171864
GENERAL INFORMATION:
APPLICANT: Coughlan, Sean J.
TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND USES NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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Pred. No. 2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                            Score 8.4; DB 1; Length 10;
Pred. No. 2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPUTES: TakentIn Felease #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,816
FILING DATE: 05-010-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6711864fenburg, Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 750027.401
REGISTRATION NUMBER: 39,317
REFERENCE DOCKER NUMBER: 750027.401
REPERENCE DOCKER NUMBER: 750027.401
TELECHONE: (206-622-4900
TELEPRA: (206)-682-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39,317
39,317
39,317
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Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (206-622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (206)-682-6031
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
                                                                                                                                                                                                                                                                                                 11.5%;
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Best Local Similarity 90.0.
Thes 9; Conservative
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Best Local Similarity 90.0°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                 90S TCATTTTCTT 914
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                                                                                                                                                                                                                                      linear
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ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
STREET: 70:
CITY: Seat!
                                                                                                                                                                                                                                    ; TOPOLOGY:
US-08-675-816-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-675-816-15
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US-08-675-816-10
Sequence 10. Application US/08675816
Fatent No. 6171864
Fatent No. 6171864
FATEL TREPARATION:
APPLICANT: Coughlan, Sean J.
TITLE OF INVENTION: CALRETICULIN AND CALMEXIN GENES AND PROMOTER REGIONS AND USES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 701 Fifth Ave. Suite 6300
CITY: Seattle

"Magnington
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                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:

APPLICANT: LOPEZ-NIETO, CARLOS E
APPLICANT: LOPEZ-NIETO, CARLOS E
APPLICANT: MIGAM, SANJAY KUMAR
TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
FILE REFERENCE: 2458-4029
CURRENT APPLICATION NUMBER: US/08/522,384
CURRENT PILING DATE: 1996-11-15
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 11
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Primer
                                                                                                                                                        Query Match 11.5%; Score 8.4; DB 1; Length 10; Best Local Similarity 90.0%; Pred. No. 2e+02; Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.5%; Score 8.4; DB 1; Length 10; illarity 90.0%; Pred. No. 2e+02; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
US/08/675,816
FILING DATE: .05-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/08522384 Patent No. 6110667
                                                                            ; TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic) US-09-008-303-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Unknown Organism
                 10 base pairs
                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                          933 CCTCCTCTTC 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    933 CCTCCTCTTC 942
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-522-384-11
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schultz1-899.rn:
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11.5%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 2e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS S.O
SOFTWARRE: WORD Ferfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,011B
FILING DATE: 05-UUL-1995
CLASSIFICATION: CURNOWN-
PRIOR APPLICATION NUMBER: 07/882,438
FILING DATE: May 13, 1993
APPLICATION NUMBER: 08/08,766
FILING DATE: May 13, 1993
APPLICATION NUMBER: 08/060,952
APPLICATION NUMBER: 08/060,952
APPLICATION NUMBER: 08/060,952
FILING DATE: May 13, 1993
ATTORNEY/AGENT INFORMATION:
NAME: WATDUEY, RICHARD J.
REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
TELECOMMUNICATION NUMBER: 32,327
                                      CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09154750A; Sequence 4, Application US/09154750A; Bettert No. 6432640; Bettert No. 6432640; APPLICANT: Vogelstein, Bert APPLICANT: Winzler, Kenneth APPLICANT: Winzler, Kenneth APPLICANT: POLYAK, Kornella TITLE OF INVENTION: D53-Induced Apoptosis; FILE REFERENCE: 1107.75357; CURRENT APPLICATION NUMBER: 06/059,153 FILE RIGHTON TILING DATE: 1998-09-17; PRIOR PILING DATE: 1999-03-30; NUMBER OF SEQ ID NOS: 93; SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 4; LENGTHUS NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDESS: aingle

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-08-464-0118-11
                  Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHREACTERISTICS:
LENGTH: 10
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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) ORGANISM: Homo sapiens
US-09-154-750A-4
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US-09-154-750A-4
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                                                  Sequence 11, Application US/08464011B
Patent No. 6568789
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Michael D. West
Mocdaring E. Wright
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
RELARIED TO TELOMERE LENGTH AND/OR
TELOMERASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.5%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 2e+02; tive 0; Mismatches 1; Indels
                Sequence 4, Application US/08894324A Patent No. 6204437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: DNA (genomic); ORIGINAL SOURCE:
; ORGINAL SOURCE:
; ORGANISM: TCA MOTIF
US-08-894-324A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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     US-08-894-324A-4
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CTHER INFORMATION: Theoretical sequence designed to show proper and improper joining OTHER INFORMATION: elements
US-09-914-259-129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE:
, OTHER INFORMATION: Hypothetical sequence to demonstrate application.
US-09-709-596A-7
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Pred. No. 2e+02;
0; Mismatches 1; Indels
                                                                                           Sequence 7. Application US/09709596A

Betent No. 6458945

GENERAL INFORMATION:
APPLICANT: Variagenies, Inc.
TITLE OF INVENTION: A Method for Analyzing Polynucleotides
FILE REFERENCE: 258/239

CURRENT FILING DATE: 2002-02-1

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Variagenics, Inc.
TITLE OF INVENTION: A Method for Identifying Polymorphisms
FILE REFERENCE: 257/078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Sequence 129, Application US/09914259 | Sequence 129, Application US/09914259 | Patent No. 649536 | GENERAL INFORMATION: | APPLICANT: Makowski, Lee | APPLICANT: Williams, Mark | TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES | TITLE FERENCE: 8471-010-99/914,259 | CURRENT APPLICANION NUMBER: US/09/914,259 | CURRENT FILING DATE: 2000-11-21 | NUMBER OF SEQ ID NOS: 180 | SOFTWARE: FastSEQ for Windows Version 4.0 | SEQ ID NO 129 | LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09655104A Patent No. 6500650 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.5%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 90.0
Matches 9; Conservative
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Matches 9; Conserv
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                                                                  RESULT 312
US-09-709-596A-7
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NUMBER OF SEQ ID NOS: 78
SOFTWARE: PATENTH Ver. 2.1
SEQ ID NO 61
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , OTHER INFORMATION: Hypothetical sequence to demonstrate application. US-09-394-457C-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ), OTHER INFORMATION: Description of Artificial Sequence: Customized
), OTHER INFORMATION: oligonucleotide
US-09-261-115-61
                                                .
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0
                                                                                                                                                                                                                      Sequence 7, Application US/09394457C;
Patent No. 6440705;
Patent No. 6440705;
GENERAL INFORMATION:
APPLICANT: Variagenics, Inc.
TITLE OF INVENTION: A Method for Analyzing Polynucleotides
FILE REFERENCE: 246/020
CURRENT FILING DATE: 1999-09-10;
NUMBER OF SEQ ID NOS: 16;
SOFTWARE: Patentin version 3.1;
SEQ ID NO 7;
LENGTH: 10
Score 8.4; DB 1; Length 10; Pred. No. 2e+02; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 8.4; DB 1; Length 10;
Pred. No. 2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 8.4; DB 1; Length 10;
Pred. No. 2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 61, Application US/09261115
Patent No. 6458584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: MIRZABEKOV, ANDREI
APPLICANT: GUSCHIN, DMITRY Y.
APPLICANT: GUSCHIN, ALEKSEI
APPLICANT: POTIN, ALEKSEI
APPLICANT: POTIN, ALEKSEI
APPLICANT: POTIN, ALEKSEI
APPLICANT: YERSHOV, GENNADIY
APPLICANT: LYSOV, YU
    11.5%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.5%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.5%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 90.0
Matches 9, Conservative
                         Best Local Similarity 90.0
Matches 9; Conservative
                                                                                         932 CCCTCCTCT 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           929 TATCCCTCCT 938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    915 TGGTCTTTGC 924
                                                                                                                                    1 ccccccrcrr 10
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                                                                                                                                                                                                    RESULT 310
US-09-394-457C-7
         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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CURRENT APPLICATION NUMBER: US/09/655,104A CURRENT FILING DATE: 2000-09-05 NUMBER OF SEQ ID NOS: 25 SSOUTHARE: Patentin version 3.1 SEQ ID NO 7 LENGTH: 10
Mon Oct 18 14:40:1/ 2004
                                                                                                                                                                                                                                                                   TYPE: DNA
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ö Gaps OTHER INFORMATION: Hypothetical sequence to demonstrate application. ö Query Match
11.5%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels ORGANISM: Artificial Sequence FEATURE: 929 TATCCCTCCT 938 1 TATTCCTCT 10 US-09-867-915-22/c US-09-655-104A-7 ò

APPLICANT: Generation:
APPLICANT: Generation:
APPLICANT: Generation:
APPLICANT: Finkel, Kevin
APPLICANT: Forkel, Kevin
APPLICANT: Forkel, Kevin
APPLICANT: Lee, Helen H.
TITLE OF INVENTION: HAPLOTYPES OF THE AGTRI GENE
FILE REPERRANCE: AGTR1-1136 test
CURRENT FILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: 60/228,542
PRIOR FILING DATE: 2000-08-28
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 22
LENGTH: 10 Sequence 22, Application US/09867915 Patent No. 6521747 GENERAL INFORMATION: TYPE: DNA

0; Gaps 11.5%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 2e+02; tive 0; Mismatches 1; Indels Query Match
Best Local Similarity 90.0
Matches 9; Conservative ; ORGANISM: Homo sapiens US-09-867-915-22

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902 TGGTCATTTT 911 10 recrearity 1 g à

RESULT 316
US-09-394-467-7
US-09-394-467-7
Sequence 7, Application US/09394467
Sequence 7, Application US/09394467
Setent No. 6566059
GENERAL INFORMATION:
APPLICANT: VARIAGENICS, Inc.
TITLE OF INVENTION: A Method for Analyzing Polynucleotides
FILE REFERENCE: 245/287
CURRENT APPLICATION NUMBER: US/09/394,467
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 14
SOFTWARR: PatentIn Version 3.0
SEQ ID NO 7
LENGTH: 10

TYPE: DNA ORGANISM: Artificial Sequence

; OTHER INFORMATION: Used to demonstrate how indicated aspect of invention works. US-09-394-467-7 FEATURE:

ô Gaps ; FEATURE: ; OTHER INFORMATION: Hypothetical sequence to demonstrate application. US-10-104-818-7 ö RESULT 317

US-10-104-0810-7

i Sequence 7, Application US/10104818

Patent No. 658223

GENERAL INFORMATION:

APPLICANT: VARIGON: A Method for Analyzing Polynucleotides

TITLE OF INVENTION: A Method for Analyzing Polynucleotides

TITLE OF INVENTION: A Method for Analyzing Polynucleotides

CURRENT PRICATION UNMER: US/10/104,818

CURRENT FILING DATE: 209-05-14

PRIOR APPLICATION UNMER: 09/394,774

PRIOR FILING DATE: 1999-09-10

NUMBER OF SEQ ID NOS: 16

SOFTWARE: PatentIn Version 3.1

SEQ ID NO 7 Score 8.4; DB 1; Length 10; Pred. No. 2e+02; 0; Mismatches 1; Indels 11.5%; 90.0%; TYPE: DNA ORGANISM: Artificial Sequence Query Match
Best Local Similarity 90.0
Matches 9; Conservative 1 TATTCCTCCT 10 929 TATCCCTCCT LENGTH: 10 ò g

. 0 Query Match 11.5%; Score 8.4; DB 1; Length 10; Best Local Similarity 90.0%; Pred. No. 2e+02; Matches 9; Conservative 0; Mismatches 1; Indels

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929 TATCCCTCCT 938 1 TATTCCTCT 10 ò d CRS-05-989-789-1659/C

18-09-989-789-1659/C

18-09-989-789-1659/C

18-09-989-789-1659/C

18-09-989-789-1659/C

18-09-989-789-1659/C

18-09-989-789-1659/C

18-09-18-09-18-09-18-09/C

18-09-18-09-18-09/C

18-09-18-09-18-09/C

18-09-18-09-18-09/C

18-09-18-09/C

1 TYPE: DNA ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFERMATION: DNA
US-09-989-789-1659 .. 0 11.5%; Score 8.4; DB 1; Length 10; 90.0%; Pred. No. 2e+02; tive 0; Mismatches 1; Indels Query Match
Best Local Similarity 90.07

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RESULT 319

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) MOLECULE TYPE: other nucleic acid US-08-344-695-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Kelber, Steven B.
REGISTRATION NUMBER: 30,073
REFRENCE/DOCKET NUMBER: 2747
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.5%;
90.0%;
               Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 11.5
Best Local Similarity 90.0
Matches 9; Conservative
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EDNESS: unknown
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                                                                                                926 TITTATCCCT 935
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U
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                                                                                                                                                                                                                                                                                                                                              ) OTHER INFORMATION: Description of Artificial Sequence: example target; OTHER INFORMATION: DNA US-09-989-789-1663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
    Sequence 163, Application US/09989789

Patent No. 6588746
GENERAL INFORMATION:
APPLICANT: LIU, Qiang
APPLICANT: LIU, Qiang
TITLE OF INVENTION:
FILE REPRENCE: 8325-0011.20 / S11-US2
CURRENT APPLICATION NUMBER: US/09/989,789
CURRENT FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1663
LENGTH: 10
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0
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Patent No. 5614398
Patent No. 5614398
Patent No. 5614398
Patent No. 5614398
Patent No. 580CHTA, DAVID
PAPLICANT: WARREN, WILLIAM
APPLICANT: WARREN, WILLIAM
APPLICANT: ATKINSON, PETER
ITILE OF INVENTION: A GENE TRANSFER SYSTEM FOR INSECTS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 8.4; DB 1; Length 10;
Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: P.C.
1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,695
FILING DATE: 18-NOV-1994
CLASSIPICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown

MOLECULE TYPE: other nucleic acid
US-08-344-695-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Kelber, Steven B.
REGISTRATION NUMBER: 30,073
REFRENCE/DOCKET NUMBER: 2747.
TELECOMMUNICATION: TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 90.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (703) 413-2220
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   933 CCTCCTCTTC 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U.S.A.
US-09-989-789-1663/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 320
US-08-344-695-24/c
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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                                               Gaps
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                                                                                                                                                                                       Sequence 25, Application US/08344695

Sequence 25, Application US/08344695

Sequence 25, Application US/08344695

Sequence 25, Application US/08344695

SERERAL INFORMATION:
APPLICANT: O'BROCHTA, DAVID
APPLICANT: ATKINGON, PERS
TILLE OF INVENTION: A GENE TRANSFER SYSTEM FOR INSECTS
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STREET: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 8.4; DB 1; Length 11; Pred. No. 2.2e+02; 0; Mismatches 1; Indels
Length 11;
                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 26, Application US/08344695
; Sequence 26, Application US/08344695
; Parent No. 5644398
; GENERAL INFORMATION:
APPLICANT: WARREN, WILLIAM
APPLICANT: ATKINSON, PETER
TITLE OF INVENTION: A GENE TRANSFER SYSTEM FOR INSECTS
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,695
FILING DATE: 18-NOV-1994
CLASSIFICATION: 536
Score 8.4; DB 1;
Pred. No. 2.2e+02;
0; Mismatches 1.
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                       11.5%; Score 8.4; DB 1; Length 11; 90.0%; Pred. No. 2.2e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                          unknown
E: other nucleic acid
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US-08-344-695-29
      REFERENCE/DOCKET NUMBER: 274
TELECOMONICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-220
TELEFAX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          926 TITTAICCCT 935
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                                                                                                                                                                                                                                                                                          ; TOPOLOGY: un;
; MOLECULE TYPE:
US-08-344-695-27
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US-08-344-695-29
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APPLICANT: WARREN, DAVID
APPLICANT: WARREN, MILLIAM
APPLICANTON: A GENE TRANSFER SYSTEM FOR INSECTS
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: DELON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 & Jefferson Davis Highway, Suite 400
CITY: Arlington
STREET: U.S.A.
COUNTRY: U.S.A.
ALINGTON TO SA.A.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,695
FILING DATE: 18-NOV-1994
CLASSIFICATION: S36
ATTORNEY/GENT INFORMATION:
NAME: Kelber, Steven B.
REGISTRATION NUMBER: 30,073
CORRESPONDENCE ADDRESS:
ADDRESSE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
11.5%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                    COMPUTER EARABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,695
FILING DATE: 18-NOV-1994
CLASSIPICATION: 536
ATTORNEY AGENT INFORMATION:
NAME: Kelber, Steven B.
REFERENCE/DOCKET NUMBER: 2747-058-27
TELEPHONE: (703) 413-220
TELEPHONE: (703) 413-220
TELEPHONE: (703) 413-220
TELEPHONE: (703) 413-220
TELEPHONE: CARACTERISTICS:
LENGTH: 11 base pairs
TYPE: Incleic caid
STRANDEDNESS: unknown
MITERITER TANDE UNKNOWN
MITERITER 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: other nucleic acid
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; Sequence 27, Application US/08344695
; Patent No. 5614398
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Score 8.4; DB 1; Length 11;
Pred. No. 2.2e+02;
0; Mismatches 1; Indels
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Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C.-G.
APPLICANT: W
                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMER:
FILING DATE: 105/08/152,443A
FILING NUMBER: 33,943
REPRENCE/COCKET NUMBER: 33,943
RELEPHONE: (415) 813-5600
TELEFAX: (415) 813-5600
TELEFAX: (415) 813-5600
TELEFAX: (415) 813-5600
TELEF AT 706141
INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRESPONDENCE ADDRESS:
STREET: 510 EAST 73RD STREET,
CITY: NBW YORK
STATE: NBW YORK
COUNTRY: USA
COMPUTER: NBW YORK
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFWWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
PRIOR APPLICATION 1957
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
REGISTRAITON NUMBER: 26,179
REFERENCE/DOCKET NUMBER: 26,179
REFERENCE/DOCKET NUMBER: 26,179
                                                                            ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDIUFER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         930 ATCCCTCCTC 939
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California
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US-08-173-489C-64
                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
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APPLICANT: BARR, PHILIP J.
APPLICANT: SHAPINO, JOHN P.
TITLE OF INVENTION: NOVEL FAS FROTEIN AND METHODS OF USE TITLE OF INVENTION: THERROF NOVEL FAS FROTEIN AND METHODS OF USE TITLE OF INVENTION: THERROF NOVELS: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER STREET: 755 Page Mill Road CITY: Palo Alto
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: CALL STATE OF THE STAT
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90.0%; Pred. No. 2.2e+02;
tive 0; Mismatches 1.
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APPLICATION NUMBER:
FILING DATE: 15-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                     ; Sequence 16, Application US/08444231
; Patent No. 5652210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS: LENGTH: 11 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             930 ATCCCTCTC 939
         1 TITCAICCCI 10
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US-08-444-231-16
                                                                                                                                          RESULT 325
US-08-444-231-16/c
         С
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US-08-173-489C-121

US-08-173-489C-121

US-08-173-489C-121

US-08-173-489C-121

US-08-121-1 Application US/08173489C

PREDICANT: HERBURN, A. G.

APPLICANT: HERBURN, A. G.

APPLICANT: HERBURN, A. G.

TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA TITLE OF INVENTION: TALPLE-STRAND FORMATION.

NUMBER OF SEQUENCES: 365

CORRESPONDENCE ADDRESS:

ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC., STREET, SIQ RAST 73RD STREET,
CITY: NEW YORK

COUNTY: NEW YORK

STATE: NEW YORK

COUNTY: NEW YORK

STATE: NEW YORK

CONFUTER: LEADABLE FORM:

MEDIUM TYPE: 3. inch, 1.44MD storage

COMPUTER: BEADABLE FORM:

MEDIUM TYPE: 3. inch, 1.44MD storage

COMPUTER: DOTE TOWN NUMBER: US-07/968,436

FILING DATE: 2. DEC 1993

CLASSIFICATION NUMBER: US-07/968,436

FILING DATE: 2. DEC 1993

CLASSIFICATION NUMBER: US-07/968,436

FILING DATE: 2. DCT 1992

ATTORNEY-AGENT NUMBER: US-1880

TELEPHONE: GALCOMPY) (212) 246-8959

INFORMATION FOR SEQ ID NO: 121:

SEQUENCE CHARACTERISTICS:

LENGTH 1 base pairs

TYPE: NICH ASIGNATION:

TELEPHONE: LENGTH 1 base pairs

TYPE: NICH ASIGNATION:

TELEPHONE: LENGTH NUMBER: US-07/968,436

TYPE: NICH ASIGNATION:

LENGTH 1 base pairs

TYPE: NICH ASIGNATION:

TELEPHONE: LENGTH NUMBER: US-07/968,436

TYPER: NICH ASIGNATION:

LENGTH 1 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
11.5%; Score 8.4; DB 1; Length 11
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
POSITION IN GENOME:
CHROMOSOME/SEGMENT: chromosome 18
MAP POSITION: 18q11.2-12.1
PUBLICATION INFORMATION:
AUTHORS: M.
AUTHORS: M.
TITLE: Structure and expression of
TITLE: the mutant prealbunin gene associated with
TITLE: familial amyloidotic polyneuropathy
JOURNAL: Molecular Biological Medicine
VOLUME: 3 29-338
                                                                                                                                                                                                                                                                                                                                      | PAGES: 329-338
| DATE: 1986
| RELEVANT RESIDUES IN SEQ ID NO: 99 :FROM 1 TO 11
| US-08-173-489C-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: genomic DNA
DESCRIPTION: alpha-2-globin gene (accession
DESCRIPTION: V00516) nucleotides 139 to 149
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 926 TITTATCCCT 935
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                                                                                                                                                                             SIGNATORY:

DESCRIPTION: third strand derived from gamma-
DESCRIPTION: third strand derived from gamma-
DESCRIPTION: crystallin sequence region in Seq ID No. 586124463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 11.5%; Score 8.4; DB 1; Length 11; Best Local Similarity 90.0%; Pred. No. 2.2e+02; Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-173-489C-99
; Sequence 99, Application US/08173489C
; Patent No. 5861244
; Generation: Mand, C. -G.
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G. -G.
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
; STREET: NEW YORK
; STATE: NEW YORK
; STATE: NEW YORK
                                                                                                                                                                                                                                                                                               HYPOTHETICAL: Yes

MATI-SENSE: No

PUBLICATION INFORMATION:

RELEVANT RESIDUES IN SEQ ID NO: 64 :FROM 1 TO 11
US-08-173-489C-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 10021.
ZIP: 10021.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION NUMBER: US/08/173,489C
FILING DATE: 20 DC 1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 20 OCT 1992
ATTORNEY APPLICATION NUMBER: US 07/968,436
FILING DATE: 20 OCT 1992
ATTORNEY ABOUT INFORMATION:
NAME: Handelman, JOSEPH H.
REFERENCE/DOCKET NUMBER: U9518-6
TELEPRANE (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDENESS: double stranded
STRANDENESS: Gooble stranded
STRANDENESS: GOOBLE STRANDENES
                                                          INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGHH: 11 bases
TYPE: Nucleic Acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  920 TITGCCTTTT 929
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ORIGINAL SOURCE:
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GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Gristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: WICLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                           COUNTRY: CALLICOLIDA

COUNTRY: CALLICOLIDA

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: Storage

COMPUTER: IBM COMPATIBLE

COMPUTER: EBM COMPATIBLE

COMPUTER: FEATSON FOR WINDOWS 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/460,890A

FILING DATE: DATE: 1995

CLASSIFICATION AND ST. 1995

FILING DATE: DECEMBER: 0/167,641

FILING DATE: MARCH 20, 1993

APPLICATION NUMBER: 07/855,389

FILING DATE: MARCH 20, 1993

APPLICATION NUMBER: 07/855,389

FILING DATE: MARCH 19, 1993

APPLICATION NUMBER: PCT/US91/02725

FILING DATE: MARCH 19, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: Other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-460-890A-16
; Sequence 16, Application US/08460890A
; Patent No: 5994109
; GENERAL INFORMATION:
Sequence 2, Application US/08460890A
Patent No. 5994109
                                                                                                                                                                                                                                       ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REPERCOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEX: (67-3510
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
EDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                   Score 8.4; DB 1; Length 11;
Pred. No. 2.2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-U8-29-571-5/7-5/7
Sequence 57. Application US/08590571
Patent No. 5861246
GENERAL INFORMATION:
APPLICANT: Sherman Weissman and Girish N. Nallur
TITLE OF INVENTION: MULTIPLE SELECTION PROCESS
NUMBER OF SEQUENCES:
ADDRESSE: Yahwak & Associates
STREET: 25 Skyrop Drive
CTTY: Trumbull
STREET: Osnecticut
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIOM TYPE: floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/590,571
                                                                                                                                                                               ; DATE: 1981.
; RELEVANT RESIDUES IN SEQ ID NO: 121 :FROM 1 TO 11
US-08-173-489C-121
                                                  Hechtman, R L.
                                              AUTHORS: Orkin, S H, Goff, S C, Hechtman, R L. TITLE: Mutation in an intervening TITLE: Sequence splice junction in man JOURNAL: Proceedings of the National Academy of JOURNAL: Sciences, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak
REGISTRATION NUMBER: 26,824
REFERENCE/DOCKET UNMER: Yale
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (203)268-1951
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative C
      ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
AUTHORS: Orkin, S H, G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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; MOLECULE TYPE: DNA
US-08-590-571-57
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Best Local Similarity
Matches 9; Conserv
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US-08-590-571-57/c
                                                                                                                                                           VOLUME:
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. 0 Gaps 0 11.5%; Score 8.4; DB 1; Length 11; 90.0%; Pred. No. 2.2e+02; tive 0; Mismatches 1; Indels APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richad J.
APPLICANT: Gritchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND OTHER INFORMATION: "C" stands for 5-methylcytosine

RESULT 331 US-08-460-890A-2

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Gaps
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US-08-167-461C.
US-08-167-461C.
Patent No. 6033884

APPLICANT: Swith, Louis C.
APPLICANT: Swith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE 400
STREET: Suite 4700
CITY: Los Angeles
STREET: Suite 4700
CONDURY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: EMCOMPATIBLE
COMPUTER: EMESTATION COMPATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,641C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 90.0%; Pred. No. 2.2e+02; Matches 9; Conservative 0; Mismatches 1.
          COUNTRY: U.S.A.

ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS S.O
SOFTWARE: FastSEQ for Windows 2.O
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,641C
FILING DATE: December 14, 1993
CLASSIPICATION DATA:
APPLICATION NUMBER: 0'855.389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
APPLICATION NUMBER: 20,1993
APPLICATION NUMBER: 205/012
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard U.
REGESTRATION NUMBER: 205/012
TELEPHONE: (213) 955-0440
TELEPHONE: (213) 955-0440
TELEFRAX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TELENGTH: 11 base pairs
TELENGTH: 11 base pairs
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: Other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   931 TCCCTCCTCT 940
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US-08-167-641C-16
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Patent No. 6033884

GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Gritiano, Richard J.
APPLICANT: Gritiano, Richard J.
APPLICANT: Gottchark, Stephen
ITTLE OF INVENTION: NUCLEIC FOR USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.5%; Score 8.4; DB 1; Length 11; 90.0%; Pred. No. 2.2e+02; tive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ); OTHER INFORMATION: "C" stands for 5-methylcytosine US-08-460-890A-16
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STREET: Scalifornia
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Journal English
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: BROOMBER: US/08/460,890A
MEDIUM TYPE: TRESTEM: 1995
CURRENT APPLICATION NUMBER: US/08/460,890A
FILING DATE: December 14, 1993
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 10, 1993
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 10, 1993
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 10, 1993
ATTORNEY/AGENT INFORMATION:
TELEFAM: (213) 489-1600
TELEFAM: (213) 489-1600
TELEFAM: (213) 955-0440
TELEFAM: (213) 955-0440
TELEFAM: (213) 955-0440
TELEFAM: MARACTERISTICS:
LENGTH 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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US-08-167-641C-2
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Sequence 15, Application US/0879331
| Sequence 15, Application US/0879331
| Patent No: 6071877
| Patent No: 6071877
| GENERAL INFORMATION:
| APPLICANT: DELECLUSE, ARMELLE
| APPLICANT: THIERY, ISABELLE
| TITLE OF INVENTION: INSECTS OF THE DIPFERAE FAMILY
| TITLE OF INVENTION: INSECTS OF THE DIPFERAE FAMILY
| FILE REFERENCE: 6660-0116-0 PCT
| CURRENT APPLICATION NUMBER: 1997-05-13
| CURRENT FILING DATE: 1997-05-13
| FARLIER PELIGN DATE: 1995-08-25
| EARLIER APPLICATION NUMBER: FR 94/10299
| EARLIER APPLICATION NUMBER: FR 94/10299
| SARLIER PILING DATE: 1994-08-25
| SOFTWARE: PATENTING DATE: 1994-08-25
                                                                                                                                                                                                                                                                Gaps
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Patent No. 6150168

GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Gottehank, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 1056Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence:RIBOSOME; OTHER INFORMATION: BINDING SITE (FIGURE 5)
US-08-793-331-15
                                                                                                                                                                                             11.5%; Score 8.4; DB 1; Length 11; 90.0%; Pred. No. 2.2e+02; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 11.5%; Score 8.4; DB 1; Length 11; Best Local Similarity 90.0%; Pred. No. 2.2e+02; Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                           Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                           925 CTTTTATCCC 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      932 CCCTCCTCTT 941
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                                                                                                                                                                                                                                                                                                                                                                                                              10 cerrrarcce
                      ; STRANDEDNESS: si.
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-906-691-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-460-971A-2
                                                                                                                                                                                                     Query Match
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US-08-906-691-44/C
15 Sequence 44, Application US/08906691
5 Patent No. 6066452
5 Patent No. 6066452
5 Patent No. 6066452
5 Patent No. 6066452
6 Patent No. 6066452
7 Tribe OF INVENTION: MULTIPLEX SELECTION TECHNIQUE FOR TITLE OF INVENTION: MULTIPLEX SELECTION TECHNIQUE FOR TITLE OF INVENTION: IDENTIFYING PROTEIN-BINDING SITES FOR DNA-BINDING PROTEINS NUMBER OF SEQUENCES: 50
7 CORRESPONDENCE ADDRESS:
7 CORRESPONDENCE ADDRESS:
7 CORRESPONDENCE ADDRESS:
7 TREET: 6300 Columbia Center, 701 Fifth Avenu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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ZIP: 981094
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,691
FILING DATE: 31-JUL-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6066452tenburg Ph.D., Carol
REFERENCE/DOCKET NUMBER: 39036.403C1
TELEFOND: (206) 622-4900
TELEFAK: (206) 622-4900
TELEFAK: (206) 622-631
TELEFAK: (206) 622-631
TELEFAK: (206) 622-631
TELEFAK: (206) 622-631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: "C" stands for 5-methylcytosine
FILING DATE: December 14, 1993
CLASSIFICATION: 435
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/855,389
FILING DATE: MARCH 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: MARCH 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 205/012
REFERENCE/DOCKET NUMBER: 205/012
TELEPHONE: (213) 489-1600
TELEFRAX: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 11.5
Best Local Similarity 90.0
Matches 9; Conservative
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nucleic acid
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APPLICANT: Smith Louis C.
APPLICANT: Smith Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gristiano, Richard J.
APPLICANT: MUCLEIC ACID TRANSPORTER SYSTEMS AND TITLE OF INVENTION: METHODS OF USE NUMBER OF SEQUENCES: 65
CORRESPONDENCES: 65
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
CITY: Los Angeles
STREET: Galifornia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
11.5%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: "C" stands for 5-methylcytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY.

COUNTRY.

ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: storage
COMPUTER: IBM COMPATIALE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTENG FOR WINGOWS 2.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/462,040
FILING DATE: June 5, 1995
CLASSIFICATION NUMBER: 08/167,641
APPLICATION NUMBER: 08/167,641
APPLICATION NUMBER: 07/955,389
FILING DATE: MARCH 19, 1993
APPLICATION NUMBER: 07/955,389
FILING DATE: MARCH 19, 1993
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: MARCH 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: WARDURG, Richard J.
                                                            FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/85,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: 07/85,389
FILING DATE: March 19, 1993
ATTORNEY AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REERENCE/DOCKET NUMBER: 32,327
REERENCE/DOCKET NUMBER: 212/063
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MUSCULE TYPE: Other nucleic acid
                                        08/167,641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-462-040-2
; Sequence 2. Application US/08462040
Patent No. 6177554
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          931 TCCCTCCTCT 940
                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-460-971A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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US-08-400-571A-16

ESTEREL NO. 6150168

GENERAL INPORMATION:

APPLICANT: WOO. Savio L.C.

APPLICANT: Smith, Louis C.

APPLICANT: Smith, Louis C.

APPLICANT: Gavio L.C.

APPLICANT: Gavio L.C.

APPLICANT: Smith, Louis C.

APPLICANT: Smith, Louis C.

APPLICANT: Smith, Louis C.

APPLICANT: Smith, Louis C.

APPLICANT: METHODS OF USE

NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDERSOS:

ADDRESSEE: Lyon & Lyon

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

CONDUTER: LAM Compatible

COMPUTER: LAM Compatible

CORPUTER: LAM COMPATIBLE

SOFTWARE: FastSEQ for Windows 2.0

CURRENTING SYSTEM: 18M Compatible

CORPUTER: LAM COMPATIBLE

CORPUTER: LAM COMPATIBLE

SOFTWARE: FastSEQ for Windows 2.0

CURRENT APPLICATION NUMBER: US-08/08/460,971A

FILING DATE: JUNE 5, 1995

COLORATION NUMBER: US-08/08/460,971A

FILING DATE: JUNE 5, 1995

COLORATION NUMBER: US-08/08/460,971A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
11.5%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: "C" stands for 5-methylcytosine US-08-460-971A-2
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,971A
FILING DATE: Une 5, 1995
CLASSIPFCATION A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
APPLICATION NUMBER: 20, 1993
APPLICATION NUMBER: 32,327
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
TELEPHONE (213) 955-0440
ITELEFAX: (213) 955-0440
ITELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 2:
ENGURNCE CHARACTERISTICS:
IENGTH: 11 base pairs
ITELERY: ATTORNEY STRAIL STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              931 TCCCTCCTCT 940
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; OTHER INFORMATION: Description of Artificial Sequence: Homopyrimidine; OTHER INFORMATION: Oligonucleotide
US-09-358-664-1
                                                                                                                                                                                                    Ouery Match
11.5%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 90.0%; Pred. No. 2.2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.5%; Score 8.4; DB 1; Length 11;
                                                                   TOPOLOGY: linear:
| MOLECULE TYPE: Other nucleic acid | FRATURE: |
| FRATURE: | OTHER INFORMATION: "C" stands for 5-methylcytosine US-08-462-040-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , OTHER INFORMATION: Synthetic Oligonucleotide. US-08-722-015A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
       LENGIH: 11 base pairs
                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                    931 TCCCTCCTCT 940
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US-09-358-664-1
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LENGTH: 11
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US-08-462-040-16

Sequence 16, Application US/08462040

Patent No. 6177554

GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gritiano, Richard J.
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND TITLE OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                            11.5%; Score 8.4; DB 1; Length 11; 90.0%; Pred. No. 2.2e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: "C" stands for 5-methylcytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,641
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/078
TELEOPMUNICATION INFORMATION:
TELEPHONE: (213) 469-1600
TELEFAX: (213) 955-0440
TELEFAX: (713) 955-0440
TELEFX: 67-3510
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM COMPALIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,040
FILING DATE: Unne 5, 1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/078
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                              MOLECULE TYPE: Other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (213) 489-1600
TELERAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,3
                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       931 TCCCTCCTCT 940
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STATE: California
                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                   US-08-462-040-2
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                                                                                                                                                                                                                                                                                                           FEATURE:
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OSCITATE 4, Application US/08722015A
Patent No. 637981
GENERAL INFORMATION:
APPLICANT: FOUCHIER: A.M.
APPLICANT: SCHUILE MAKEN, GOADANA
TITLE OF INVENTION: INDUCING AND NON SYNCYTIUM INDUCING VARIANTS OF THE HUMAN IMMUNOI
FILE REFERENCE: 9250.25
CURRENT FILING DATE: 1996-11-19
NUMBER OF SEC ID NOS: 258
NUMBER OF SEC ID NOS: 258
SOFTWARE: Patentin version 3.1 . 0 ö Sequence 1, Application US/09358664

Batent No. 6495320

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LOCKHART, DAVID J.
APPLICANT: LAI, CHAO-QIANG
APPLICANT: GUNDERSON, KEVIN
FILE REFERENCE: 23879:0004
CURRENT APPLICATION NUMBER: US/09/358,664
CURRENT FILING DATE: 1999-07-21
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver: 2.1 Gaps Gaps

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RESULT 345
US-08-031-147A-20/c

| Sequence 20, Application US/08031147A |
| Patent No. 5514577 |
| GENERAL INFORMATION: |
| APPLICANT: Draper et al. |
| TITLE OF INVENTION: | Modulating the Effects of Herpesviruses |
| TITLE OF SEQUENCES: |
| OWBERS OF SEQUENCES: |
| ADDRESSEE: | Woodcock Washburn Kurtz |
| ADDRESSEE: | Mackiewicz & No. 5514577ris |
| STREET: One Liberty Place - 46th Floor |
| CITY: | Philadelphia |
| STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.5%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MD STORAGE
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
SOFTWARE: IBM PS/2
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/031,147A
FILING DATE: MACCAL 12, 1993
CLASSIFICATION DATA:
APPLICATION NUMBER: 485,297
FILING DATE: February 26, 1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 952,1992
FILING DATE: SEPEMBER: 954,185
FILING DATE: SEPEMBER: 954,185
FILING DATE: SEPEMBER: 954,185
APPLICATION NUMBER: 954,185
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REGISTRATION NUMBER: 32,257
REDEPHONE: (215) 568-3499
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                  TELEX:
INPOMBATION: 00: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: circular
FEATURE:
         202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Conservative
                                         202-371-8856
                                                                                                                                                                                                                                                                                                  NAME/KEY:
COCATION:
DENTIFICATION METHOD:
COTHER INFORMATION:
US-07-668-517-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               905 TCATTTTCTT 914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 TTATTTTCTT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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'US-07-668-517-44

'Sequence 44, Application US/07668517

'Patent No. 5262309

'GENERAL INFORMATION:
'TITLE OF INVENTION: No. 5262309el Physiologically Active

TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism

TITLE OF INVENTION: Polypeptide, Recombinant Plasmid, Recombinant Microorganism

TITLE OF INVENTION: Polypeptide, Recombinant Microorganism

TITLE OF INVENTION: Cell, Pharmaceutical Composition and Method of Recovering

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

STREET: 805 Fifteenth Street, N.W., #700

STREET: B.C.

COUNTRY: U.S.A.

ZIP: 2005

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb

COMPUTER: IBM Compatible

OPERATING SYSTEM: MS.DOS

SOFTWARE: DisplayWrite

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 19910322

CLASSIFICATION SATA:

PRIOR APPLICATION NUMBER:

PATTER DATE: D
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                                     Gaps
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11.5%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred, No. 2.2e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
   Pred. No. 2.2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                            FACESTIANCE NO. 5422251
FACENT NOWBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
FILING DATE: 28-JAN-1994
FILING DATE: 28-JAN-1994
FILING DATE: 27-FEB-1992
APPLICATION NUMBER: 841,218
FILING DATE: 27-FEB-1990
APPLICATION NUMBER: 622,330
FILING DATE: 27-NOV-1990
FILING DATE: 27-NOV-1990
FILING DATE: 27-NOV-1990
APPLICATION NUMBER: 366,244
FILING DATE: 09-UN-1989
FILING DATE: 26-NOV-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Matthew Jacob
REGISTRATION NUMBER: 25,154
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION;
      90.06;
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                           931 TCCCTCCTCT 940
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RESULT 347
US-08-173-489C-315/c
Sequence 315, Application US/08173489C
; Patent No. 5861244
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                    RESULT 346
US-08-211-820-5
i Sequence 5, Application US/08211820
j Patent No. 5533859
i GENERAL INFORMATION:
APPLICANT: Prockop, Darwin J.
APPLICANT: Sertala, Andraej
APPLICANT: Sieron, Aleksander
APPLICANT: Geddis, Amy
ITLE OP INVENTION: Synthesis of Human Procollagens
NUMBER OF SEQUENCE:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5593859ris
CITY: Philadelphia
                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Pred. No. 2.4e+02;
0; Mismatches 1; Indels
                                                     11.5%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 2.4e+02; cive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTER: USAR
ZIF: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,820
FILING DATE: 11-AUG-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US92/09061
FILING DATE: 22-007-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 32-007-1991
ATTORNEY/AGENT INFORMATION:
FLEEDRANG OF SEG 1D NO: 5:
SEGUENCE CHARACTERISTICS:
LENGETH: 12 DASE PAILS

INFORMATION FOR SEG 1D NO: 5:
LENGETH: 12 DASE PAILS

LENGETH: 12 DASE PAILS

LENGETH: 12 DASE PAILS

LENGETH: 12 DASE PAILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative
                                                 Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
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; LOCATION: 1..1
US-08-211-820-5
; ANTI-SENSE: yes
US-08-031-147A-20
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Gaps
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TITLE: Transfer of Kingella

TITLE: indologenes (Snell and Lapage 1976) to the
TITLE: indologenes (Snell and now as Suttonella
TITLE: indologenes comb now transfer of Bacteroides
TITLE: indologenes comb now transfer of Bacteroides
TITLE: nodosus (Beveridge 1941) to the genus
TITLE: Dichelobacter gen now as Dichelobacter nodosus
GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANT: WENG, C. -G.
APPLICANT: HEPBURN, A. G.
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSED: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
CITY: NEW YORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: genomic DNA
DESCRIPTION: 16s rRNA gene from Haemophilus
DESCRIPTION: influenzae (Accession # M15019, M59433)
DESCRIPTION: nucleotides 406 to 417
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) DATE: 1991
; RELEVANT RESIDUES IN SEQ ID NO: 315 :FROM 1 TO 12
US-08-173-489C-315
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTES: 1MM 'EV/KIVA'
COMPUTES: 1MM 'EV/KIVA'
COMPENING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATE: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFFATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: US OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, JOSEPH H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: U9518-6
TELECOMUNICATION INFORMATION:
TELEPHONE: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 315:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                          STATE:
COUNTY: USA
ZIP: 10021.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
MEDIUM TYPE: MS-DOS version 6.2
MS-DOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Haemophilus influenzae PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
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936 CCTCTTCATT 945

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                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: BEALFILL
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/676,782
FILING DATE: 08-JUL-1996
CLASSIFICATION 1435
PRING APPLICATION NUMBER: US/08/248,505
FILING DATE: 25-MAY-1994
ATTONNEY/AGENT INPORMATION:
NAME: MCGOWAN, MAICOIM K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 39,300
REFERENCE/OFFORTER: 386-620
ITELEPPAK: (703) 836-620
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHRARATERISE:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHRARATERISE:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHRARACTERISTICS:
ILL Dase pairs
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Sequence 27, Application US/08442809A

Patent No. 5976873

APPLICANT: Bohinski, Robert J.,

APPLICANT: Whitestt, Jeffrey A.,

ITILE OF INVENTION: Controlling Lung Cell -

TITLE OF INVENTION: Specific Gene Expression

NUMBER OF SEQUENCES: 76

CORRESPONDENCE ADDRESS:

ADDRESSEE: Caccala, Stree, Bain, Gilfillan,
ADDRESSEE: Caccala, Stewart & Olstein

STREET: 6 Becker Farm Road

CITY: Roseland

STREET: New Jørsey

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY.

ZIP: 07068

COMPUTER READABLE FORM:
MEDUM TYPE: 3.5 inch diskette
COMPUTER: 18P $5/2

COMPUTER: 18P $6/2

FILING DATE: 18P $6/2

APPLICATION NUMBER: 08/245,356

FILING DATE: 18P $6/2

APPLORNEY, AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025

REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic) US-08-676-782-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  905 TCATTTTCTT 914
          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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RESULT 348

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Pred. No. 2.4e+02;
0; Mismatches 1; Indels
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Patent No. 5976792
Patent CHEUNG, Ambrose
Papelicant: FISCHETTI, Vincent A.
TITLE OF INVENTION: REGULATION OF EXOPROFEIN IN
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. Box 1404
CTTY: Alexandria
STREET: Virginia
STAFE: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 90.0.
Thes 9; Conservative
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11 CTTCTTCATT
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US-08-676-782-15
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APPLICANT: Nandabalan, Krishnan
APPLICANT: Nandabalan, Krishnan
APPLICANT: Nandabalan, Matian
APPLICANT: Yang, Metjia
APPLICANT: Yang, Metjia
APPLICANT: Kright, James
APPLICANT: Manager of Fortial Traction of TITLE OF INVENTION: PROTEIN INTERACTIONS THAT OCCUR IN POPULATIONS
TITLE OF INVENTION: AND IDENTIFICATION OF INHIBITORS OF THESE INTERACTORS
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 89, Application US/08663824

Batent No. 6083693

GENERAL INFORMATION:
APPLICANT: Nandabalan, Krishnan
APPLICANT: Rothberg, Jonathan
TITLE OF INVENTION: INDEMTIFICATION AND COMPARISON OF PROTEIN-PROTEIN
TITLE OF INVENTION: INVERACTIONS THAT OCCUR IN POPULATIONS
FILE REFERENCE: 7934-006
CURRENT APPLICATION NUMBER: US/08/663,824

CURRENT PILING DATE: 1996-06-14

NUMBER OF SEQ ID NOS: 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.5%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Law Comparing to COMPUTER: Law Comparing SYSTEM: DOS SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/874,825 FILING DATE: 13-UTN-1997 CLASSIFICATION 1935 PRIOR APPLICATION 10458 08/63,824 PILING DATE: 14-UTN-1996 ATTORNEY/AGENT INFORMATION: NAME: Misrock, S. Leslie REGISTRATION NUMBER: 18,872 REGISTRATION NUMBER: 18,872 REGISTRATION NUMBER: 18,872 REGISTRATION NUMBER: 19,872 REGISTRATION NUMBER: 19,872 REGISTRATION NUMBER: 19,872 TELECOMMUNICATION NUMBER: 19,872 TELECOMMUNICATION NUMBER: 1999-9090
                                                                  Sequence 89, Application US/08874825
Patent No. 6057101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 Dase pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIÚM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       935 TCCTCTTCAT 944
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                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1155 Ave
CITY: New York
STATE: NY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-874-825-89
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                                                                                                                                                                                                                                                                         11.5%; Score 8.4; DB 1; Length 12; 90.0%; Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 22, Application US/08474700B
Patent No. 6001990
GENERAL INFORMATION:
APPLICANT: Wands, Jack
APPLICANT: Markita, Takaji
APPLICANT: Moradpour, Darius
TITLE OF INVENTION: ANTISENSE INHIBITION OF HEPATITIS C
TITLE OF INVENTION: VINUS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: NUCCE.
COUNTRY: U.S.A.
ZIP: 02110-2864
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION NUMBER: US/08/474,700B
                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Fish & Richardson P.C. 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 07-JUN-1995
PRICK APPLICATION DATA:
APPLICATION NUMBER: 08/240,382
FILING DATE: 10 May 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
US-08-442-809A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 200154
INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS: TYPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEPHONE: 201-994-1700
TELEPAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 bases
                                                                                                                                                                                                                                                  Query Match
11.5
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-474-700B-22
                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                       917 GTCTTTGCCT 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     913 TITGGICTIT 922
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US-08-474-700B-22
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STREET: 23
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Gaps

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; OTHER INFORMATION: Description of Artificial Sequence: proCaspase-1; OTHER INFORMATION: substrate recognition sequence
US-09-513-783A-55
                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence: linker US-09-231-303-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-513-783A-55

Sequence 55, Application US/09513783A

Sequence 55, Application US/09513783A

PAPELICANT: 6416599

APPLICANT: Giuliano, Kenneth A.

APPLICANT: Rapur, Ravi

TILLE OF INVENTION: A System for Cell Based Screening

FILE REFERENCE: 97-022-11

CURRENT APPLICATION NUMBER: US/09/513,783A

CURRENT PILING DATE: 2000-02-25

NUMBER OF FILING DATE: 2000-02-25

SOPTWARE: Patentin Ver. 2.0
                                                                                                                                                                            Length
                                                                                                                                                                         Query Match
Best Local Similarity 90.0%; Pred. No. 2.4e+02;
Matches 9; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 90.0%; Pred. No. 2.4e+02;
Matches 9; Conservative 0; Mismatches 1.
      TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 39
LENGTH: 12
TYBE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                        935 TCCTCTTCAT 944
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US-09-151-890B-39/c
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LENGTH: 12
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APPLICANT: Nandabalan, Krishnan
APPLICANT: Nandabalan, Krishnan
APPLICANT: Nandabalan, Krishnan
APPLICANT: Nandabalan, Krishnan
APPLICANT: Nathan
TITLE OF INVENTION: INTERACTIONS THAT OCCUR IN POPULATIONS AND
TITLE OF INVENTION: INTERACTIONS THAT OCCUR IN POPULATIONS AND
TITLE OF INVENTION: INTERACTIONS THAT OCCUR IN POPULATIONS AND
TITLE OF INVENTION: 108701/108
TILE REFERENCE: 7934-087
CURRENT FILING DATE: 1999-01-12
EARLIER PILING DATE: 1996-06-14
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 89
LENGTH: 12
                                                                                                                                                                                                                                                                                                                       Gaps
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LOCATION: (1)...(12)
COTHER INFORMATION: synthesized test oligonuclectide for binding
US-09-393-783A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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US-09-393-783A-39/C
US-09-393-783A-39/C
Sequence 39, AppDication US/09393783A
Patent No. 6355420
GENERAL INFORMATION:
APPLICANT: Schroth, Gary P.
APPLICANT: Schroth, Gary P.
TILLE OF INVENTION: Wucleic Acid Ligand Interaction Assays
TILLE OF INVENTION: WUCLE: 1999-10-09
PRIOR PRILICATION NUMBER: US/09/393,783A
CURRENT APPLICATION NUMBER: US 09/151,890
PRIOR PRILICATION NUMBER: US 09/151,890
PRIOR APPLICATION NUMBER: US 09/151,890
                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: linker
US-08-663-824-89
                                                                                                                                                                                                                                                    Query Match
11.5%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 2.4e+02;
Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 8.4; DB 1; Length 12;
Pred. No. 2.4e+02;
0; Mismatches 1; Indels
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90.0%;
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 89
LENGTH: 12
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Best Local Similarity 90.0
Matches 9; Conservative
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US-09-231-303-89
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Gaps

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FEATURE:

NAME/KEY: misc_binding

LOCATION: (1)...(12)

OTHER INFORMATION: synthesized test oligonucleotide for binding

US-09-1S1-890B-39
Sequence 39, Application US/09151890B
Patent No. 6420109
Patent No. 6420109
GENERAL INFORMATION:
APPLICANT: Gary P. Schroth
APPLICANT: Thomas Wayne Bruice
TITLE OF INVENTION: Nucleic Acid Ligand Interaction Assays
FILE REFERENCE: 4600-0128
CURRENT APPLICATION NUMBER: US/09/151,890B
CURRENT FILING DATE: 1998-09-11
NUMBER OF SEQ ID NOS: 80
NUMBER OF SEQ ID NOS: 80
NUMBER OF SEQ ID NOS: 80
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 8.4; DB 1;
Pred. No. 2.4e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wakita, Takaji
APPLICANT: Wands, Jack
ITTLE OF INVENTION: ANTISENSE INHIBITION OF
ITTLE OF INVENTION: ANTISENSE INHIBITION OF
ITTLE OF EQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 02110-2804
COMUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
COMPUTER: IBM PS/2 Model 502 or 55SX
SOFRATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION DATA:
PRICA APPLICATION DATA:
APPLICATION NUMBER: 08/240,382
FILING DATE: 10 MMY 1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T:
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/221001
TELECOMMUNICATION INFORMATION:
                                         ISIS-0469
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISIS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22:
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Best Local Similarity 90.0%;
Matches 9; Conservative (
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(617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
ANTL SENSE: yes
PCT-US94-02471-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     913 TTTGGTCTTT 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         899 CCCTGGTCAT 908
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                                                                                                                                                                                                                                                              Sequence 7, Application US/09324803C
Patent No. 6420547
Batent No. 6420547
GENERAL INFORMATION:
APPLICANT: MAIT!, Indu B.
APPLICANT: DEY, Nrisingha
APPLICANT: DEY, Nrisingha
APPLICANT: SHEPERD, ROBERT J.
TITLE OF INVENTION: USE OF THE FULL LENGTH TRANSCRIPT (FLL) FROM
TITLE OF INVENTION: WIRABILIS MOSAIC CAULIMOVIRUS TO EXPRESS CHIMERIC GENES IN PLANT
FILE REFERENCE: 50229-148
CURRENT APPLICATION NUMBER: US/09/324,803C
URRENT FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin ver. 2.0
SEQ ID NO 7
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                Gaps
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PCT-US84-02471-20/C
; Sequence 20, Application PC/TUS9402471
; GENERAL INFORMATION:
APPLICANT: Draper et al.
ITLE OF INVENTION: Modulating the Effects of Herpesviruses;
ITLE OF INVENTION: Modulating the Effects of Herpesviruses;
NUMBER OF SEQUENCES:
ADDRESSEE: Mocdcock Washburn Kurtz
ADDRESSEE: Macdiewicz & Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
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Best Local Similarity 90.0%; Pred. No. 2.46+02;
Matches 9; Conservative 0; Mismatches 1; Indels
                1; Indels
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COUNTRY: USA
ZIP: 19103
ZIPITE 2103
ZIPITE 2
                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA (promoter)
; ORGANISM: mirabilis mosaic caulimovirus
US-09-324-803C-7
                   9; Conservative
                                                                                908 TITICITIGG 917
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                      Matches
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Gaps
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Sequence 285 Application US/08859954

Parent No. 6083695

GENERAL INFORMATION:
APPLICANT: Hardin, Susan H.
APPLICANT: Hardin, Paul E.
TITLE OF INVENTION: Gene Sequencing and Method Thereof
ITLE OF INVENTION: Gene Sequencing and Method Thereof
NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STREET: 1301 McKinney, Suite 5100

CITY: Houston
STREET: 1301 McKinney, Suite 5100

CITY: Houston
STREET: 1308-856

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
PILING DATE:
PLING DATE:
PLING DATE:
PLING DATE:
PLING DATE:
PREADER DATE:
PLING DATE:
PLING DATE:
PLING DATE:
PLING DATE:
PREADER DATE:
PLING DATE:
PLING DATE:
PREADER DATE:
PLING DATE:

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REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEPRAX: 713/651-5246
INFORMATION FOR SEQ ID NO: 262:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
BECRIPTION: /desc = "cligonuclectide"
HYDOLEGY: YES: other nucleic acid
DESCRIPTION: /desc = "cligonuclectide"
HYDOLETICAL: YES
AMTI-SENSE: YES
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PRIOR APPLICATION:
PROOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: D.5900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5245
TELEPHONE: 713/651-5246
INFORMATION FOR SEQ ID NO: 285:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 base pairs
TYPE: mucleic acid
STARNBEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                other nucleic acid
/desc = "oligonucl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE:
US-08-859-954-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        엄
                                                                                                                                                                                                                                                                                                 Sequence 26, Application US/09163485

Patent No. 627571

GENERAL INFORMATION:

APPLICANT: BILLMORE, HELEN

APPLICANT: BICANDENG, WILLIAM

APPLICANT: GILLIES, GEORGE

TITLE OF INVENTION: SEQUENTIAL CONSENSUS REGION-DIRECTED AMPLIFICATION OF

TITLE OF INVENTION: NUMBER: US/09/163,485

CURRENT APPLICATION NUMBER: US/09/163,485

CURRENT FILING DATE: 1988-08-30

SOFTWARE: Patentin Ver. 2.0

LENGTH: 12

TYPE: DNA

TYPE: DNA

TYPE: DNA

TYPE: DNA

CONSENSUS ARTIFICIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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US-08-659-954-262/C
Sequence 262, Application US/0885954
Fatent No. 6083655
GENERAL INFORMATION:
APPLICANT: Hardin, Susan H.
APPLICANT: Hardin, Ramin
APPLICANT: Hardin, Paul E.
TITLE OF INVENTION: Gene Sequencing and Method Thereof
NUMBER OF SEQUENCES: 566
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.
COUNTRY: U.S.
COUNTRY: U.S.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/859,954
FILING DATE:
CLASSIFICATION NUMBER: 08/632,782
FILING DATE:
CLASSIFICATION NUMBER: 08/632,782
FILING DATE:
FILING 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: oligonucleotide, consensus sequence from human
OTHER INFORMATION: matrix metalloproteinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: MOD_RES
LOCATION: (9)
CHER INFORMATION: A, T, C, G, other or unknown
US-09-163-485-26
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Best Local Similarity 58.3
Matches 7; Conservative
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                                                                                                   1 TTTGGTTTTT 10
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COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Minneapolis STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL: )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-021-667A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                              Sequence 319, Application US/08859954
; Patent No. 6083695
; General Information:
    APPLICANT: Hardin, Susan H.
    APPLICANT: Hardin, Paul E.
    TILLE OF INVENTION: Design and Optimized Primer Library for TITLE OF INVENTION: Design and Optimized Primer Library for TITLE OF INVENTION: Gene Sequencing and Method Thereof NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS: ADDRESSEE: L101 MCKinney, Suite 5100
                                                                                 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.0%; Score 8; DB 1; Length 8; 100.0%; Pred. No. 1.9e+03; ive 0; Mismatches 0; Indels
                                    Query Match 11.0%; Score 8; DB 1; Length 8; Best Local Similarity 100.0%; Pred. No. 1.9e+03; Matches 8; Conservative 0; Mismatches 0; Indel@
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Houston
STATE: Texas
CONTRY: To.3.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BATCHILL Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "oligonucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 365
US-08-021-667A-4/c
; Sequence 4, Application US/08021667A
; Parent No. 5434049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: PAUL, Thommas 32,714
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-59C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEPAX: 713/651-5326
INFORMATION FOR SEQ ID NO: 309:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 8 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  934 CICCICIT 941
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ANTI-SENSE: YES
US-08-859-954-309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
                                                                                                                                                                                                                                  RESULT 364
US-08-859-954-309
US-08-859-954-285
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Gaps
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APPLICANT: Magner, Fred W.
APPLICANT: Stout, Jay
APPLICANT: Henrikeen, Dennis
APPLICANT: Henrikeen, Dennis
APPLICANT: Partridge, Bruce
APPLICANT: Manning, Shane
TITLE OF INVENTION: Enzymatic Method for Modification of
TITLE OF INVENTION: Recombinant Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5707826west Center
CITY: Minneapolis
STREET: M.
                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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                                                                                                                                                                                                                                                                                                                                                      11.0%; Score 8; DB 1; Length 9; 100.0%; Pred. No. 1.7e+03; tive 0; Mismatches 0; Indele
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11.0%; Score 8; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 8; Conservative 0; Mismatches 0; Indel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Batenium Release #1.0, Version #1.25
SOFTWARE: Patenium DATA:
APPLICATION DATA:
CLASSIFICATION DATA:
FLING DATE: O6-JUN-1995
FRICASIFICATION DATA:
PRICASIFICATION DATA:
APPLICATION NUMBER: U8 08/095,162
FILING DATE: 20-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: ACCOUNT INFORMATION:
REFERENCE/DOCKET NUMBER: 8648.32-US01
TELEFONNICATION INFORMATION:
TELEFONNICATION INFORMATION:
TELEFONNICATION INFORMATION:
TELEFONNICATION TOWNICATION:
TELEFONNICATION TOWNICATION
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TELEFONNICATION TOWNICATION
TELEFONNICATION
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MOLEGULE TYPE: DNA (genomic)
INMEDIATE SOURCE:
CLONE: Ubiquitin cleaving enzyme
US-08-470-220A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-470-220A-13/c
; Sequence 13, Application US/08470220A
; Patent No. 5707826
; GENERAL INFORMATION:
                                                          LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
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US-08-410-544-4
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US-08-410-544-4/c

US-08-410-544-4/c

US-08-410-544-4/c

US-08-410-544-4/c

US-08-410-544-4/c

Patent No. 5607646

FRIENCAL INPORMATION RAZUNOTI

APPLICANT: KAMBARA, Hideki

TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION

TITLE OF INVENTION: METHOD USING SAME

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDERSS:

ADDESSEE: Antonelli, Terry, Stout & Kraus

STREET: Suite 600, 1919 Pensylvania Ave., NW

STREET: Suite 600, 1919 Pensylvania Ave., NW

COUNTRY: USA

INPERIORATION NAMER: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/410,544

FILING DATE:

CLASSIFICATION NUMBER: US/08/410,544

FILING DATE:

TILNG DATE:

TILNG DATE:

TILNG DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: S20.31930X00

TELEPHONE: APRICATION NUMBER: 520.31930X00

TELEPHONE: 202-828-0380

TELEPHONE: 202-828-0380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 8; Conservative 0; Mismatches 0; Indel
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/095,162
FILING DATE: 20-JUL-1993
CLLASSIPICATION: 514
ATTORNEY AGENT INPORMATION:
NAME: Nelson, Albin J.
REGISTRATION NUMBER: 84.69
REGISTRATION NUMBER: 84.69
REGISTRATION NUMBER: 84.69
REFERENCE POCKET NUMBER: 86.48.32-USO1
TELEPHONE: 612-332-9081
INPORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

INMEDIATE SOURCE:

CLONE: Ubiquitin cleaving enzyme
US-08-095-162-13
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TELEX: 248545
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              933 CCTCCTCT 940
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Sequence 8, Application US/08680350
| Sequence 8, Application US/08680350
| Sequence No. 5955590
| GENERAL INFORMATION:
| APPLICANT: Lawina, Asya
| APPLICANT: Lamecnik, Paul C
| TITLE OF INVENTION: Conjugates of Minor Grocve DNA Binders
| TITLE OF INVENTION: With Antisense Oligonucleotides
| NUMBER: OF SEQUENCES: 18
| CORRESPONDENCE ADDRESS: 18
| ADDRESSEE: Wolf, Greenfield & Sacks PC
| STREET: 600 Atlantic Avenue
| CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 9; . 1.7e+03;
FITLE OF INVENTION: with Antisense Oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/680,350
FILING DATE:
                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/680,350
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.0%; Score 8; DB 1
100.0%; Pred. No. 1.7
tive 0; Mismatches
                                                                 E: Wolf, Greenfield & Sacks PC 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDRESS: single
TOPOLOGY: linear
TOPOLOGY: linear
HYPE: Oligodeoxyribonucleotide
                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: KINDEGRATION:
NAME: KINDEGRATION:
NAME: KINDEGRATION:
NUMBER: 39,248
REPERENCE/DOCKET NUMBER: W046
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
INFORMATION OR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39,248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kindregan, Helen C
                                                                                                                                       STATE: MA
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 11.0
Best Local Similarity 100.
Matches 8; Conservative
                     NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Gree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          945 TGGTTTAA 952
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                                                                                                                    Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
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                                                                                                     RESULT 369
US-08-728-785A-4/C

i Sequence 4, Application US/08728785A

j Patent No. 5817506

d APPLICANT: Okano, Kazunori

APPLICANT: CAMBARA, HOLVANTION:

TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND

TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION

TITLE OF INVENTION: POLYNUCLEOTIDE REPARATIVE METHOD AND DETECTION

TITLE OF INVENTION: POLYNUCLEOTIDE REPARATIVE METHOD AND DETECTION

TITLE OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Antonelli, Terry, Stout & Kraus

STREET: Suite 1800, 1300 No. 5817506th Seventeenth St.
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US-08-680-350-2/c
US-08-680-350-2/c
; Sequence 2, Application US/08680350
; Patent No. 5955590
; GENERAL INNCEMATION:
; APPLICANT: Levina, Asya
; APPLICANT: Zamecnik, Paul C
; TITLE OF INVENTION: Conjugates of Minor Groove DNA Binders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,785A
FILING DATE: 10-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/410,544
FILING DATE: 21-MAR-1995
PRIOR APPLICATION NUMBER: 08/21,667
APPLICATION NUMBER: 08/021,667
RILING DATE: 24-FEB-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       520.31930X00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 22209
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Terry, David T.
REGISTRATION NUMBER: 20,178
REPERDICE/POCKET UMBER: 520
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-312-6600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 703-312-6666
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         952 ATGTATCG 959
         CCTCCTCT 940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ANTI-SENSE: NO
US-08-728-785A-4
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Gaps

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Squence 15, Application US/08680350
Patent No. 595550
GENERAL INFORMATION:
APPLICANT: Levina, Asya
APPLICANT: Zamecnik, Paul C
TITLE OF INVENTION: Conjugates of Minor Groove DNA Binders
TITLE OF INVENTION: With Antisense Oligonucleotides
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks PC
STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESUL: 3.44
US-08-967-374-13/c
; Sequence 13, Application US/08967374
; Patent No. 6037143
; GENERAL INFORMATION:
; APPLICANT: Wagner, Fred W.
; APPLICANT: Henriksen, Dennis
; APPLICANT: Hartidge, Bruce
; APPLICANT: Bartidge, Bruce
; APPLICANT: Ranning, Shane
; TITLE OF INVENTION: Enzymatic Method for Modification of TITLE OF INVENTION: Recombinant Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/680,350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.0%; Score 8; DB 1
100.0%; Pred. No. 1.7
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: KINDREGAN, Helen C
REGISTRATION NUMBER: 39,248
REFERENCE/DOCKET NUMBER: W0461
TELEPCOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGIH: 9 base pairs
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   945 TGGTTTAA 952
                                                                          1 TGGTTTAA
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CITY: Boston
STATE: MA
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US-08-680-350-15
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                                                                                                                                                                               RESULT 373
US-08-680-350-15/c
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Sequence 13, Application US/08680350
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Levina, Asya
APPLICANT: Zamecnik, Paul C
TITLE OF INVENTION: Conjugates of Minor Groove DNA Binders
TITLE OF INVENTION: with Antisense Oligonucleotides
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woll, Greenfield & Sacks PC
STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 11.0%; Score 8; DB 1; Length 9; Best Local Similarity 100.0%; Pred. No. 1.7e+03; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 9;
5. 1.70+03;
cches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boscon
COUNTRY: USA
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 11.0%; Score 8; DB 1
Best Local Similarity 100.0%; Pred. No. 1.7
Matches 8; Conservative 0; Mismatches
                                 REFERENCE/DOCKET NUMBER: W0461/7040
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEPAX: 617-720-3441
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Oligodeoxyribonucleotide
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: Oligodeoxyribonucleotide
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:

ATTORNEY AGENT INFORMATION:
NAME: KINDERGRATION:
REGISTRATION NUMBER: 39,248
REFERENCE/DOCKTY NUMBER: W0461
TELECOMMUNICATION INFORMATION:
TELEPAN: 617-720-341
INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
LENGTH: 9 bace pairs
TYPE: nucleic acid
STRANDENRESS: single
REGISTRATION NUMBER: 39,248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 945 TGGTTTAA 952
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US-08-680-350-8
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US-08-680-350-13
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Gaps

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Mon Oct 18 14:40:17 2004

Query Match

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Sequence 9, Application US/09063450
Patent No. 6109776
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Method and System for Computationally Identifying TITLE OF INVENTION: Clusters Within a Set of Sequences
TITLE OF INVENTION: Clusters Within a Set of Sequences
TITLE OF INVENTION: Clusters Within a Set of Course Precision of Course of Sequences
CURRENT FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
) ORGANISM: Artificial Sequence
; FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:example
; OTHER INFORMATION: sequence illustrating a computational methodology
US-09-063-450-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stout, or,
Henriksen, Dennis
Partridge, Bruce
Manning, Shane
TITLE OF INVENTION: Enzymatic Method for Modification of
Recombinant Polypeptides
Best Local Similarity 100.0%; Pred. No. 1.7e+03; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.0%; Score 8; DB 1; Length 9; 100.0%; Pred. No. 1.7e+03; tive 0; Mismatches 0; Indel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS: ADDRESSE: Merchant & Gould STREET: 3100 No. 6403361west Center CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/505,991
FILING DATE: 17-Feb-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/520,485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13, Application US/09505991
Patent No. 6403361
GENERAL INFORMATION: Fred W. APPLICANT: Wagner, Fred W. Stout, Jay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                             930 ATCCCTCC 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  955 TATCGCTA 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
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Sequence 62 Application US/08297395A

GENERAL INFORMATION:
APPLICANT: David A. Hafler

TITLE OF INVENTION: PERTIDES DERIVED FROM IMMUNODMINANT

TITLE OF INVENTION: PERTIDES OF WYELIN BASIC PROTEIN
FILE REFERENCE: 1010/05723US3

CURRENT APPLICATION NUMBER: US/08/297,395A

CURRENT FILING DATE: 1994-001.1

EARLIER PILING DATE: 1993-05-06

EARLIER FILING DATE: 1993-05-06

EARLIER FILING DATE: 1980-03-30

EARLIER FILING DATE: 1980-06-24

EARLIER FILING DATE: 1980-06-24

EARLIER FILING DATE: 1980-06-24

EARLIER FILING DATE: 1980-06-24

EARLIER FILING DATE: 1987-06-24

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 9

LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 11.0%; Score 8; DB 1; Length 9; Best Local Similarity 100.0%; Pred. No. 1.7e+03; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                              ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: FOPOPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTEN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8648.32-USD1
3100 No. 6037143west Center
                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/520,485
FILING DATE: 29-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.32-TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | IMMEDIATE SURCE:
| CLONE: Ubiquitin cleaving enzyme
| US-08-967-374-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 933 CCTCCTCT 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Homo sapiens
US-08-297-395-62
                           Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                 FILING DATE:
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US-08-297-395-62
                                                                             COUNTRY:
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Gaps

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ORGANISM: Artificial Sequence
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US-09-989-789-538/c
; Sequence 538, Application US/09989789
; Patent No. 6588746
; GENERAL INFORMATION:
; ATTLE OF INVENTION:
; TITLE OF INVENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) OTHER INFORMATION: Description of Artificial Sequence: example target; OTHER INFORMATION: DNA US-09-989-789-537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pacture 537, Application US/09989789

Pacture No. 6588746

GRNERAL INFORMATION:
APPLICANT: LIU, Qiana
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REPRESENCE: 8325-0011.20 / S11-US2
CURRENT APPLICATION NUMBER: US/09/989,789

CURRENT FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 537
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.0%; Score 8; DB 1; Length 9; 100.0%; Pred. No. 1.7e+03; tive 0; Mismatches 0; Indel.
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                                                8648.32-USD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLONE: Ubiquitin cleaving enzyme; SEQUENCE DESCRIPTION: SEQ ID NO: 13: US-09-505-991-13
REGISTRATION NUMBER: 35,093
REPERENCE/DOCKET NUMBER: 8648
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-980
TELEPRAX: 612-332-980
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECTLE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 11.0
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            933 CCTCCTCT 940
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US-09-989-789-537/c
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RESULT 380
PCT-US31-0360-85
PCT-US31-0360-85
Sequence 85, Application PC/TUS9103680
Sequence 85, Application PC/TUS9103680
Sequence 85, Application PC/TUS9103680
TOTAL INFORMATION:
APPLICANT: Marked D. Application Sequence SPECIFIC NONPHOTOACTIVATED
TITLE OF INVENTION: CROSSLINKING AGENTS WHICH BIND TO THE MAJOR GROOVE OF TITLE OF INVENTION: DUPLEX DNA
NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESSE:
ADDRESSEE: MORTISON & FOGTSTER
STREET: 545 Middlefield Road, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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CTHER INFORMATION: /mod base= OTHER
OTHER INFORMATION: /note= "T-T, linking group o-xyloso (nucleotides OTHER INFORMATION: that have xylose sugar linked via the o-xylene PCT-US91-03680-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                      Gaps
) OTHER INFORMATION: Description of Artificial Sequence: example target ; OTHER INFORMATION: DNA US-09-989-789-538
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                                                                                                                                                                0; Indels
                                                                                                            Length 9;
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COMPUTER READABLE FORM:

MEDIUM TYPE: Flopyy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATE:

APPLICATION NUMBER: PCT/US91/03680

FLING DATE: 19910524

CLASSIFICATION: 435

ATTORNEY/AGANT INFORMATION:

NAME: MURASHIGE, Kate H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 29,959

RELEPAN: 415-327-2951

INFORMATION FOR SEQ ID NO: 85:

SEQUENCE CRAAACTERISTICS:

LENGTH: 9 base pairs

TELENCHMULLICATION

STRANDBRESS: single

COMPUTER: 0000LGY: linear
                                                                                                          Query Match
11.0%; Score 8; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 8; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mod_base= OTHER
/note= "5-methylcytosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: modified base LOCATION: 5 OTHER INFORMATION: /mod b. OTHER INFORMATION: /note=FRATURE: NAME/KEY: modified base LOCATION: 9
                                                                                                                                                                                                                      935 TCCTCTTC 942
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STATE: California
                                                                                                                                                                                                                                                                             TCCTCTTC 1
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ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5641625ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSE: Woodcock Washburn Kurtz Mackiewicz and No. 5641625ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 43, Application US/08088658
Patent No. 5641625
GENERAL INFORMATION:
APPLICANT: Ecker, David J.
APPLICANT: Buchardt, Ole
APPLICANT: Bedolm, Michael
APPLICANT: Berg, Rolf H.
APPLICANT: Melsen, Peter E.
APPLICANT: Milegard, Niels E.
TITLE OF INVENTION: HIGH ORDER STRUCTURE AND BINDING OF PEPTIDE
TITLE OF INVENTION: MCLEIC ACIDS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.0%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 2.3e+02; ive 0; Mismatches 0; Indels
                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/088,658
FLING DATE: 19930702
PLING DATE: 19930702
PRICE APPLICATION NUMBER: 08/054,363
ATTORNEY/AGENT INFORMATION:
NAME: Lucci, Joseph
REGISTRATION NUMBER: 33,307
REFRENCE/COMMINICATION INFORMATION:
TELEPHONE: 215-568,3100
TELEPHONE: 215-568,3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/088,658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CLASSIFICATION: 435
PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                908 TTTTCTTT 915
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                                                 STATE: FA
COUNTRY: U.S
COUNTRY: U.S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
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GENERAL INFORMATION:
APPLICANT: Hybridon, Inc.
APPLICANT: Worcester Foundation for
APPLICANT: Experimental Biology
TITLE OF INVENTION: Transcription Inhibitors and Methods of Their Use
TITLE OF INVENTION: Transcription Inhibitors and Methods of Their Use
CORRESPONDENCES. 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lappin & Kusmer
STREET: 200 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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APPLICANT: Ecker, David J.
APPLICANT: Buchardt, Ole
APPLICANT: Babolm, Michael
APPLICANT: Nielsen, Peter E.
APPLICANT: Nielsen, Niels E.
APPLICANT: Milegard, Niels E.
APPLICANT: Milegard, Niels E.
APPLICANT: Milegard, Niels E.
TITLE OF INVENTION: NUCLEIC ACIDS
TITLE OF INVENTION: NUCLEIC ACIDS
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100.0%; Pred. No. 1.7
trive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
ATTORNEY, AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REPREMENCE/DOCKET NUMBER: 4FYZ-037PCT
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-330-1310
TELEFAX: 617-330-1310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/01008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5641625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS: LENGTH: 9 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                            Massachusetts
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    TITICITY 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: singl
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MOLECULE TYPE: C

HYPOTHETICAL: NO

ANTI-SENSE: NO

PCT-US96-01008-18
                                                                                                                                                                                                                                                                                                                                                                 STREET: 200 S
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                     \mathbf{usa}
                                                                                                          RESULT 381
PCT-US96-01008-18/c
                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U
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US-08-088-658-4/c
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Pred. No. 2.3e+02;
Pred. No. 2.3e+02;
Mismatches 0;
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100.0%; Pred. No. ...
                     0; Mismatches
  100.08;
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Best Local Similarity 100.
Best Local Similarity 100.
Matches 8, Conservative
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;
STRANDEDNESS: single
;
TOPOLOGY: linear
US-08-686-116A-49
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                                                             906 CATTTTCT 913
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US-08-122-43-39/C
US-08-122-43-39/C
Sequence 39, Application US/08122433
Fatent No. 5683985
GENERAL INFORMATION:
APPLICANT: Chu, Barbara C.F.
APPLICANT: Orgel, Leslie
TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDES AND
TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDES AND
TITLE OF INVENTION: OLIGONUCLEOTIDES USEFUL AS DECOYS FOR PROTEINS WHICH
TITLE OF INVENTION: SCHECTIVELY BIND TO DEFINED DNA SEQUENCES
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS.
ADDRESSEE: PRETTY, SCHEOEDER, BRUEGGENANN & CLARK
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: Callifornia
COUNTRY: USA
ZIP: 20071
ZIP: 20071
ZIP: 20071
ZIP: 20071
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 10;
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CZEP: 90071

CZEP: 90071

MEDIUM TYPE: Floppy disk
CCOMPOTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/122,433
FILING DATE: 22-SEP-1993
CLASSTRICATION: S14
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/687,337
FILING DATE: 18-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Relter, Stephen E.
REGISTRATION NUMBER: 931 9308
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: muclaic acid
TYPE: muclaic acid
TYPE: muclaic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                FILING DATE: 26-ARRIL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lucci, Joseph
REGISTRATICN NUMBER: 33,307
REFERENCE/DOCKET NUMBER: 181S-1052
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3439
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.0%; Score 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: other nucleic acid US-08-122-433-39
    08/054,363
                                                                                                                                                                                                  TYPE: nucleic acid STRANDEDNESS: single ; TOPOLOGY: linear US-08-088-658-43
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                             908 TITITITE 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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RESULT 365

US-08-686-116A-49/C

Sequence 49, Application US/08686116A

FRETEN NO. 574331

TITLE OF INVENTION: Peptide Nucleic Acids Having Enhanced

TITLE OF INVENTION: Binding Affinity, Sequence Specificity

TOTRIE TO INVENTION: Binding Affinity Application And Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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US-08-686-116A-51/c
US-08-686-116A-51/c
Sequence 51, Application US/08686116A
PACENT NO. 5714331
GENERAL INFORMATION:
APPLICANT NEUCHARCH et al.
APPLICANT NEUCHARCH PEDEIGE Nucleic Acids Having Enhanced
TITLE OF INVENTION: Binding Affinity, Sequence Specificity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ans Solubility
53
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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GENERAL INFORMATION:
APPLICANT: Buchardt et al.
TITLE OF INVENTION: Side Chains
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5719262ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                              DB 1; Length 10; 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
11.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                11.0%; Score 8; DB 1
100.0%; Pred. No. 2.3
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: BM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: MOTHER: DOS/MS-DOS
SOFTWARE: WORDERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,484
FILING DATE: 24-UUL-1996
CLASSIPICATION: 435
REGISTRATION NUMBER: 38,325
REFRENCE/DOCKET NUMBER: ISIS-2270
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISIS-2270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/108,591
FILING DATE: 22-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: MIChael P. Straher
REGISTRATION NUMBER: 38,325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5-08-685-484-51/c
Sequence 51, Application US/08685484
Patent No. 5719262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: IS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215-568-3439
                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 10 bases
TYPE: nucleic acid
STRANDEDNESS: single
US-08-685-484-51
                                                                                                                                                                                                                                                                                                                                                                                                           908 TTTTCTTT 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             908 TTTTCTTT 915
                                                                                                                                                                                                                                       ; TOPOLOGY: linear
US-08-685-484-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 TTTTCTTT 3
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US-08-685-484-49/c
Sequence 49, Application US/08655484
Patent No. 5719262
GENERAL INFORMATION:
APPLICANT: Buchardt et al.
TITLE OF INVENTION: Peptide Nucleic Acids Having Amino Acid
TITLE OF INVENTION: Side Chains
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & No. 5719262ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5714331ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ilarity 100.0%; Score 8; DB 1; Length 10; ilarity 100.0%; Pred. No. 2.3e+02; Conservative 0; Mismatches 0; Indels
                                                                                                            COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/686,116A
FILLING DATE: UNJY 24, 1996
CLASSIPICATION DATA:
APPLICATION NUMBER: 08/108,591
FILING DATE: 22-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAWE: MACHAEL P. SCHAPET
REGISTRATION NUMBER: 38,325
REPREMENCE/DOCKET NUMBER: ISIS-2271
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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ZIP: 19103.

ZIP: 19103.

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC comparible
COMPUTER: 24-UUL-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/108,591
FILING DATE: 22-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Michael P. Straher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               908 TTTTCTTT 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                  PA
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WESUL 391
US-08-686-113A-56/c

| Sequence 56, Application US/08686113A |
| Patent No. 576685 |
| GENERAL INFORMATION: Beptide Nucleic Acids Having Enhanced TITLE OF INVENTION: Pffinity And Sequence Specificity ITLE OF INVENTION: Affinity And Sequence Specificity FADRESPENDENCE ADDRESS: ADDRESSE: ADDRESSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
11.0%; Score 8; DB 1
Best Local Similarity 100.0%; Pred. No. 2.3
Matches 8; Conservative 0; Mismatches
                                        COMPUTER READABLE FORM:
MEDITM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: 18 FC compatible
OPERATING SYSTEM: PC-DoS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/847,108
FILING DATE: 01-MAY-1997
CLASSIFICATION 124, 1996
FILING DATE: July 24, 1996
FILING DATE: July 24, 1996
APPLICATION NUMBER: 08/108,591
FILING DATE: 22-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: MAChael P. Straher
REGISTRATION NUMBER: 38,325
REFERENCE/DOCKET NUMBER: 1SIS-2271
TELECOMMUNICATION INPORMATION:
TELEPONE: 215-568-310
TELEPONE: 215-568-310
TELEPONE: 215-568-310
TELEPONE: 10 bases
TWOET: 10 bases
TWOET: 10 bases
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REGISTRATION NUMBER: 38,325
REFERENCE/DOCKET NUMBER: ISIS-2273
                             ZIP: 19103
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        908 TTTTTTT 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
US-08-847-108-51
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U.S.A.
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; Sequence 51, Application US/08847108
; Patent No. 573638
; GENERAL INFORMATION:
    APPLICANT: Buchardt et al.
    TITLE OF INVENTION: Binding Affinity, Sequence Specificity
; TITLE OF INVENTION: Binding Affinity, Sequence Specificity
; TITLE OF INVENTION: Binding Affinity
; Patent No. 5736336
; TITLE OF INVENTION: and Solubility
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5736336ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
                                                                                Sequence 49, Application US/08847108
Sequence 49, Application US/08847108
Patent No. 5736336
GENERAL INFORMATION:
APPLICANT: Buchardt et al.
TITLE OF INVENTION: Peptide Nucleic Acids Having Enhanced
TITLE OF INVENTION: Binding Affinity, Sequence Specificity
Patent No. 5736336
TITLE OF INVENTION: and Solubility
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5736336ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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11.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Philadelphia
SIATE: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 MD
COMPUTER: DW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordberfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/847,108
FILING DATE: 0.1-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/686,116
FILING DATE: 0.1-MAY-1997
FILING DATE: 0.1-MAY-1997
FILING DATE: 0.1-MAY-1997
FILING DATE: 0.1-MAY-1997
FILING DATE: 1.38,325
REFERENCE/DOCKET NUMBER: 18:S1S-2271
TELECOMMUNICATION INFORMATION:
TELEPHORE: 215-568-3439
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LEBRACE: United acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    908 TTTTCTTT 915
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US-08-847-108-51/c
                                                                     US-08-847-108-49/c
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ISIS-2270
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CLASSIFICATION
PRIOR APPLICATION
PRIOR APPLICATION
PRIOR APPLICATION
THING DATE: 24-UL-1996
FILING DATE: 22-NOV-1993
ATTORNEY/ASMIT INFORMATION:
NAMB: Michael P. Straher
REGISTRATION NUMBER: 38,325
REFERENCE/DOCKET NUMBER: 151S-227
TELEPHONE: 215-568-3100
TELEPHONE: 215-568-3409
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.08; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          908 TTTTCTTT 915
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Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 TTTTCTTT 3
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                      JS-08-847-095A-49/c
                                                                                                                                                                                                                                                                           STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-847-095A-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 58, Application US/08686113A
Patent No. 576685
GENERAL INFORMATION:
PAPLICANT: Buchardt et al.
TITLE OF INVENTION: Peptide Nucleic Acids Having Enhanced
TITLE OF INVENTION: Affinity And Sequence Specificity
Patent No. 5766855
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5766855ris
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                 Query Match 11.0%; Score 8; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 2.3e+02; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.0%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 2.3e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: PA
COUNTRY: U.S.A.
ZIF: 19103 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COPERATING SYSTEM: DEMPCROUPDING
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
PILING DATE: JULY 24, 1996
CLASSIFICATION NUMBER: US/00/686,113A
PILING DATE: JULY 24, 1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/108,591
FILING DATE: Z2-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: MICHAEL P. STRABET
REGISTRATION NUMBER: 38,325
RESISTRATION NUMBER: 38,325
RESISTRATION NUMBER: 1SIS-2273
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/686,113A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISIS-2273
TELECOMMUNICATION INFORMATION
               TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 10 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
EDNESS: single
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   215-568-3439
                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                    908 TTTTCTTT 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 908 TTTTCTTT 915
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                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 392
US-08-686-113A-58/c
                                                                                                                                                                     : TOPOLOGY:
US-08-686-113A-56
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TOPOLOGY:
US-08-686-113A-58
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Sequence 49, Application US/08847095A

Batent No. 5786461

GENERAL INFORMATION:
APPLICANT: Buchardt et al.
TITLE OF INVENTION: Peptide Nucleic Acids Having Amino Acid
TITLE OF INVENTION: Side Chains
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5786461ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5786461ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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| Sequence 51, Application US/08847095A
| Patent No. 5786461
| Patent No. 5786461
| GENERAL INFORMATION:
| APPLICANT: Buchardt et al.
| TITLE OF INVENTION: Peptide Nucleic Acids Having Amino Acid
| TITLE OF INVENTION: Side Chains
| NUMBER OF SEQUENCES: 53
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.0%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 2.3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 MD
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/847,095A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
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BCDUITCZI-899.rni
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Gaps ö

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Query Match
11.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred, No. 2.38+02;
Matches 8; Conservative 0; Mismatches 0; Indels
        STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: ED
                                                                                                                                                                                                                                                                                                                                                                         960 CTACCAAC 967
                                                                                                                                                                                                                                                                                                                                                                                                                           10 CTACCAAC 3
                                                                                                                                                              ; NAME/KEY:
; LOCATION:
US-08-597-467-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-590-571-24
                                                                                                                                           FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 395
US-08-597-467-8/C

i Sequence 8, Application US/08597467

i Patent No. 5824787

i GENERAL INFORMATION:
APPLICANT: Shinger, Paul A.
ITILE OF INVENTION: POLYNUCLEOTIDE SIZING REAGENT
NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA

ZIP: 90067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ENAPHABLE FORM:
COMPUTER: ENAPH DEC-DOS/MS-DOS
COMPUTER: DatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/597,467
FILING DATE:
CLASSIPICATION DATA:
APPLICATION NUMBER: US 08/161,901
FILING DATE:
CLASSIPICATION NUMBER: US 08/161,901
FILING DATE:
APPLICATION NUMBER: US 08/161,901
FILING DATE:
CLASSIPICATION NUMBER: US 08/161,901
FILING DATE: 03-DEC-1993
ATTORNEY AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D., John R.
REGISTRATION NUMBER: 31,678
REFERENCE/POCKET NUMBER: PD-3006
TELEPHONE: (619) 455-5110
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Worderfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/847,095A
FILING DATE:
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,484
FILING DATE: 24-UU-1996
APPLICATION NUMBER: 08/108,591
FILING DATE: 22-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: MACHAIN NUMBER: 38,325
FILING DATE: 22-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: MACHAEL P. SLYABER
REFERENCE/DOCKET NUMBER: 151S-270
TELEPHONE: 215-568-3109
SEQUENCE CHARACTERISTICS:
LENGTH: 10 Dases
TYPE: NUCleic acid
STRANDENDESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 8; Conservative
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Query Match
11.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
RESULT 396
US-08-590-571-24/C

JS Sequence 24, Application US/08590571
Patent No. 5861246
GENERAL INFORMATION:
APPLICANT: Sherman Weissman and Girish N. Nallur
TITLE OF INVENTION: MULTIPLE SELECTION PROCESS
NUMBER OF SEQUENCES: 66
CORRESPONDENCES: 66
CORRESPONDENCES: Associates
STREET: 25 SKytop Drive
CITY: Trumbull
STATE: Connecticut
CCUNTRY: USA
ZIP: 06611
STATE: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/590,571
FILING DATE:
CLASSIFICATION NUMBER: Yale
TELECOMMUNICATION NUMBER: Yale
TELECOMENING POCKET NUMBER: Yale
TELECOMENING CORTENTION:
REPRENDENCE CHARACTERISTICS:
LENGRATION POR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: MICHOSIC STATES
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-471-907A-4/c
; Sequence 4, Application US/08471907A
; Patent No. 5966053
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           958 CGCTACCA 965
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RESULT 399
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                 APPLICANT: Buchardt, Ole
APPLICANT: Egholm, Michael
APPLICANT: Nielsen, Peter E.
APPLICANT: Nielsen, Peter E.
APPLICANT: Milegaard, Niels E.
TITLE OF INVENTION: HICH ORDER STRUCTURE AND BINDING OF PEPTIDE
TITLE OF INVENTION: NUCLEIC ACIDS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSES: Woodcock Washburn Kurtz Mackiewicz and No. 5986053ris
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5986053ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MS-08-471-907A-43/C

Sequence 43, Application US/08471907A

Sequence 43, Application US/08471907A

Sequence 43, Application US/08471907A

PERFORMATION:
APPLICANT: Buchardt, Ole
APPLICANT: Befolm, Michael
APPLICANT: Berg, Rolf H.

APPLICANT: M llegazd, Niels E.

TITLE OF INVENTION: NICLEIC ACIDS

TITLE OF INVENTION: NUCLEIC ACIDS

TITLE OF INVENTION: NUCLEIC ACIDS
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                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/471,907A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.0%; Score 8; DB 1
100.0%; Pred. No. 2.3
ttive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PILING DATE:
CLASSIFICATION
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/088,658
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lucci, Joseph
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: ISIS-105
TELECHNOR: 215-568-3100
David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
;
STRANDEDNESS: double
;
TOPOLOGY: linear
US-08-471-907A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 11.0
Best Local Similarity 100.
Matches 8; Conservative
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COMPUTER: IN PROJECT RELEASE #1.0, Version #1.25
COMPUTER: THE PLOSDY GIVEN
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Sequence 228, Application US/0838353
Patent No. 6010895
GENERAL INFORMATION:
APPLICANT: Deacon, Nicholas J.
APPLICANT: Deacon, Nicholas J.
APPLICANT: McPhee, Dale A.
APPLICANT: Cooper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Barden City Plaza
CITY: Garden City Plaza
CITY: Barden City Plaza
CUNTRY: United States
ZIP: 11530
COMPUTER: New York
COUNTRY: United States
ZIP: 11530
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DoS/MS-DOS
SOFTWARE: BATOMINE: US/08/388,353
FILLING DAFE: Patent In Release #1.0, Version #1.25
CLASSIPICATION: 424
ATTORNEY/AGENT INFORMATION:
TELEPHONE: Gill) 742-4343
TELEFENCE/DOCKET NUMBER: 31,346
REPERENCE/DOCKET NUMBER: 31,346
REPERENCE/DOCKET NUMBER: 31,346
TELECOMMUNICATION INDEMER: 9606
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 228:
SEQUENCE CHARACTERSTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
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11.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                   11.0%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 2.3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: euc
CORRESPONDENCE ADDRESS:
ADDRESSE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
L1530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OCMPUTER: IBM CASION
OCMPUTER: IBM CASI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Deacon, Nicholas J.

APPLICANT: McPhes Dale A.

APPLICANT: McPhes, Dale A.

APPLICANT: Crowe, Suzanne

APPLICANT: Crowe, Suzanne

APPLICANT: Crower, David

TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1

NUMBER OF SEQUENCES: 800

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 400
US-08-388-353-227/c
; Sequence 227, Application US/08388353
; Patent No. 6010895
                         ; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-181
                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          934 CTCCTCTT 941
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10 CTCCTCTT 3
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ö Gaps 0 Query Match 11.0%; Score 8; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 2.38+02; Matches 8; Conservative 0; Mismatches 0; Indels RESULT 402
US-08-388-35-231/C
isequence 231, Application US/08388353
Fatent No. 6010895
Fatent No. 6010895
GENERAL INFORMATION:
APPLICANT: Dearont, Jennifer C.
APPLICANT: McPhee, Dale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Crowe, Suzanne
APPLICANT: Crowe, Suzanne
APPLICANT: Crowe, Suzanne
APPLICANT: Copper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States ; MOLECULE TYPE: DNA (genomic) US-08-388-353-228 ZIP: 11530 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk 914 TIGGICIT 921 9 TTGGTCTT 2 linear TOPOLOGY:

RESULT 401 US-08-388-353-228/c

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0
                                                                                                                                                                                   11.0%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 2.3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.0%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 2.3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/38,353

FILING DATE: 14-FEB-1995

CLASSIFICATION NUMBER: US/08/38,353

FLING DATE: 14-FEB-1995

CLASSIFICATION NUMBER: 31,346

REGISTRATION NUMBER: 31,346

REGISTRATION NUMBER: 9606

TELECOMMUNICATION INFORMATION:

TELEPAX: (516) 742-4343

TELEPAX: (516) 742-4366

TELEPAX: (516) 742-4368

TEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Deacon, Nicholas J.
APPLICANT: Deacon, Jennifer C.
APPLICANT: McPhee, Dale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Crowe, Suzanne
APPLICANT: Coper, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
CORRESPONDENCE: 800
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City STATE: New York COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-388-353-273/c
; Sequence 273, Application US/08388353
; Partent No. 6010895
; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 405
US-08-388-353-274/c
; Sequence 274, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
          ; STRANDEDNESS: single
POPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: DNA (genomic) US-08-388-353-273
                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 8; Conservative
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Best Local Similarity 100.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                              941 TCATTGGT 948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Learmont, Jennifer C.
APPLICANT: Learmont, Jennifer C.
APPLICANT: Crowe, Suzanne
APPLICANT: Cooper, David
TITLE OF INVEXTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COMPUTRY: United States
ZIP: 11530
COMPUTRY: LEM PC Compatible
COMPUTRY: LEM PC Compatible
COMPUTER: LEM PC Compatible
COMPUTRY: LEM PC Compatible
COMPUTRY: LEM PC Compatible
COMPUTRY: LEM PC Compatible
COMPUTRY: LIM SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PLANTING SYSTEM: VG-DOS/MS-DOS
SOFTWARE: LIM FEALENT DATH:
APPLICATION NUMBER: US/08/388,353
FILLING DATE: 14-FEB-1995
CLASSIPICATION: 42-4
COMPUTER: IBM PC compatible
COMPRAING SYSTEM: PC-DOS/MS-DOS
SOUTHARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FLING DATE: 14-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERRICE/DOCKET NUMBER: 9606
TELECOMMUNICATION INFORMATION:
TELEPAX: (516) 742-4343
TELEEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 231:
SEQUENCE CHARACTERISTICS:
LYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 232, Application US/08388353; Patent No. 6010895; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Didigilo, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9606
TELECOMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-436
TELEFAX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 232:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-388-353-231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 10 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        941 TCATTGGT 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-388-353-232/c
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0; Indels
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100.0%; Pred. No. 2...
... 0; Mismatches
14-FEB-1995
N: 424
                            CURRENT AFFILCATION DAYS

PELING DATE: 14-FEB-195

CLASSIFICATION 1424

ATTORNEY/AGENT INFORMATION:
NAME: Didiglio, Frank S.
REGISTRATION NUMBER: 31,346

REGISTRATION NUMBER: 31,346

REFRENCE/DOCKET NUMBER: 9606

TELEPHONE: (516) 742-4343

TELEPHONE: (516) 742-4346

TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 308:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs

TYPE: nucleic acid

STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 10 base pairs
nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         910 TICTITICG 917
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STRANDEDNESS:
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                               APPLICANT: Learmont, Jennifer C.
APPLICANT: McPhee, Dale A.
APPLICANT: Crowe, Suzanne
APPLICANT: Crowe, Suzanne
APPLICANT: Crowe, Suzanne
APPLICANT: Crowe, David
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCES: 800
CORRESPONDENCES: 800
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
COMPUTER: Use Vork
COMPUTER: Use Poppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATH:
APPLICATION TYPE: TOPOS/MS-DOS
SOFTATING SYSTEM: PC-DOS/MS-DOS
SOFTATING SYSTEM: PC-DOS/MS-DOS
SOFTATION DATE: 14-FEB-1995
CLASSIFICATION NUMBER: 31,346
FILLERENCE DOCKET NUMBER: 31,346
FILLERENCE DOCKET NUMBER: 31,346
FILLERENCE CONCET NUMBER: 31,346
FILLERENCE: (516) 742-4346
TELLERX: (516) 742-4346
TELLERX: (516) 742-4346
TELLERX: (516) 742-4346
TELLERX: (516) 742-436
TELLERX: (516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 10; 2.3e+02;
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Patent No. 6010895
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Learmont, Jennifer C.
APPLICANT: Crowe, Suzanne
APPLICANT: Crowe, Suzanne
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONDUCTOR SOULLY, SCOTT, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City Plaza CITY: Garden City STREET: New York COUNTRY: United States ZIP: 11530 COMPUTER: ISAN PC COMPUTER: STATEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 11.0%; Score 8; DB 1
Best Local Similarity 100.0%; Pred. No. 2.3
Matches 8; Conservative 0; Mismatches
                     Deacon, Nicholas J.
Learmont, Jennifer C.
McPhee, Dale A.
Crowe, Suzanne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     908 TTTTCTTT 915
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11.0%; 5c.
100.0%; Pre
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INFORMATION FOR SEQ ID NO: 227:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 10 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
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                                                                                                                                                  Gaps
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0
                                                                   11.0%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 2.3e+02; live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: GRALE STATE: COUNTRY: U.S.A.

ZIP: 11530-0299
COMPUTAT: U.S.A.

ZIP: 11530-0299
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
GOFTWARE: PatentIn Release #1.0, Version #1.25
GOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-UN-1995
APPLICATION NUMBER: PM364 (AU)
FILING DATE: 1-FEB-1994
APPLICATION NUMBER: PW30284 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: US/08/388,353
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: US/08/388,353
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: US/08/388,353
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: US/08/383
APPLICATION US/08/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhee
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 GARDEN CITY PLAZA
                                                                                                                                                                                                                                                                                                                                                                                       RESULT 408
10.08-488-551B-181/c
1.5equence 181, Application US/08488551B
1. Patent No. 6015661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 181:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (516) 742-4343
                                                               Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 base pairs
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STRANDEDNESS: single
                                                                                                                                                                                                              910 TTCTTTGG 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                934 CTCCTCTT 941
US-08-388-353-309
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RESULT 409 US-08-488-551B-227/c

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Sequence, 60156b1
| Patent No. 60156b1
| Patent No. 60156b1
| APPLICANT: Nicholas J. Deacon
| APPLICANT: Nicholas J. Deacon
| APPLICANT: David Cooper
| APPLICANT: David Cooper
| TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
| UNMBER OF SEQUENCES: 841
| CORRESPONDENCE ADDRESS: 841
| ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
| STREET: 400 GARDEN CITY PLAZA
| CITY: GARDEN CITY
| NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 8; DB 1; Length 10;
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; Sequence 228, Application US/08488551B
; Patent No. 6015561
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
                                                                                                                                                                                                                                                                                                                                STATE: GARLEN CLII
STATE: MEM YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER: ELOPPY disk
COMPUTER: TEM PC COMPATIBLE
COMPUTER: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTING DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 12-FEB-1994
APPLICATION NUMBER: PM364 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM3021/95
FILING DATE: 17-MS-1995
APPLICATION NUMBER: US/08/38,353
FILING DATE: 17-MS-1995
APPLICATION NUMBER: US/08/38,353
FILING DATE: 17-MS-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 17-MS-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 17-MS-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGILO
REFERENCE/POCKET NUMBER: 9606Z
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4343
```

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Sequence 222, Application US/08488551B
Sequence 222, Application US/08488551B
GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. Morbne
CORRESONDENCES: G41
CORRESONDENCES: G41
CORRESONDENCES: G41
CORREST: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY PLAZA
CITY: GARDEN CITY
STREET: NEW YORK
COUNTRY: US.A.
COMPUTER: ISO-0299
COMPUTER: ISO-0299
MEDIUM TYPE: Ploppy disk
COMPUTER: DALE COMPABLE PORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: DALE COMPABLE
COMPUTER: DALE COMPABLE
COMPUTER: DALE COMPABLE
APPLICATION NUMBER: DAJ64 (AU)
FILING DATE: 07-UUN-1995
PRIOR APPLICATION NUMBER: DAJ64 (AU)
FILING DATE: 21-FEB-1995
APPLICATION NUMBER: BN024 (AU)
FILING DATE: 11-MAY-195
FILING DATE: 11-MAY-195
APPLICATION NUMBER: BN024 (AU)
FILING DATE: 11-MAY-195
AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 11.0%; Score 8; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 2.3e+02; Matches 8; Conservative 0; Mismatches 0; Indels
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PN0244 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PN3021/95
FILING DATE: 17-MAY-1995
ATTONNEY, AGENT INFORMATION:
NAME: FRANK S. DIGIGLIO
NAME: FRANK S. DIGIGLIO
TELEPHONE: (516) 742-4346
INFORMATION FOR SEQ ID NO: 231:
TELEPHONE: (516) 742-4366
INFORMATION FOR SEQ ID NO: 231:
TELEPHONE: (516) 742-4366
INFORMATION FOR SEQ ID NO: 231:
TELEPHONE: (516) 742-4366
INFORMATION SEQ ID NO: 231:
TELEPHONE: (516) 742-4366
INFORMATION FOR SEQ ID NO: 231:
TELEPHONE: (516) 742-4366
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INFORMATION FOR SEQ ID NO: 231:
TELEPHONE: (516) 742-4366
INFORMATION FOR SEQ ID NO: 231:
TELEPHONE: (516) 742-4366
INFORMATION FOR SEQ ID NO: 231:
TELEPHONE: (516) 742-4366
INFORMATION FOR SEQ ID NO: 231:
TELEPHONE: (516) 742-433
INFORMATION FOR SEQ ID NO: 231:
TELEPH
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Sequence 231, Application US/08488551B
Falent No. 6018661
GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhee
APPLICANT: SCOPER S. 841
CORRESPONDENCES: 841
CORRESPONDENCES: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 1153-0.299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PILING DATE: O'-UUN-1995
                                               COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-UN-1995
PRILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 17-MAY-1995
APPLICATION NUMBER: PM3021/95
APPLICATION NUMBER: PM3021/95
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGIO
NUMBER: SEAD INFORMATION:
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4366
INFORMATION FOR SEQ ID NO: 228:
ERNGTH: 10 base pairs
TYRANDEDISSS: single
TYRANDEDISSS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
PILING DATE: 14-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          914 TTGGTCTT 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear;
MOLECULE TYPE: DNA
US-08-488-551B-228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
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Gaps
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                                                                                                                                                                                                                                                                                                                                                      GENERAL INCORMATION:

APPLICANT: Dale A. McPhee
APPLICANT: Dale A. McPhee
APPLICANT: Dale A. McPhee
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
CITY: GAADEN CITY
STATE: NOW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COUNTRY: IBN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: W3/08/488,551B
FILING DATE: 07-JUM-1995
RILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 11-FEB-1994
APPLICATION NUMBER: PN0284 (AU)
FILING DATE: 11-FEB-1995
APPLICATION NUMBER: PN0284 (AU)
FILING DATE: 11-FEB-1995
APPLICATION NUMBER: PN0284 (AU)
FILING DATE: 11-FEB-1995
APPLICATION NUMBER: PN0284 (AU)
FILING DATE: 17-MAY-1995
ATTORNEY ARBORNATION:
NAME: FRANK S. DIGIGILO
REFERENCE/DOCKET NUMBER: 9606Z
TREECOMMUNICATION INFORMATION:
THE PROMONEY FRANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.0%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 2.3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                  US-08-488-551B-274/c
; Sequence 274, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-488-551B-308/c
; Sequence 308, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INPORMATION FOR SEQ ID NO: 274:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                          908 TITICITY 915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-488-551B-274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 415
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0
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Best Local Similarity 100.0%; Pred. No. 2.38+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                               DB 1; Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTATION OF THE STATE OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhe
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY
CITY: GARDEN CITY
                                                                                                                                                                                                                                                                                                                                     Query Match
11.0%; Score 8; DB 1
Best Local Similarity 100.0%; Pred. No. 2.3
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 413
42.08-488-551B-273/c
; Sequence 273, Application US/08488551B
; Patent No. 6015661
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TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 273
SEQUENCE CHARACTERISTICS:
TELEFAX: (516) 742-4366
INPORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 base pairs
                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
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EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       941 TCATTGGT 948
                                                                                                                                                                                                  ; TOPOLOGY: linear;
; MOLECULE TYPE: DNA
US-08-488-551B-232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 TCATTGGT 1
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US-08-488-551B-273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                           CURRENT APPLICATION DATA:

APPLICATION NUMBER: PAGE (AU)
FILING DATE: O'-JUN 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 14-FEB-1994

APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 23-DEC-1994

APPLICATION NUMBER: PM384 (AU)
FILING DATE: 14-FEB-1995

APPLICATION NUMBER: PM3021/95

FILING DATE: 13-MAY-1995

APPLICATION NUMBER: US 08/388,353

FILING DATE: 17-MAY-1995

APPLICATION NUMBER: PM3021/95

FILING DATE: 17-MAY-1995

APPLICATION NUMBER: 9606Z

FERENCE/DOCKET NUMBER: 9606Z

TELEPHONE: (516) 742-4343

TELEPHONE: (516) 742-4343

TELEPHONE: (516) 742-4366

INFORMATION FOR SEQ ID NO: 309:
SEQUENCE CHARACTERISTICS:

LENGTH: 10 base pairs

LENGTH: 10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAPUTER RELABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,691
FILING DATE: 31-JUL-1997
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: NO. 6066432tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/POCKET NUMBER: 39,317
REFERENCE/POCKET NUMBER: 39,317
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   910 TICTITIG 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 Trctridg 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: lii
; MOLECULE TYPE:
US-08-488-5518-309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
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APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCES: 841
CORRESPONDENCES: ADDRESS:
ADDRESSE: SCULLY, SCOTT, MURPHY & PRESSER
CITY: GARDEN CITY PLAZA
CITY: TOO GARDEN CITY PLAZA
CITY: STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.25
CURRUT APPLICATION DATA: APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: BN0284 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: US/08/388,353
FILING DATE: 21-FEB-1995
APPLICATION NUMBER: US/08/388,353
FILING DATE: 21-FEB-1995
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: US/08/388,353
FILING DATE: 17-FEB-1995
APPLICATION NUMBER: US/08/388,353
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGALIO
REFERENCE/DOCKET NUMBER:
TELESPONE: G161 74-2433
TELESPONE: G161 74-24-343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3109, Application US/08488551B
Fatent No. 6015661
GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhee
APPLICANT: Dale A. McPhee
ITILE OF INVENTION: NON PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STREET: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
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100.0%; Pred. No. 2.3e+02;
tive 0; Mismatches 0;
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INFORMATION FOR SEQ ID NO: 308:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
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US-08-488-551B-309/c
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) OTHER INFORMATION: Description of Artificial Sequence: No. 6228982el Sequence US-08-088-661F-20
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GENERAL INFORMATION:
APPLICANT: Wittung, Pernila
APPLICANT: Wittung, Pernila
APPLICANT: Wittung, Pernila
APPLICANT: Wittung, Pernila
APPLICANT: Buchardt, Ole
APPLICANT: Bacholm, Michael
APPLICANT: Berg, Rolf
APPLICANT: Nielsen, Peter E.
APPLICANT: Nielsen, Peter E.
APPLICANT: BERG, Nolf
TITLE OF INVENTION: Double-Stranded Peptide Nucleic Acids
TITLE OF INVENTION: Double-Stranded Peptide Nucleic Acids
CURRENT FILING DATE: 1993-07-02
PRIOR APPLICATION NUMBER: 08/054,363
PRIOR FILING DATE: 1993-04-26
PRIOR APPLICATION NUMBER: PCT/EP92/01219
PRIOR FILING DATE: 1992-05-19
                                                                                                                                                                                                                                                                                                               GENERAL INCRAFILOR:
APPLICANT: No. 625992den, Benget
APPLICANT: Wittung, Pernilla
APPLICANT: Wittung, Pernilla
APPLICANT: Buchardt, 01e
APPLICANT: Buchardt, 01e
APPLICANT: Buchardt, 01e
APPLICANT: Bacham, Michael
APPLICANT: Nielsen, Peter E.
APPLICANT: Nielsen, Pouble-Stranded Peptide Nucleic Acids
FILE REFERENCE: 15151108
CURRENT APPLICATION NUMBER: 08/054,363
PRIOR FILING DATE: 1993-07-02
PRIOR FILING DATE: 1993-07-05
PRIOR FILING DATE: 1992-05-19
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.0%; Score 8; DB 1; Length 10;
100.0%; Pred. No. 2.3e+02;
Aative 0; Mismatches 0; Indels
100.0%; Pred. No. 2.3e+02; rative 0; Mismatches 0; Indels
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, Sequence 20, Application US/08088661F
, Patent No. 6228982
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                         901 CIGGICAT 908
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LENGTH: 10
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VES-08-522-384-74

Sequence 74, Application US/08522384

Sequence 74, Application US/08522384

GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION: PROCESSES, APPRATUS AND COMPOSITIONS FOR TILLE OP INVENTION: PROCESSES, APPRATUS AND COMPOSITIONS FOR TILLE OP INVENTION: PROCESSES, APPRATUS AND COMPOSITIONS FOR TILLE OP INVENTION: 1958-4029

FILE REFERENCE: 2458-4029

CURRENT FILING DATE: 1996-11-15

NUMBER OF SEQ ID NOS: 122

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 74

LENGTH: 10
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Sequence 102, Application US/08522384
Sequence 102, Application US/08522384
FEBERAL INFORMATION:
APPLICANT: LOPEZ-NIETO, CARLOS E
FAPLICANT: NIGAM! SANJAY KUNAR
TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
FILE REPERBUCE: 2458-4029
CURRENT APPLICATION NUMBER: US/08/522,384
CURRENT FILING DAIR: 1996-11-15
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 102
LENGTH: 10
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COTHER INFORMATION: Description of Unknown Organism: Primer US-08-522-384-74
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                                                                                                                                                                                                                                                       Length 10;
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                                                                                                                                                                                                                                                       DB 1; Len
                                                                                                                                                                                                                                                     Query Match 11.0%; Score 8; DB 1
Best Local Similarity 100.0%; Pred. No. 2.3
Matches 8; Conservative 0; Mismatches
     TELEFAX: (206) 682-6031
INPORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Unknown Organism
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ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 11.0
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                      TYPE: nucleic acid
STRANDEDNESS: sing
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                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA
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OTHER INFORMATION: Description of Artificial Sequence: No. 6228982el Sequence 11.0%; Score 8; DB 1; Length 10;

Query Match

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Gaps
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TITLE OF INVENTION:
TOMPUTER OF SEQUENCES:
COMPUTER:
TEMP PC Compatible
OPERATING SYSTEM:
PC-DOS/MS-DOS
SOFTWARE:
WOADGERFEET PC-DOS/MS-DOS
SOFTWARE:
WOADGERFEET S.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/150,156A
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11.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0986/91
FILING DATE: 24-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0987/91
FILING DATE: 24-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0510/92
FILING DATE: 15-APR-1992
INPORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/150,156A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; DOCUMENT NUMBER: WO PCT/EP92/01220
; FILING DATE: 22-MAY-1992
US-08-150-156A-5
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PUBLICATION INFORMATION:
DOCUMENT NUMBER: WO PCT/EP92/01220
                                                                                                                PFILING DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0986/91
FILING DATE: 24-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0987/91
FILING DATE: 24-MAY-1991
PRIOR DATE: 24-MAY-1991
PRIOR DATE: 15-APR-1992
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 424
US-08-150-156A-14
Sequence 14, Application US/08150156A
Partent No. 6357163
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PUBLICATION INFORMATION:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      908 TITICITY 915
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US-08-150-156A-5/c

| Sequence 5, Application US/08150156A
| Patent No. 6357163
| CANDERAL INFORMATION:
| TITLE OF INVENTION:
| TITLE OF INVENTION: DAGNOSTICS AND ANALYTICAL PROCEDURES
| NUMBER OF SEQUENCES
| MEDIUM TYPE: Floppy disk
| COMPUTER: IBM PC Compatible
| COMPUTER: IBM PC Compatible
| COMPUTER: IBM PC COMPATION: DOS COMPUTER: OF SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
DIAGNOSTICS AND ANALYTICAL PROCEDURES
NUMBER OF SEQUENCES: 40
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION NUMBER: US/08/150,156A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.0%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 2.3e+02; tive 0; Mismatches 0; Indels
                                                           11.0%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 2.3e+02; tive 0; Mismatches 0; Indels
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FILING DATE: 22-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0986/91
FILING DATE: 24-MAY-1991
PRIOR APPLICATION NUMBER: DK 0987/91
FILING DATE: 24-MAY-1991
PRIOR APPLICATION NUMBER: DK 0987/91
FILING DATE: 24-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0510/92
FILING DATE: 15-APR-1992
INFORMATION POR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TYPE: Nucleic acid
TYPE: NUCL
                                                                                                                                                                                                                                                                                                                                                                                           US-08-150-156A-2/c; Sequence 2, Application US/08150156A; Patent No. 6357163
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Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                              8; Conservative
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PUBLICATION INFORMATION:
                                                                                                                                                                                                 908 TTTTCTTT 915
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                                                           Query Match
Best Local Similarity
Matches 8; Conserva
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US-08-088-661F-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 427
US-08-108-591B-9/C
US-08-108-591B-9/C
Sequence 9, Application US/08108591B
Factor No. 6395474
GENERAL INFORMATION:
APPLICANT: Buchardt, Ole
APPLICANT: Bergholm, Michael
APPLICANT: Berg, Rolf Henrik
TITLE OF INVENTION: Peptide Nucleic Acids
FILE REFERENCE: ISISOS40
CURRENT APPLICATION NUMBER: US/08/108,591B
CURRENT APPLICATION NUMBER: US/08/108,591B
CURRENT FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 428
US-08-108-591B-10/C
Sequence 10, Application US/08108591B
Patent No. 6335474
GENERAL INFORMATION:
APPLICANT: Buchardt. Ole
APPLICANT: Berder Egiol
APPLICANT: Berg, Rolf Henrik
TITLE OF INVENTION: Peptide Nucleic Acids
FILE REFERENCE: IS150540
CURRENT APPLICATION NUMBER: US/08/108,591B
CURRENT FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.1
                                                                                                                                                          PEATURE:
; OTHER INFORMATION: No. 6395474el Sequence
US-08-108-591B-8
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: No. 6395474el Sequence
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                   NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.1
                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
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Matches 8; Conservative
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CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 9
                                                                 SEQ ID NO 8
LENGTH: 10
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LENGTH: 10
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COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.0%; Score 8; DB 1; Length 10; 100.0%; Pred. No. 2.3e+02; ative 0; Mismatches 0; Indels
                                                                 Query Match
11.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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Sequence 8, Application US/08108591B
Sequence 8, Application US/08108591B
Sequence 8, Application US/08108591B
September 1 No. 6395474
SEPELICANT: Buchardt, Ole
APPLICANT: Bablolm, Michael
APPLICANT: Bespin, Peter Eigil
APPLICANT: Berg, Rolf Henrik
TITLE OF INVENTION: Peptide Nucleic Acids
FITLE REPERENCE: ISISOS40
CURRENT APPLICATION NUMBER: US/08/108,591B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DCS/MS-DOS SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/150,156A
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PUBLICATION INFORMATION:
DOCUMENT NUMBER: WO PCT/EP92/01220
FILING DATE: 22-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0986/91
FILING DATE: 24-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0987/91
PRIOR APPLICATION NUMBER: DK 0510/92
PRIOR APPLICATION NUMBER: DK 0510/92
PRIOR APPLICATION NUMBER: DK 0510/92
INFORMATION FOR SEC ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                   sequence 16, Application US/08150156A
Patent No. 6357163
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
  ; FILING DATE: 22-MAY-1992
US-08-150-156A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 100.
Matches 8; Conservative
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US-08-150-156A-16
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US-08-108-591B-10

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US-08-68-1148-56/C

Sequence 56. Application US/08686114B

Patent No. 6414112

GENERAL INFORMATION:
PERIODIN: Peptide Nucleic Acids Having 2,6-Diaminopurine Nucleob
NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6414112ris LLP
CITY: Philadelphia
STARE: De Liberty Place - 46th Floor
CITY: Philadelphia
STARE: De Liberty Place - 46th Floor
COUNTY: U.S.A.
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
COMPUTER: U.S.A.
ZIP: 19103
COMPUTER: U.S.A.
ZIP: 19103
COMPUTER: IBM PC compatible
CO
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Best Local Similarity luv...
Best Local Similarity Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  908 TITICITY 915
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  RESULT 431
US-08-686-114B-56/c
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TOPOLOGY:
US-08-686-114B-56
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Length 10;
                                                    0; Indels
Query Match
11.0%; Score 8; DB 1; Le:
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 0; Mismatches 0;
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Patent No. 6395474
GENERAL INFORMATION:
APPLICANT: Buchardt, Ole
APPLICANT: Egholm, Michael
APPLICANT: Berg, Rolf Henrik
ITILE OF INVENTION: Petter Eigil
APPLICANT: Berg, Rolf Henrik
ITILE OF INVENTION: Peptide Nucleic Acids
FILE REFERENCE: ISISO540
CURRENT APPLICATION NUMBER: US/08/108,591B
CURRENT FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
                                                                                                                                                                                                                                                                                           GENERAL INCOMPATION:
Sequence 12, Application US/08108591B
Patent No. 639544
GENERAL INFORMATION:
APPLICANT: Buchardt, Ole
APPLICANT: Beholm, Michael
APPLICANT: Mielsen, Peter Eigil
APPLICANT: Berg, Rolf Henrik
TITLE OF INVENTION: Peptide Nucleic Acids
FILE REFERENCE: ISISO540
CURRENT APPLICATION NUMBER: US/08/108,591B
CURRENT FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.1
SEC ID NO ID
LENGTH: 10
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US-08-108-591B-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: NO. 6395474el Sequence
US-08-108-591B-12
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     908 TTTTCTTT 915
                                                                                                           908 TTTTCTTT 915
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US-08-108-591B-12
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US-08-108-591B-14
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GENERAL INFORMATION:
APPLICANT: Vasuhiro FURUICHI
APPLICANT: Yuko SHIBATA
APPLICANT: Hiroko FUNAKI
APPLICANT: Hiroko FUNAKI
APPLICANT: Hiroko FUNAKI
APPLICANT: Hiroko FUNAKI
APPLICANT: Masanori WATAHIKI
TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
APPLICANT: Eiji OHARA
APPLICANT: Masanori WATAHIKI
TITLE OF INVENTION: Method for Synthesizing CDNA from mRNA sample
FILE REFERENCE: 00162/HG
CURRENT APPLICATION NUMBER: US/09/508,753B
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: JP 9/270324
PRIOR APPLICATION NUMBER: JP 9/270324
NUMBER OF SEQ ID NOS: 472
SEQ ID NO 20
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APPLICANT: Eiji OHARA
APPLICANT: Biji OHARA
TYLE OF INTENTION: MEANAHIKI
TITLE OF INVENTION: MEANAHIKI
FILE REPERENCE: 00162/HG
CURRENT APPLICATION NUMBER: US/09/508, 753B
CURRENT APPLICATION NUMBER: US/09/508
PRIOR APPLICATION NUMBER: US/09/508
PRIOR PILING DATE: 1997-09-18
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CRGANISM: Artificial Sequence
PEATURE:
CONTRACTURE:
CONTRACT
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; OTHER INFORMATION: Description of Artificial Sequence: Primer US-09-508-753B-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
11.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.38+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 2.38+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 27, Application US/09508753B
Patent No. 6544736
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Akira SHIMAMOTO
APPLICANT: Yasuhiro FURUICHI
APPLICANT: Yuko SHIBATA
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SEQ ID NO 27
LENGTH: 10
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US-09-508-753B-50/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.0%; Score 8; DB 1; Length 10; llarity 100.0%; Pred. No. 2.3e+02; Conservative 0; Mismatches 0; Indels
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CURRENT FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/059,153
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1998-03-30
NUMBER OF SEQ ID NOS: 93
SOFTWARE: FESTSEQ for Windows Version 3.0
SEQ ID NO 18
LENGTH: 10
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Sequence 18, Application US/09154750A

PAtent No. 6432640

GENERAL INFORMATION:

APPLICANT: Vogelstein, Bert

APPLICANT: Kinzler, Kenneth

APPLICANT: Kinzler, Kenneth

TILLE OF INVENTION: p33-Induced Apoptosis

FILE REFERENCE: 1107.75357
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/686,114B
FILING DATE: U1/12 4, 1996
CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/108,591
FILING DATE: 22-NOV-1993
ATTORNEY/AGENT INPORMATION:
NAME: Michael P. Straher
REGISTRATION NUMBER: 18IS-2272
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 434
US-09-508-753B-20/C
US-09-508-753B-20/C
Sequence 20, Application US/09508753B
Sequence No. 6544736
GENERAL INFORMATION:
APPLICANT: Akira SHIMAMOTO
APPLICANT: Yasuhiro FURUICHI
APPLICANT: Yuko SHIBATA
APPLICANT: Hiroko FUNAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 11.0
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 10 bases
TYPE: nucleic acid
STRANDEDNESS: single
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US-09-154-750A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCTCCTC 939
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Best Local Similarity
Matches 8; Conserva
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US-08-686-114B-58
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APPLICANT: Akira SHIMAMOTO

APPLICANT: Yasuhiro FURUICHI

APPLICANT: Yasuhiro FURUICHI

APPLICANT: Yave SHEBATA

APPLICANT: Hiroko FUNAKI

APPLICANT: Hiroko FUNAKI

APPLICANT: Hiroko FUNAKI

TITLE OP INVENTION: MATHAHIKI

TITLE OP INVENTION: MACHOG for Synthesizing cDNA from mRNA sample

FILE REFERENCE: 00162/HG

CURRENT APPLICATION NUMBER: US/09/508,753B

CURRENT APPLICATION NUMBER: US/09/508,753B

CURRENT APPLICATION NUMBER: US/09/508,753B

FRIOR APPLICATION NUMBER: US/09/508,753B

NUMBER: OF SEQ ID NOS: 472

SEQ ID NO 113

LENGTH: 10
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US-09-508-753B-440/c
Sequence 440, Application US/09508753B
Patent No. 6544736
GENERAL INFORMATION
APPLICANT: Atax SHIMAMOTO
APPLICANT: Vasuhiro FURUICHI
APPLICANT: Hirok PURNICH
APPLICANT: Hirok PURNAXI
APPLICANT: Masanori WATAHIKI
TITLE OF INVENTION: Method for Synthesizing oDNA from mRNA sample
FILE REFERENCE: 00162/HG
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; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-113
                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: Primer US-09-508-753B-50
                                                                                                                                                                                                                                                                                                                                              Query Match
11.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
               CURRENT APPLICATION NUMBER: US/09/508,753B
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: JP 9/270324
PRIOR FILING DATE: 1997-09-18
NUMBER OF SEQ ID NOS: 472
LENGTH: 10
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CURRENT FILING DATE: 2000-06-16
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; Sequence 113, Application US/09508753B
; Patent No. 6544736
                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
FILE REFERENCE: 00162/HG
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Sequence 56, Application US/09337304

Sequence 56, Application US/09337304

Patent No. 6613673

GENERAL INFORMATION:
PAPLICANT: Buchard.
APPLICANT: Bard, Michael
APPLICANT: Berg, Rolf Henrik
TITLE OF INVENTION: Peptide Nucleic Acids Having 2, 6-Diaminopurine Nucleobases
CURRENT APPLICATION NUMBER: US/09/337,304

CURRENT APPLICATION NUMBER: US/09/337,304

CURRENT FILING DATE: 1999-06-21

PRIOR APPLICATION NUMBER: 08/847,110

PRIOR APPLICATION NUMBER: 08/866,114

PRIOR FILING DATE: 1996-07-24

PRIOR FILING DATE: 1996-07-24

PRIOR FILING DATE: 1993-11-22

PRIOR FILING DATE: 1993-11-22

PRIOR FILING DATE: 1991-05-24
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                                                                                                                                                                                                                                                                                                            .
                                                                                                                    TYPE: DNA

ORGANISM: Artificial Sequence

PEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Primer

US-09-753B-440
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Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Squence 5, Application US/09924346

Patent No. 6555674

GENERAL INCORMATION:
FILE PREFERENCE: 19313-005

FILE REFERENCE: 19313-005

CURRENT APPLICATION NUMBER: US/09/924,346

CURRENT FILING DATE: 2001-08-08

PRIOR FILING DATE: 2000-08-09

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin Ver. 2.1

SSEQ ID NO 5

LENGTH: 10
PRIOR APPLICATION NUMBER: JP 9/270324
PRIOR FILING DATE: 1997-09-18
NUMBER OF SEQ ID NOS: 472
SEQ ID NO 440
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
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US-09-337-304-56/c
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US-09-924-346-5
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nucleic acid
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Patent No. 6613873

GENERAL INFORMATION:

APPLICANT: Buchardt, Ole

APPLICANT: Beholm, Michael

APPLICANT: Beholm, Michael

APPLICANT: Benown Nielsen, Peter E.

APPLICANT: Berg, Rolf Henrik

TITLE OF INVENTION: Peptide Nucleic Acids Having 2, 6-Diaminopurine Nucleobases

FILE REFERENCE: ISTS-3809

CURRENT FILING DATE: 1999-06-21

PRIOR PILING DATE: 1999-06-21

PRIOR PILING DATE: 1997-05-01

PRIOR PILING DATE: 1997-05-24

PRIOR PILING DATE: 1991-05-24

PRIOR PILING DATE: 1992-04-15

NUMBER OF SEQ ID NOS: 60

SOFTWARE: PatentIn Version 3.1
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                                                                                                                                                                                                                                                                                                     Length 10;
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11.0%; Score 8; DB 1; Lei
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 0; Mismatches 0;
                                                                                                                                                                                                             FEATURE:
, OTHER INFORMATION: Synthetic Construct
US-09-337-304-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Synthetic Construct US-09-337-304-58
PRIOR APPLICATION NUMBER: 987/91
PRIOR FILING DATE: 1991-05-24
PRIOR PELLING DATE: 1992-04-15
PRIOR FILING DATE: 1992-04-15
NUMBER OF SEQ ID NOS: 60
SEQ ID NO 56
LENGTH: 10
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US-08-246-373-6/c
; Sequence 6, Application US/08246373
; Patent No. 5550018
; PAPLICANT: LEVENBOOK, Inessa
                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 8; Conservative
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US-09-337-304-58/c
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SEQ ID NO 58
LENGTH: 10
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APPLICANT: POWNERS, Laurie mutin
APPLICANT: POWNERS, Laurie mutin
APPLICANT: POWNERS, Laurie mutin
APPLICANT: POWNERS, Laurie mutin
TITLE OF INVENTION: "TEST POR VIRGILENT REVERTANTS IN
TITLE OF INVENTION: "TEST POR VIRGILENT REVERTANTS IN
TITLE OF INVENTION: ATTENDATED LIVE WACCINES;
COMBERGE OF SOURCES;
THE STATE: VIRGINES STEWARY COLACCH & BIRGH
STATE: VIRGINES TO NO. 55 501016 N Meshington Street
TITL: Alls Chira Companies
COMPANIES WAS A COMPANIES OF THE COMPANIES OF THE COMPANIES WAS A COMPANIES. THE MAS A COMPANIES WAS A COMPANIES WAS A COMPANIES WAS A COMPANIES. THE WAS A COMPANIES WAS A COMPANIES. THE WAS A COMPANIES WAS A COMPANIES. THE WA
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Sequence 27, Application US/08910632B

Sequence 27, Application US/08910632B

Sequence 27, Application US/08910632B

SEXELI UNFORMATION:
APPLICATION:
APPLICATION:
CURRENT APPLICATION UNMBER: US/08/910,632B

CURRENT FILING DATE: 1997-08-13

SARLIER APPLICATION NUMBER: 08/805,631

SARLIER APPLICATION NUMBER: 08/805,631

SARLIER PILING DATE: 1997-02-23

SARLIER PILING DATE: 1995-02-23

SARLIER PILING DATE: 1993-04-15

NUMBER OF SEQ ID NOS: 83

SOFTWARE: PARENTIN PARENT: 1993-04-15

NUMBER OF SEQ ID NOS: 83

SEQ ID NO 27

LENGTH: 11
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Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from esterase D
DESCRIPTION: sequence region in Seq ID No. 586124473
HYPOTHETICAL: Yes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; FUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 74 :FROM 1 TO 11
US-08-173-489C-74
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOCTAARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 2.2 DEC 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 2.9 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: U95.179
REFERENCE/DOCKET NUMBER: U95.18-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (atcorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 74:
EROTHER CHARACTERISTICS:
LENGTH: 11 bases
TYPE: Nucleic Acid
STRANDENESS: single stranded
TTPE: Nucleic Acid
STRANDENESS: single stranded
TOTOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
FATORE:
OTHER INFORMATION: ligation adaptor
US-08-910-632-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        908 TITICITI 915
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US-08-910-632-27
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US-108-173-489C-74

i Sequence 74, Application US/08173489C

i Patent No. 586-1244

i GENERAL INFORMATION:

APPLICANT: WANG. C. -G.

APPLICANT: HEBRURN, A. G.

ITILE OF INVENTION: TRIPLE-STRAND FORMATION.

INUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,

STREET: S10 EAST 73RD STREET,

CITY: NEW YORK

COUNTY: NEW YORK

COUNTY: USA

ZIP: 10021.

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.0%; Score 8; DB 1; Length 11; 100.0%; Pred. No. 2.6e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
DESCRIPTION: esterase D gene (Accession # M13450)
DESCRIPTION: mucleotides 777 to 787
HYPOTHETICAL: No
ANTI-SENSE: No
ORIGINAL SOURCE:
ORGANICM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: chromosome 13
MAP POSITION: 13141.1-q14.2
PUBLICATION: 13141.1-q14.2
AUTHORS: Lee, E Y H P, Lee, W H.
TITLE: Molecular cloning of the
TITLE: molecular cloning of the
TITLE: retinoblastoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) DATE: 1986
; RELEVANT RESIDUES IN SEQ ID NO: 73 :FROM 1 TO 11
US-08-173-489C-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proceedings of the National Academy of Sciences, USA
     OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION DATA:
CLASSIFICATION DATA:
CLASSIFICATION DATA:
FILING DATE: 22 DEC 1993
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGIGSTRATION NUMBER: U9518-6
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (attorney) (212) 708-1880
TELEFRAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 8; Conservative
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JOURNAL:
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CORPUTER: 1-10ppy disk
COMPUTER: 1-10ppy disk
CURRENT APPLICATION NATA:
APPLICATION NATA:
FILING DATE: 11-May-2000
CLASSIFICATION: -4Unknown>
PRIOR APPLICATION -4Unknown>
PRIOR APPLICATION NATA:
APPLICATION NATA:
APPLICATION NATA:
APPLICATION NATA:
FILING DATE: 23-FEB-97
FILING DATE: 23-FEB-1995
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 11.0%; Score 8; DB 1; Length 11; Best Local Similarity 100.0%; Pred. No. 2.6e+02; Matches 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Patent No. 6472154
FAPENT INFORMATION:
APPLICANT: Wren, Jonathan D.
FAPELICANT: Wren, Jonathan D.
TITLE OF INVENTION: Polymorphic Repeats in Human Genes
FILE REPERSANCE: UTSD667
CURRENT APPLICATION NUMBER: US/09/475,947A
CURRENT FILING DATE: 1999-12-31
NUMBER OF SEG ID NOS: 346
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 220,00010140
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                           NAME: SANDBERG, VICTORIA A. REGISTRATION NUMBER: 41,287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 11 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
ZIP: 55401
COMPUTER READABLE FORM:
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 448
US-09-475-947A-230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-475-947A-230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: UNIVERSITY OF ROCHESTER
TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                ; Sequence 27; Application US/08805631A
; Patent No. 6096880
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF ROCHESTER
APPLICANT: UNIVERSITY OF ROCHESTER
; TITLE OF INVENTION: DIA
; TITLE OF INVENTION: DIA
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CORRESPONDENCE ADDRESS:
ADDRESSEE: WUETING, RAASCH & GEBHARDT, P.A.
STREET: 119 No. 6368802th Fourth Street, Suite 201
CITY: Minneapolis
STATE: Minnesota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 8; DB 1; Length 11; Pred. No. 2.6e+02; 0; Mismatches 0; Indels
                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 72
CORRESSPONDENCE ADDRESS.
ADDRESSES: WIETING, FAASCH & GEBHARDT, P.A.
STREET: 119 No. 6096880th Fourth Street, Suite 201
CITY: Minneapolis
STATE: Winnesota
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/805,631A
FILING DATE: 26-FEB-97
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/393,439
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/393,439
FILING DATE: 23-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/47,860
FILING DATE: 15-APR-1993
ATORNEY/AGENT INFORMATION:
NAME: SANDBERG: VICTORIA A.
REGISTRATION NUMBER: 41,287
REGISTRATION NUMBER: 41,287
REGISTRATION INFORMATION:
TELEPHONE: 612-305-1226
                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 27, Application US/09569344 Patent No. 6368802 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 base pairs
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EDNESS: single
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Best Local Similarity
Matches 8; Conserv
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                                                            US-08-805-631A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-805-631A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -09-569-344-27
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RESULT 453
US-07-754-918A-4/C
US-07-754-918A-4/C
Sequence 4, Application US/07754918A
Federat No. 5286484
GENERAL INFORMATION
TITLE OF INVENTION: NUCLEOTIDE SEQUENCE CODING FOR AN
TITLE OF INVENTION: OUTER MEMBRANE PROTEIN FROM NEISSERIA MENINGITIDIS AND USE
TITLE OF INVENTION: OF SAID PROTEIN IN VACCINE PREPARATIONS
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Sequence 251, Application US/09249155A |
| Sequence 251, Application US/09249155A |
| Patent No. 653473 |
| GENERAL INFORMATION: |
| APPLICANT Heber-Katz, Ellen |
| TITLE OF INVENTION: Compositions and Methods for Wound |
| TITLE OF INVENTION: Healing |
| FILE REFERENCE: 00486.78503 |
| CURRENT APPLICATION NUMBER: US 60/074,737 |
| PRIOR PILING DATE: 1999-02-13 |
| PRIOR FILING DATE: 1998-02-13 |
| PRIOR FILING DATE: 1998-02-13 |
| PRIOR FILING DATE: 1998-02-66 |
| PRIOR FILING DATE: 1998-09-26 |
| NUMBER OF SEQ ID NOS: 346 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| LENGTH: 11
APPLICANT: Heber-Katz, Ellen
TITLE OF INVENTION: Compositions and Methods for Wound;
TITLE OF INVENTION: Healing
TITLE OF INVENTION: Healing
CURRENT APPLICATION NUMBER: US/09/249,155A
CURRENT FILING DATE: 1999-02-13
FRICR APPLICATION NUMBER: US 60/074,737
FRICR FILING DATE: 1998-08-26
FRICR FILING DATE: 1998-08-26
FRICR FILING DATE: 1998-09-28
NUMBER OF SEQ ID NOS: 346
SEQ ID NO 191
LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
11.0%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
CRGANISM: Mus musculus
US-09-249-155A-251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       932 cccrccrc 939
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
CORGANISM: Mus musculus
US-09-249-155A-191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            964 CAACGGIG 971
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US-09-249-155A-251
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US-09-249-155A-31/C

is Gaquence 31, Application US/09249155A

patent No. 6538173

GENERAL INVORMATION:

APPLICANT: Heber-Katz, Ellen

TITLE OF INVENTION: Compositions and Methods for Wound

TITLE OF INVENTION: Healing

FILE REFREENCE: 00486.78503

CURRENT APPLICATION NUMBER: US 60/249,155A

CURRENT FILING DATE: 1999-02-13

PRIOR APPLICATION NUMBER: US 60/074,737

PRIOR PILING DATE: 1998-02-13

PRIOR PILING DATE: 1998-09-26

NUMBER OF SEQ ID NOS: 346

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 31

LENGTH: 11
                                 US-09-249-155A-18/C

Sequence 18, Application US/09249155A
Fatent No. 6538173
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Compositions and Methods for Wound;
TITLE OF INVENTION: Healing
TITLE OF INVENTION: Healing
FILE REFERENCE: 00486 78503
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US/09/249,155A
CURRENT FILING DATE: 1999-02-13
FRIOR PILING DATE: 1998-08-15
FRIOR PILING DATE: 1998-08-16
FRIOR FILING DATE: 1998-09-28
NUMBER OF SEQ ID NOS: 346
SSO ID NOS: 346
SSO ID NOS: 346
SSO ID NOS: 346
LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
11.0%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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US-09-249-155A-191/c
Sequence 191, Application US/09249155A
Parent No. 6538173
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA; ORGANISM: Mus musculus
US-09-249-155A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
CORGANISM: Mus musculus
US-09-249-155A-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          943 ATTGGTTT 950
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US-08-363-475-27/C

US-08-363-475-27/C

US-08-363-475-27/C

US-08-363-475-27/C

GENERAL INFORMATION:

PAPLICANT: Chinag, Shu-Jen

APPLICANT: Chinag, Shu-Jen

ADDRESSES: Thomas R. Savitsky

STREET: P.O. Box 4000

CITY: Princeton

STATE: New Jersey

COUNTYER READALE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER READALE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 31,661

REGISTRATION 1435

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 31,661

REGISTRATION NUMBER: 31,661

REGISTRATION NUMBER: 31,661

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION NUMBER: 31,661

TELECOMMUNICATION INFORMATION:

TELECOMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMUN
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                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-115-497-11
   TELEX: 230 901 SANS UR
INFORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                908 TITICITY 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 921 TTGCCTTT 928
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US-08-363-475-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 456
US-08-280-441-8
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Refer No. 5514546

GENERAL INFORMATION

TITLE OF INVENTION: STEM-LOOP OLIGONUCLEOTIDES CONTAINING
TITLE OF INVENTION: PARALLEL AND ANTIPARALLEL BINDING DOMAINS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: Scully, Scott, Murphy & Presser
STREET: ADDRESSES: Scully, Scott, Murphy & STREET: ADDRESSES: STREET: ADDRESSES: STREET: ADDRESSES: STREET: New York

CITY: Garden City
STREET: New York

COUNTRY: USA
                       ADDRESSEE: Stanger, Michaelson, Spivak and Wallace, Ebg. STREET: Parkway 109 Office Center, 328 Newman Springs STREET: Rad May P. O. Box 8489
CITY: Red Bank
STATE: New Jersey
COUNTRY: USA
ZIP: 07701
                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDLIN TYPE: 5 1/4" 360KD IBM compatible diskette
COMPUTER: 1BM PS/2 Model 80
COMPUTER: 1BM PS/2 Model 80
COPERATING SYSTEM: MS-DCS 5.0
SOFTWARE: Microsoft Word 5.5
CURRENT APPLICATION DATA:
PLILING DATE: 19910905
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Michaelson, Peter L.
REGISTRATION NUMBER: 30090
REPERBORE/COCKET NUMBER: Centro-2R
TELECHOMICATION INFORMATION:
TELECHOME: (908)530-6684
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 bases
LENGTH: 12 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 8; DB 1; Length 12;
Pred. No. 2.8e+02;
0; Mismatches 0; Indels
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ZIP: 11530
ZIP: 11530
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/115,497
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/ACENT INFORMATION:
NAME: DIGIGIO, Frank S.
REGESTRATION NUMBER: 31,346
REPERADICATION NUMBER: 31,346
REPERADICATION NUMBER: 31,346
REPERADICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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(516) 742-436
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Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: NUCLEOTIDE
STRANDEDNESS: single
; TOPOLOGY: linear
US-07-754-918A-4
CORRESPONDENCE ADDRESS:
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US-08-115-497-11
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Sequence 26, Application US/08410116B
Patent No. 5599675
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sydney Brenner, Glenn Albrecht, Andrew J. Blasband
TILLE OF INVENTION: DNA Sequencing by Stepwise Ligation and Cleavage
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics, Inc.
STREET: 3832 Bay Center Place
CITY: Hayward
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.0%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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ZUP: 94545

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: 1BM compatible
COMPUTER: 1BM compatible
COMPUTER: 1BM compatible
COMPUTER: 1BM compatible
COMPUTER: 24.Macrosoft Word for Windows, vers. 2.0
SOCTWARE: Microsoft Word for Windows, vers. 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/22,300
FILING DATE: 24-MAR-95
CLASSIFICATION NUMBER: 08/22,300
FILING DATE: 08/280,441
FILING DATE: 25-JUL-94
ATTORNEY/AGENT INFORMATION:
NAME: Stephen C. Macevicz
REGISTRATION NUMBER: 30,285
REGISTRATION NUMBER: 30,285
REGISTRATION NUMBER: 30,285
REGISTRATION NUMBER: 30,285
TELEFRAX: (510) 670-9305
TELEFRAX: (510) 670-9305
TELEFRAX: (510) 670-9305
                  NAME: Kezer, William B.
REGISTRATION NUMBER: 37,369
REFERENCE/DOCKER NUMBER: 37,369
REFERENCE/DOCKER NUMBER: 37,369
REFERENCE/DOCKER NUMBER: 37,369
TELEPHONE: (415) 543-5600
TELEPHONE: (415) 543-5603
INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS: LENGTH: 12 base pairs
TENETH: 13 base pairs
TENETH: 14 base pairs
TENETH: 15 base pairs
TENETH: 16 base pairs
TENETH: 17 base pairs
TENETH: 18 base pairs
TENETH:
ATTORNEY/AGENT INFORMATION: NAME: Kezer, William B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (510)670-9302
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            908 TITICITI 915
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Best Local Similarity
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US-08-410-116B-26
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       Sequence 8, Application US/08280441
Patent No. 5552278
GENERAL INFORMATION:
APPLICANT: Sydney Brenner
TITLE OF INVENTION: DNA Sequencing by Stepwise Ligation and Cleavage
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequent No. 5596091
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SWITZER, Christopher
APPLICANT: SWITZER, Christopher
TITLE OF INVENTION: NOVEL ANTISENSE CLICONUCLECTIDES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/214,603
FILING DATE: 18-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Microsoft Windows 3.1/DOS 5.0 SOFTWARE: Microsoft Word for Windows, vers. 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/280,441 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-214-603-11/c
; Sequence 11, Application US/08214603
; Patent No. 5596091
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 3.1/D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222,300
FILING DATE: 04-APR-94
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                ADDRESSEE: Stephen C. Macevicz
STREET: 21890 Rucker Drive
CITY: Cupertino
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       935 TCCTCTTC 942
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Gaps
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APPLICANT: Kool, Eric T.
TILLE OF INVENTION: STEM-LOOP AND CIRCULAR OLIGONUCLEOTIDES NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 11.0%; Score 8; DB 1; Length 12; Best Local Similarity 62.5%; Pred. No. 2.8e+02; Matches 5; Conservative 3; Mismatches 0; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408,656
FILING DATE: 21-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 9373
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAK: (516) 742-4366
TELEFAK: (516) 742-4366
TELESK: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2:
SEQUINCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Flappy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408,656
FILING DATE: 21-MAR-1995
CLASSIFICATION: 1435
ATTORNEY/AGENT INFORMATION:
NAME: DiGIGIO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9373
TELECOMMUTCATION INFORMATION:
TELEPHONE: (516) 742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08408656
Patent No. 5674683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                    12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          931 TCCCTCCT 938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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US-08-408-656-2
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           Gaps
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Patent No. 5574693
GENERAL INFORMATION:
APPLICANT: Kool, Eric T.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSES: Scully, Scott, Murphy & Presser
STREET 400 Garden City Plaza
CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 460
US-08-408-656-2
Sequence 2, Application US/08408656
Fatent No. 5674683
GENERAL INFORMATION:
APPLICANT: Kool, Eric T.
TITLE OF INVENTION: STEM-LOOP AND CIRCULAR OLIGONUCLEOTIDES
OURSESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 400 Garden City Plaza
CITY: Garden City Plaza
CITY: Garden City
           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: OLIVER STATE: COUNTRY: U.S.A.

ZIP: 11530-0299
COMPUTEX: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC-COMPACTION
COMPUTER: TEM PC-COMPACTION
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408,656
FILING DATE: 21-MAR-1995
CLASSIFFCATION: 435
ATTORNEY AGENT INPORMATION:
NAME: DiGiglio, Frank S.
RECISTRATION NUMBER: 93.73
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION SEQ ID NO: 1:
CONTENT SEQ SEQ ID NO: 1:
       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
    8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                               935 TCCTCTTC 942
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US-08-408-656-1
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                                                                                                                                                           RESULT 459
US-08-408-656-1
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    Matches
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APPLICALLO...
FILING DATE.
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGALO, FEAR S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8085ZXX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-434
TELEFAX: (516) 742-436
TELEFAX: 230 910 SANS UR
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
LENGTH: 12 base pairs
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-413-813-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               908 TITICITI 915
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                                           Gaps
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US-08-413-813-13/c
US-08-413-813-13/c
US-08-413-813-13/c
Sequence 13, Application US/08413813
Patent No. 5683874
Farent No. 5683874
TITLE OF INVENTION: SINGLE-STRANDED, CIRCULAR OLIGONUCLEORIDES
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULIJ, SCOLL, Murphy & Presser
STREET: 400 Garden City Plaza
COUNTRY: USA
COUNTRY: USA
                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: KOOJ, Eric T.

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: New York

COUNTRY: USA
                                         ..
                  Pred. No. 2.8e+02;
; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.0%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 2.8e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIF: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Diddiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFRENCE/DOCKET NUMBER: 8085ZX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4346
TELERX: 239 910 SANS UR
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STREET TYPE: nucleic acid
STREET TYPE: nucleic acid
                                                                                                                                                                                                           US-08-413-813-12/c
; Sequence 12, Application US/08413813
; Patent No. 5683874
100.0%; Pre
                Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 8; Conservative
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COMPUTER READABLE FORM:
                                                                                931 TCCCTCCT 938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-413-813-12
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RESULY 404
US-08-413-413-813
IS GQUENCE 30, Application US/08413813
Fetent No. 5683874
Fetent No. 5683874
FAPLICANT: KOOL, Eric T.
FILLE OF INVENTION:
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
FITLE OF INVENTION: SINGLE-STRANDED, CIRCULAR OLIGONUCLEOTIDES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
FITLE OF INVENTION: At Old Garden City Plaza
CITY: Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
11.0%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/413,913
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TITLE OF INVENTION: RNA APTAMERS BASED ON SHAPE SELECTION NUMBER OF SEQUENCES: 16 CORRESPONDENCE ADDRESS: ADDRESSE: Schwegman, Lundberg, Woessner & Kluth, P.A. STREET: P.O. Box 2938 CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 11530
COMPUTER READBLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,670
                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/662,335A
FILING TER: 12-UW-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: No. 5792613e
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30,440
--- 423.001US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Woesner, Warren D
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 42
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity luv...
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
                                                                                                                                                                                          ZIP: 55402
COMPUTER READABLE FORM:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear ; MOLECULE TYPE: CDNA US-08-662-335A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 CCTGGTCA 12
                                                                                                                                                                         USA
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                                                                                                                                                 STATE: M
COUNTRY:
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                                                                                                                                                                                                                                                              Sequence 26, Application US/08667689A
Patent No. 5714330
GENERAL INVALION:
GENERAL INVALION:
APPLICANT: Sydney Brenner, Robert B. DuBridge
TITLE OF INVENTION: DNA Sequencing by Stepwise Ligation and Cleavage
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen C. Macevicz, Lynx Therapeutics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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         Query Match 11.0%; Score 8; DB 1; Length 12; Best Local Similarity 12.5%; Pred. No. 2.8e+02; Matches 1; Conservative 7; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 11.0%; Score 8; DB 1; Length 12; Best Local Similarity 100.0%; Pred. No. 2.8e+02; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: 1BM compatible
OPERATING SYSTEM: Windows 3.1/DOS 5.0
SOFTWARE: Microsoft Word for Windows, vers. 2.0
SOFTWARE: 1DM OBTA:
APPLICATION NUMBER: US/08/667,689A
FILING DATE: 21-JUN 1996
CLASSIFICATION NUMBER: 08/410,116
FILING DATE: 24-MAR-95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222,300
FILING DATE: 24-MAR-95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222,300
FILING DATE: 04-APR-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/280,441
FILING DATE: 25-JUL-94
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 30,285
REFERENCE/DOCKET NUMBER: 801-06
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Sequence 16, Application US/08662335A
Patent No. 5792613
GENERAL INFORMATION:
APPLICANT: Schmidt, Francis J.
TITLE OF INVENTION: METHOD FOR OBTAINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (510) 670-9365
TELEFAX: (510) 670-9302
INPORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
EDNESS: single
                                                                                                        908 TTTTCTTT 915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Hayward
STATE: California
                                                                                                                                2 UUUUCUUU 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
US-08-667-689A-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                US-08-667-689A-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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Gaps
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US-08-466-670-11

Sequence 11, Application US/08466670

Patent No. 5808036

GENERAL INFORMATION:

APPLICANT KOOL). Eric T.

TITLE OF INVENTION: STEM-LOOP OLIGONUCLEOTIDES CONTAINING

TITLE OF INVENTION: PARALLEL AND ANTIPARALLEL BINDING DOMAINS

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCUlly, Scott, Murphy & Presser

STREET: 400 darden City Plaza

CITY: Garden City

STATE: New York

COUNTRY: USA
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                                                   0; Indels
11.0%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 2.8e+02; trive 0; Mismatches 0; Indels
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0; Indels
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100.0%; Pred. No. 2.8e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: CALLIDOLIDA

ZIP: 9445

ZIP: 9445

COMPUTER READELFORM:
MEDLINY TYPE: 3.5 inch diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 3.1/DOS 5.0

SOFTWARE: Microsoft Word for Windows, vers. 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712,011

FILING DATE: 1-SEP-96

CLASSIFICATION NUMBER: 08/410,116

FILING DATE: 24-MAR.95

PRIOR APPLICATION NUMBER: 08/222,300

FILING DATE: 04-APR.94

PRIOR APPLICATION NUMBER: 08/222,300

FILING DATE: 25-UUL-94

ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 30,285

REGISTRATION NUMBER: 30,285

REGISTRATION NUMBER: 30,285

REGISTRATION NUMBER: 30,285

REGISTRATION NUMBER: 30,285

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION:
TELECOMMUNICATION INFORMATION INFO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kim, Nam Woo
Wu, Fred
Kealey, James T.
Fruzan, Ronald
Weinrich, Scott L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 nucleotides
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (510) 670-9302
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      935 TCCTCTTC 942
                                            924 CCTTTTAT 931
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US-08-712-011-26
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
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APPLICANT: Mohr, lan J.
APPLICANT: Gluzman, Yakov
TITLE OF INVENTION: Avirulant Herpetic Viruses Useful as
TITLE OF INVENTION: Tumoricidal Agents and Vaccines
TITLE OF INVENTION: Tumoricidal Agents and Vaccines
NUMBERS OF SEQUENCES: 9
CORRESPONDENCE ADDRESS: 9
CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: American Cyanamid Plaza
CITY: Wayne
STRRET: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
COMPUTER: BEADABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: BEADABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: BEADABLE FORM:
MEDIUM TYPE: BLOSS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 31,088
REPERENCE/DOCKET NUMBER: 31,088
R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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11.0%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.0%; Score 8; I
100.0%; Pred. No.
APPLICATION NUMBER: 08/115,497
                        FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: DIGGGIO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8771
TELECOMUNICATION INFORMATION:
TELECHONE: (516) 742-4343
TELEFAX: (516) 742-4346
TELEFAX: (516) 742-436
INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/08686631 Patent No. 5824318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: DNA (genomic) US-08-466-670-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     908 TITICITY 915
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US-08-712-011-26

| Sequence 26, Application US/08712011
| Patent No. 5831065
| TILE OF INVENTION: Kits for DNA Sequencing by Stepwise Ligation and Cleavage NUMBER OF SEQUENCES: 40
| CORRESPONDENCE ADDRESS: ADDRESSEE: Stephen C. Macevicz, Spectragen, Inc. STREET: 3832 Bay Center Place CITY: Hayward CITY: Hayward STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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US-08-173-489C-83/c

Sequence 83, Application US/08173489C

Sequence 83, Application US/08173489C

Sequence 83, Application

Sequence 83, Application

Parent No. 5861244

APPLICANT: WANG, C. -G.

APPLICANT: HEPHURN, A. G.

ITLE OF INVENTION: TRIPLE-STRAND FORMATION.

ITLE OF INVENTION: TRIPLE-STRAND FORMATION.

NUMBER OF SEQUENCES: 365

CORRESPONDENCE ADDRESS: 365

ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,

STREET: 510 EAST 73RD STREET,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.0%; Score 8; DB 1; Length 12;
100.0%; Pred. No. 2.8e+02;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER EADDABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: 1BM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: WORDEFECT Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICIATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 29 DEC 1993
ATTORNEY AGENT INFORMATION:
REGISTRATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 99 OCT 1992
ATTORNEY AGENT INFORMATION:
RESERVENCE/DOCKET NUMBER: US518-6
TELECOMMUNICATION INFORMATION:
TELEBROME (attorney) (212) 708-1880
TELEBRANE: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 83:
FILING DATE: 04-APR-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/280,441
FILING DATE: 25-JUL-94
ATTORNEY/AGENT INFORMATION:
NAME: Stephen C. Macevicz
REGISTRATION NUMBER: 30,285
REFERENCE/DOCKET NUMBER: 31,281
TELEPHONE: (510) 670-9365
TELEPHONE: (510) 670-9365
TELEPHONE: (510) 670-9365
INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS:
LENGTH: 12 nucleotides
TYPE: nucleic acid
STREED SEGUENCE CHARACTERISTICS:
LENGTH: 12 nucleotides
TYPE: nucleic acid
STREED SEGUENCE CHARACTERISTICS:
LENGTH: 12 nucleotides
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 12 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (attorney) (2.
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     935 TCCTCTTC 942
                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear
US-08-478-239A-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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DESCRIPTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 10021.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: 1
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
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     TITLE OF INVENTION: Methods for Detecting the RNA Component of TITLE OF INVENTION: Telomerase CORRESPONDENCES: 26 CORRESPONDENCES: ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-478-239A-26
; Sequence 26, Application US/08478239A
; Patent No. 5856093
; GENERAL INFORMATION:
; APPLICANT: Sydney Brenner
TITLE OF INVENTION: Method of Determining Zygosity
NUMBER OF SEQUENCES: 40
; CORRESPENDENCE ADDRESS:
; ADDRESSEE: Stephen C. Macevicz, Spectragen, Inc.
STREET: 3832 Bay Center Place
; CITY: Hayward
; STATE: California
; COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: 18M compatible
COMPUTER: 18M compatible
COMPUTER: 18M compatible
OPERATING SYSTEM: Windows 3.1/DOS 5.0
SOSTWARE: Microsoft Word for Windows, vers. 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,239A
FILING DATE: 07-JUN-95
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/410,116
FILING DATE: 24-MAR-95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222,300
                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM FC compatible

COURENT ARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/770,565

FILING DATE: 20-DEC-1996

CLASSIFICATION: 435

ATTONNEY/AGENT INPORMATION:

NAME: Storella, John R:

REGISTRATION NUMBER: 32,944

REGISTRATION NUMBER: 32,944

RELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.0%; Score 8; DB 1; Lei
100.0%; Pred. No. 2.8e+02;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         935 TCCTCTTC 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 TCCTCTTC 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-770-565-4
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Gaps

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SERVERAL INFORMATION:

APPLICANT: Kool, Eric T.

TITLE OF INVENTION: SINGLE-STRANDED, CIRCULAR OLIGONUCLEOTIDES

TITLE OF INVENTION: SINGLE-STRANDED, CIRCULAR OLIGONUCLEOTIDES

CORRESPONDENCE ADDRESS:

ADDRESSER: Scully, Scott, Murphy & Presser

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: New York

COUNTRY: USA

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM FREADABLE FORM:

MEDIUM FREADABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 30, Application US/08467346

Patent No. 5872105

GENERAL INFORMATION:
TITLE OF INVENTION: SINGLE-STRANDED, CIRCULAR OLIGONUCLEOTIDES

NUMBER OF SEQUENCES: 44

ADDRESSEE: Scully, Scott, Murphy & Presser
                                                                     11.0%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 2.8e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 8; DB 1; Length 12;
Pred. No. 2.8e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IEM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,346
FILING DATE: 06-UN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/413,813
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGIO, FRANK S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8085ZXX
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEEXX: (516) 742-4343
TELEEXX: (516) 742-4343
TELEEXX: COMPUTER: SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                     US-08-467-346-13/c
; Sequence 13, Application US/08467346
; Patent No. 5872105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; P
Matches 8; Conservative 0;
                                                                  Query Match
Best Local Similarity 100.
Matches 8; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                         908 TITICITY 915
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          US-08-467-346-12
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| Sequence 12, Application US/08467346
| Pattent No. 587210.
| GENERAL INFORMATION:
| APPLICANT: Kool, Eric T.
| TITLE OF INVENTION: SINGLE-STRANDED, CIRCULAR OLIGONUCLEOTIDES NUMBER OF SEQUENCES: 44
| CORRESPONDENCE ADDRESS: ADDRESSEE: Scully, Scott, Murphy & Presser STRET: 400 Garden City Plaza CITY: Garden City Plaza CONTRY: USA
| COUNTRY: USA
ANTI-SENSE:
No
ANTI-SENSE:
No
ORGANISM: No
ORGANISM: Home sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: chromosome 13
MAP POSITION: 13414.2
PUBLICATION INFORMATION:
AUTHORS: Friend, S. H. Horowitz, J. M., Gerber, M.R.,
AUTHORS: Friend, S. P. Bogenmann, E. Li, F. P. Weinberg,
AUTHORS: R.A.
TITLE: Deletions of a DNA sequence
TITLE: Organization of the sequence and its encoded
TITLE: protein
JOURNAL: Sciences, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.0%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 2.8e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDLUM TYPE: Floppy disk
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MG-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,346
FLING DATE: 06-JUN-1995
FRIOR APPLICATION INDER: US/08/413,813
FRIDRAPHICATION NUMBER: 30-MAR-1995
ATORNEY/AGENT INFORMATION:
NAME: DIGIGIO, Frank S.
AFFERENCE/DOCKET NUMBER: 31,346
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DATE: 1987; RELEVANT RESIDUES IN SEQ ID NO: 83 :FROM 1 TO 12 US-08-173-489C-83
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Best Local Similarity 100.
Matches 8; Conservative
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PAGES:
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Gaps

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US-08-663-823B-65
; Sequence 65 Application US/08663823B
; Patent No. 5972633:
GENERAL INFORMATION:
APPLICANT: Rothberg, Jonathan
APPLICANT: Deam, Michael
APPLICANT: Simpson, John
TITLE OF INVENTION: METHOD AND APPARATUS FOR IDENTIFYING,
TITLE OF INVENTION: MIHOUT SEQUENCING
TITLE OF INVENTION: WITHOUT SEQUENCING
NUMBER OF SEQUENCES:
ADDRESSE: Pennie and Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
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Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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11.0%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CUNTRY: USA
COUNTRY: USA
ZIP: 10036-271
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: PATENTIN RElease #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/663,823B
FILING DATE: 14-Unne-1996
CLASSIFTORION: 422
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REFERENCE/DOCKET NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1934-033
TELESPONDICATION INFORMATION:
TELESPONDICATION INFORMATION INFORMATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTER STICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                         TELEPHONE: (703) 205-8000
TELEPAX: (703) 205-8050
INFORWATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                948 TITAATGI 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           937 CTCTTCAT 944
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                                                                                                                                                           COMPUTER: L1330
COMPUTER: Floppy disk
COMPUTER: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURSENIA APPLICATION DATA:
APPLICATION NUMBER: US 08/413,813
FILING DATE: 06-UN-1995
PRIOR APPLICATION NUMBER: US 08/413,813
FILING DATE: 30-MAR-1995
ATTORNEY AGENT INFORMATION:
NAME: Digislio, Frank S:
REGISTRATION NUMBER: 8085ZXX
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (516) 742-4343
TELEFAX: (516) 742-4343
TELEFAX: SO 901 SANS UR
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 Dase pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 476

US-08-232-001B-33/C

Sequence 33, Application US/08232081B

PETER NO. 586452

GENERAL INFORMATION:
APPLICANT: ONANI, HIDEYUKI
APPLICANT: WIJDENES, JOHN
APPLICANT: POGINGE, 42

CORRESPONDENCE ADDRESS:
ADDRESSE:
ADDRESSE:
CORRESPONDENCE BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747

COTTY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTER: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,081B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: SYENSSON, LEOMARD R
REGISTRATION NUMBER: 30,330
REFRENCE/DOCKET NUMBER: 20-3484
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              908 TTTTCTTT 915
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USA
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER IBM PC COMpatible
COMPUTER: IBM PC COMpatible
COMPUTER: IBM PC COMpatible
COMPUTER: IBM PC COMPatible
COMPUTER: IBM PC COMPATIBLE
CONFERNT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,355
FLING DATE: 06-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/775,993
ATTORNEY/AGRYT INFORMATION:
NAME: Kulik, David J. 6,576
REFERENCE/DOCKET NUMBER: 36,576
REFERENCE/DOCKET NUMBER: 36,576
REFERENCE/DOCKET NUMBER: 36,576
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (202)628-8800
TELEFRAX: (202)628-8844
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LEDGTH: 12 base pairs
LEDGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
SOFTWARE: FASTESTO DOS
SOFTWARE: FASTESTO VERSION 2.0
CURRENT APPLICATION NUMBER: US/08/874,825
FILING DATE: 13-UNN-1997
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 08/663,824
FILING DATE: 14-UNN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: DNA (genomic) US-08-779-355-10
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Best Local Similarity 100.
Matches 8; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         935 TCCTCTTC 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
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                                                                                                             Sequence 13, Application US/08507032
| Sequence 13, Application US/08507032
| Patent No. 5989810
| GENERAL INFORMATION:
| APPLICANT: Crabtree, Gerald R. |
| TITLE OF INVENTION: Screening Methods for Immunosuppressive TITLE OF INVENTION: Agents
| NUMBER OF SEQUENCE: 19 |
| CORRESPONDENCE ADDRESS: Appless: ADDRESSE: William M. Smith STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco STATE: California COUNTRY: USA COMPUTER: EMP PC COMPATION STATE: COMPUTER: IBM PC COMPATION SYSTEM: PC-DOS/MS-DOS SOFTWARE: IBM PC COMPATION SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: FT.LNG DATE: F
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US-08-79-355-10
US-08-79-355-10
Sequence 10, Application US/08779355
Patent No. 6017701
GENERAL INFORMATION:
APPLICANT: Sorge, Joseph A.
TITLE OF INVENTION: METHODS AND ADAPTORS FOR GENERATING TITLE OF INVENTION: SECIFIC NUCLBIC ACID POPULATIONS NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
STREET: D.C.
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 12; . 2.8e+02;
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Best Local Similarity 100.0%; Pred. No. 2.8
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIPECATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/228,944
FILING DATE:
APPLICATION NUMBER: US 07/749,385
FILING DATE: 22-AUG-1991
ATORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REFERENCE/DOCKET NUMBER: 5490A-89
TELECOMMUNICATION INFORMATION:
TELEFONE: 415-326-2402
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
EDNESS: single
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                                                            RESULT 478
US-08-507-032-13/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-507-032-13
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US-08-874-825-86

Sequence 86, Application US/08874825

Sequence 86, Application US/08874825

Sequence 86, Application US/08874825

Sequence 86, Application Sequence 86, Application Sequence 86, Applicant Nandabalan, Krishnan

APPLICANT: Nandabalan, Krishnan

APPLICANT: Nandabalan, Krishnan

APPLICANT: Kalbfleisch, Theodore

APPLICANT: Kalbfleisch, Theodore

TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF

TITLE OF INVENTION: AND IDENTIFICATION OF INHIBITORS OF THESE INTERACTORS

NUMBER OF SEQUENCES: 122

CORRESPONDENCE ADDRESS:

ADDRESSE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas ö Gaps .. 0; Indels 11.0%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 2.8e+02; tive 0; Mismatches 0; Indels

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Sequence 112 Application US/08874825
Fatent No. 6657101
GENERAL INFORMATION:
APPLICANT: Nandabalan, Krishnan
APPLICANT: Rothberg, Jonathan
APPLICANT: Yang, Maijia
APPLICANT: Kaight, James
APPLICANT: Kaight, James
TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF
TITLE OF INVENTION: PROTEIN-PROTEIN INTERACTIONS THAT OCCUR IN POPULATIONS
TITLE OF INVENTION: AND IDENTIFICATION OF INHIBITORS OF THESE INTERACTORS
NUMBER OF SEQUENCES: 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                            11.0%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 2.8e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 483
US-08-938-835A-10
; Sequence 10, Application US/08938835A
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TELEX: 66141 PENNIE
INPORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                          Query Match
Best Local Similarity 100.0
Tones 8; Conservative
                                                                                                                                   937 CTCTTCAT 944
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US-08-874-825-112
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        US-08-874-825-87
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Sequence 87. Application US/08874825

Sequence 87. Application General Sequence 87. Application Sequence 87. Application Sequence 87. Application September 9. Applicant: Northberg, Jonathan APPLICANT: Northberg, Jonathan APPLICANT: Knight, James APPLICANT: NORTHON: IDENTIFICATION AND COMPARISON OF TITLE OF INVENTION: AND IDENTIFICATION OF INHIBITORS OF THESE INTERACTORS NUMBER OF SEQUENCES: 122

CORRESPONDENCE ADDRESS:

ADDRESSE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York
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COUNTRY: USA

ZIP: 10036/2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: DISKETTE
COURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/874,825
FILING DATE: 13-UNA-1997
CLASSIFICATION: 435
FILING DATE: 14-UN-1996
ATTORNEY FYAGENT INFORMATION:
NAME: MISTOCK, S. Lesie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7934-045
REFERENCE/DOCKET NUMBER: 7934-045
TELECHONE: 212-790-9090
TELECHONE: 212-790-9090
TELECHONE: 212-790-9090
TELECHONE: 212-790-9090
TELECHONE: 212-790-9090
TELECHONE: SEQUENCE CHARATICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: Linear
TOPOLOGY: SINGA
                                                7934-045
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7934
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-909
TELERX: 212-866-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               937 CTCTTCAT 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 CTCTTCAT 11
                                                                                                                                                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: DNA US-08-874-825-86
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Gaps

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JAPELICANT: NCOLL, ERIC T.

TITLE OF INVENTION: HIGHLY SENSITIVE MULTIMERIC NUCLEIC ACID PROBES
FILE REPERENCE: 220.00010130
CURRENT APPLICATION NUMBER: 1997-08-13
CURRENT FILING DATE: 1997-08-13
EARLIER APPLICATION NUMBER: 08/805,631
EARLIER FILING DATE: 1997-08-33
EARLIER PILING DATE: 1997-08-24
EARLIER PILING DATE: 1997-02-26
EARLIER PILING DATE: 1993-04-15
NUMBER OF SEQ ID NOS: 83

NUMBER OF SEQ ID NOS: 83

SOFTWARE: PARCETIN VET: 2.0

ERROID NO 11

LENGTH: 12
                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.0%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 2.8e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                           US-08-910-632-11/c
; Sequence 11, Application US/08910632B
; Patent No. 6077668
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTHER INFORMATION: desired oligomer US-08-910-632-11
                                    TYPE: DNA
CRGANISM: Artificial Sequence
FEATURE:
CTHER INFORMATION: linear sequence
US-08-910-632-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 8; Conservative
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US-08-910-632-36/c
SEQ ID NO 8
LENGTH: 12
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APPLICANT: KOOL, ERIC T.

TITLE OF INVENTION:
FILE REFERENCE: 220.00010130

CURRENT APPLICATION UNDER: US/08/910,632B

CURRENT APPLICATION UNDER: US/08/910,632B

CURRENT APPLICATION UNDER: US/08/910,632B

EARLIER APPLICATION UNDER: 08/0905,631

EARLIER APPLICATION UNDER: 08/33,439

EARLIER APPLICATION UNDER: 08/33,439

EARLIER APPLICATION UNDER: 08/39,439

EARLIER FILING DATE: 1993-02-23

EARLIER FILING DATE: 1993-04-15

HARLIER PILING DATE: 1993-04-15

HARLIER PILING DATE: 1993-04-15

HARLIER PILING DATE: 1993-04-15

HARLIER FILING DATE: 1993-04-15

HARLIER FILING DATE: 1993-04-15

HARLIER FILING DATE: 1993-04-15

HARLIER FILING DATE: 1993-04-15
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                    GENERAL INFORMATION:
APPLICANT: SORGE, Joseph A.
APPLICANT: MULINAX, Rebecca L.
TITLE OF INVENTION: METHODS AND ADAPTORS FOR GENERATING
TITLE OF INVENTION: SPECIFIC NUCLEIC ACID POPULATIONS;
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner, L.L.P.
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
PILING DATE: 26-SEPT-1997
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/775,993
FILING DATE: 03-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/779,335
FILING DATE: 06-JAN-1997
ATPONEY/AGENT INFORMATION:
NAME: BARKEY, M. Paul
REGISTRATION NUMBER: 04121.0044-02000
TELEFOONNICATION INFORMATION:
TELEFOONNICATION INFORMATION:
TELEFOONE 202-408-4400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: MODEL COLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 8; DB 1; Le
Pred. No. 2.8e+02;
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                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 484
US-08-910-632-8/c
; Sequence 8, Application US/08910632B
; Patent No. 6077668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
11.0%; Scc
Best Local Similarity 100.0%; Pr
Matches 8; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       935 TCCTCTTC 942
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      Patent No. 6060245
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STATE: Minnesota
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                  Sequence 86, Application US/08663824

Batent No. 6083693

GENERAL INFORMATION:
GABEAL INFORMATION:
GABEAL INFORMATION:
APPLICANT: Nandabalan, Krishnan
APPLICANT: Nandabalan, Krishnan
APPLICANT: NOTEMPTION: IDEMTIFICATION AND COMPARISON OF PROTEIN-PROTEIN
TITLE OF INVENTION: INTERACTIONS THAT OCCUR IN POPULATIONS
FILE REFERENCE: 7994-006
CURRENT APPLICATION NUMBER: US/08/663,824
CURRENT FILING DATE: 1996-06-14
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Nandabalan, Krishnan
APPLICANT: Scriberg, Jonachan
APPLICANT: Scriberg, Jonachan
TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN
TITLE OF INVENTION: INTERACTIONS THAT OCCUR IN POPULATIONS
FILE REFERENCE: 7934-006
CURRENT APPLICATION NUMBER: US/08/663,824
CURRENT PILING DATE: 1996-06-14
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                    DB 1; Length 12; . 2.8e+02; ches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 11.0%; Score 8; DB 1; Length 12; Best Local Similarity 100.0%; Pred. No. 2.8e+02; Matches 8; Conservative 0; Mismatches 0; Indels
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                                                                                                                    Query Match
11.0%; Score 8; DB 1
Best Local Similarity 100.0%; Pred. No. 2.8
Matches 8; Conservative 0; Mismatches
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; Patent No. 6083693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
                                            OTHER INFORMATION: primer US-08-910-632-36
                                                                                                                                                                                                                       908 TTTTCTTT 915
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US-08-663-824-86
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US-08-663-824-87
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LENGTH: 12
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US-08-663-824-112
US-08-663-824-112
Sequence 112, Application US/08663824
Fatent No. 6083633
Fatent No. 608363
Fatent No. 6083633

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| Sequence 8, Application US/08805631A
| Patent No. 6096880
| GENERAL INFORMATION
| TILLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND TITLE OF INVENTION: DNA
| TITLE OF INVENTION: DNA
| TITLE OF SEQUENCES: 72
| CORRESPONDENCE ADDRESS: 72
| CORRESPONDENCE ADDRESS: WHETING, RAASCH & GEBHARDT, P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , OTHER INFORMATION: Description of Artificial Sequence: linker
US-08-663-824-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 11.0%; Score 8; DB 1; Length 12; Best Local Similarity 100.0%; Pred. No. 2.8e+02; Matches 8; Conservative 0; Mismatches 0; Indels
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STREET: 119 No. 6096880th Fourth Street, Suite 201
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COURERNI APPLICATION DATA:
APPLICATION NUMBER: US/08/805,631A
FILING DATE: 26-FEB-97
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/393,439
FILING DATE: 23-FEB-195
RICH APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/393,439
FILING DATE: 33-FEB-1995
RICH APPLICATION DATA:
APPLICATION NUMBER: US 08/393,439
FILING DATE: 15-APR-1993
ATTORNEY/AGENT INFORMATION:
ANDEREY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: SANDBERG, VICTORIA A. REGISTRATION NUMBER: 41,287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     612-305-1226
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4 CTCTTCAT 11
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ABELICANT: UNIVERSITY OF ROCHESTER
APPLICANT: UNIVERSITY OF ROCHESTER
TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
TITLE OF INVENTION: DNA
NUMBER OF SEQUENCES: 72
CORRESPONDENCES: 72
CORRESPONDENCES: ADDRESS:
ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
STREET: Minneapolis
STREET: Minneapolis
STATE: Minneapolis
STATE: Minneapolis
CITY: Winneapolis
STATE: Winneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
OPERATING SYSTEM:
CURRENT APPLICATION DATA:
PRILING DATE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PRILING DATE: 26-FEB-97
PRILING DATE: 28-FEB-97
PRILING DATE: 23-FEB-1995
PRILING DATE: 23-FEB-1995
PRILING DATE: 15-APR-1993
ATPORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 41.287
REGISTRATION NUMBER: 41.287
REGISTRATION NUMBER: 41.287
REGISTRATION NUMBER: 41.287
REGISTRATION NUMBER: 41.287
REFERENCE/DOCKET NUMBER: 220.00010140
TELECOMMULCATION NUMBER: 41.287
REFERENCE/DOCKET NUMBER: 220.00010140
TELECOMMULCATION NUMBER: 41.287
REFERENCE/DOCKET NUMBER: 220.00010140
TELECOMMULCATION NUMBER: 220.00010140
TELECOMMULCATION SEQ. 12.06.12.26
INFORMATION FOR SEQ. 1D NO: 36: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                          US-08-805-631A-36/c
; Sequence 36, Application US/08805631A
; Patent No. 6096880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 100.
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                       Gaps
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APPLICANT: UNIVERSITY OF ROCHESTER
TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND
TITLE OF INVENTION: DIA
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
STREET: 119 No. 6096880th Fourth Street, Suite 201
CITY: Minneapolis
STREET: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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100.0%; Pred. No. 2.8e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                 11.0%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 2.8e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/805,631A
FILING DATE: 26-FEB-97
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/393,439
FILING DATE: 23-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/047,860
FILING DATE: 15-APR-1993
ATTORNEY/AGENT INFORMATION:
ARPLICATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 220.00010140
TELEPHONE: 612-305-1226
TELEFAX: 612-305-1226
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US-08-805-631A-11/c
; Sequence 11, Application US/08805631A
; Patent No. 6096880
                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-805-631A-8
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Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 8; Conservative
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                 LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Sequence 45, Application US/09593323

GENERAL INFORMATION:
APPLICANT: Morgan, Antony R.
APPLICANT: Severini, Alberto
TITLE OF INVENTION: Compositions and Methods for Determining the Activity
TITLE OF INVENTION: of DNA-Binding Proteins and of Initiation of
TITLE OF INVENTION: Transcription
FILE REFERENCE: DNAB-02921
CURRENT APPLICATION NUMBER: US/09/593,323
PRIOR PILING DATE: 2000-06-13
PRIOR PAPLICATION NUMBER: 09/344,300
PRIOR FILING DATE: 1999-06-24
11.0%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 2.8e+02; trive 0; Mismatches 0; Indels
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Patentin Ver. 2.0
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SOFTWARE:
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Sequence 59, Application US/09354231B
Sequence 59, Application US/09354231B
Sequence 59, Application US/09354231B
GENERAL INFORMATION:
APPLICANT: DeBonte, Lorin R.
APPLICANT: Shorrosh, Basil S.
TITLE OF INVENTION: FAITY ACID DESATURASES AND MUTANT SEQUENCES THEREOF
FILE REPERENCE: 07149-063102
CURRENT APPLICATION NUMBER: US/09/354,231B
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US 08/874,109
PRIOR APPLICATION NUMBER: US 08/874,109
NUMBER OF SEQ ID NOS: 69
SEQ ID NOS: 69
LENGTH: 12
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APPLICANT: Morgan, Antony R.
APPLICANT: Morgan, Alberto
TITLE OF INVENTION: Compositions and Methods for Determining the Activity
TITLE OF INVENTION: of DNA-Binding Proteins and of Initiation of
TITLE OF INVENTION: Transcription
FILE REFERENCE: DNAB-02921
CURRENT APPLICATION NUMBER: US/09/344,300B
CURRENT FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 45
LENGTH: 12
                                                                                                                                   Gaps
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-344-300-45
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                                                                          Query Match
11.0%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 11.0%; Score 8; DB 1; Length 12; Best Local Similarity 100.0%; Pred. No. 2.8e+02; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                               Sequence 45, Application US/09344300B
Patent No. 6297013
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
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     OTHER INFORMATION: Primer
                                                                                                                                                                                     954 GTATCGCT 961
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                   11 GTATCGCT
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US-09-281-418-185
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GENERAL INFORMATION:
APPLICANT: Inoue, Takakazu
APPLICANT: Inoue, Takakazu
TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA FITLE OF INVENTION: agment, Method of Assaying Microorganisms, Method of Analyzing Mi TITLE OF INVENTION: nisms and Method of Assaying Contaminant
TITLE OF INVENTION: nisms and Method of Assaying Contaminant
TITLE OF INVENTION: nisms and Method of Assaying Contaminant
CURRENT FILING DATE: 1999-03-30
EARLIER APPLICATION NUMBER: JP/1998/87651
EARLIER PILING DATE: 1999-03-16
EARLIER FILING DATE: 1999-03-16
SEQ ID NOS: 216
SEQ ID NO 185
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 45, Application US/09594108
| Patent No. 628448|
| Patent No. 628448|
| GENERAL INFORMATION:
| APPLICANT: Morgan, Antony R. APPLICANT: Severini, Alberto | TITLE OF INVENTION: Compositions and Methods for Determining the Activity | TITLE OF INVENTION: Transcription | TITLE OF INVENTION: Transcription | TITLE OF INVENTION: Transcription | FILE REFERENCE: DNAB-02921 | CURRENT APPLICATION NUMBER: US/09/594,108 | PRIOR APPLICATION NUMBER: 09/344,300 | PRIOR PILING DATE: 1999-06-13 | PRIOR FILING DATE: 1999-06-24 | NUMBER OF SEQ ID NOS: 72 | SOFTWARE: PatentIn Ver. 2.0
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                                                                                                  FEATURE:
, OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-593-323-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-594-108-45
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11.0%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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Patent No. 6287769
                                                 TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
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US-09-281-418-185/c
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US-09-594-108-45/c
SEQ ID NO 45
LENGTH: 12
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LENGTH: 12
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity luv.
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US-09-569-344-36/c
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Sequence 11, Application US/09569344
Patent No. 6368802
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF ROCHESTER
TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND DNA
                                         Sequence 8, Application US/09569344

Sequence 8, Application US/09569344

Patent No. 6368802

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF ROCHESTER
TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND DNA
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CORRESPONDENCE ADDRESS:
ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
ADTRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
STREET: 119 No. 6368802th Fourth Street, Suite 201
CITY: Minnespolis
STATE: Minnesota
                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
STREET: 119 No. 6368802th Fourth Street, Suite 201
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.0%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 2.8e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                               ZIP: 55401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPUTER: SYSTEM: PC-DOS/MS-DOS
OPPETIUS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/569,344
FILING DATE: 11-MAY-2000
FILING DATE: 11-MAY-2000
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION WIMBER: US 08/805,631
FILING DATE: 26-FBB-97
APPLICATION NUMBER: US 08/39,439
FILING DATE: 23-FBB-1995
APPLICATION NUMBER: US 08/047,860
FILING DATE: 15-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG, VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 220.00010140
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 612-305-1226
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MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                              NUMBER OF SEQUENCES:
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RESULT 498
US-09-569-344-8/c
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; Sequence 36, Application US/09569344
; Patent No. 6368802
; GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF ROCHESTER
TITLE OF INVENTION: CIRCULAR DNA VECTORS FOR SYNTHESIS OF RNA AND DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
STREET: 119 No. 6368802th Fourth Street, Suite 201
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/569,344
FILING DATE: 11-May-2000
CLASSIFICATION NUMBER: US 08/805,631
FILING DATE: 26-FEB-97
APPLICATION NUMBER: US 08/393,439
FILING DATE: 15-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG, VICTORIA A.
REGISTRATION NUMBER: 41.287
REFERENCE/DOCKET NUMBER: 220.00010140
TELEPHONE: 612-305-1226
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARATICES:
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COMPUTER READABLE FORM:

MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/569,344
FILING DATE: 11-May-2000
CLASSIFCATION: cUnknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.0%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 2.8e+02;
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FILING DATE: 26-FEB-97
APPLICATION NUMBER: US 08/393,439
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TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                           937 CTCTTCAT 944
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Sequence 86, Application US/09231303

Patent No. 6395478

GENERAL INFORMATION:

APPLICANT: Nandabalan, Krishnan

APPLICANT: Nathberg, Jonathan

TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN

TITLE OF INVENTION: IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS

FILE REPRENCE: 7934-087

CURRENT APPLICATION NUMBER: US/09/231,303

CURRENT FILING DATE: 1999-01-12

EARLIER APPLICATION NUMBER: 08/663,824

BALLIER PLICATION DATE: 1996-06-14

NUMBER OF SEQ ID NOS: 118

SOFTWARE: PATENTING DATE: 1996-06-14

NUMBER OF SEQ ID NOS: 118

SEQ ID NO 86

LENGTH: 12
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Sequence 87, Application US/09231303
Sequence 87, Application US/09231303
GENERAL INFORMATION:
APPLICANT: Nondabalan, Krishnan
APPLICANT: Sothberg, Jonathan
TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN
TITLE OF INVENTION: IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS
TITLE OF INVENTION: IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS
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11.0%; Score 8; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
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PILING DATE: 23-FBB-1995
APPLICATION NUMBER: US 08/047,860
FILING DATE: 15-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG, VICTORIA A.
REGISTRATION NUMBER: 41,287
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1226
TELEPHONE: 612-305-1226
                                                                                                                                                                                                                                                                                   LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLGGY: linear
MOLECTLE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 36: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.0
Matches 8; Conservative
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US-09-231-303-86
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CHRENT PILE RESERVER, 1294-469, 1211-103

FRALIER PRESERVER, 1298-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-601-1295-
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Gaps
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Sequence 1, Application PC/TUS9503602
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
SCREEPONDENCE ADDRESS:
MUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scally, Scott, Murphy & Presser
STREET: Wew York
COUNTRY: Garden City Plaza
CITY: Garden City Plaza
CITY: Garden City
STREET: New York
COUNTRY: U.S.A.

ZIP: Ilso 0.0299
COMPUTER: Ilso 0.0299
COMPUTER: PLOSO 0.0290
COM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
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PCT-US95-03602-2
PCT-US95-03602-2
Sequence INFORMATION:
GENERAL INFORMATION:
APPLICANT: Research Corporation Technologies, Inc.
APPLICANT: Research Corporation Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 12;
                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                   Score 8; DB 1; Length 12;
Pred. No. 2.8e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Len
OTHER INFORMATION: /note= "5-methylcytosine"
                                                                                                              /mod_base= OTHER
/note= "5-methylcytosine"
                                                                                                                                                                                                                               11.0%;
                                                    NAME/KEY: modified_base
| LOCATION: 11
| LOCATION: 17
| OTHER INFORMATION: /mod
| CTHER INFORMATION: /mote
                                                                                                                                                                                                Query Match
Best Local Similarity 80...
Best Local Similarity 80...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                933 CCTCCTCTTC 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                  2 MCTTCTCTTC 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      931 ICCCICCT 938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 recercer 12
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Sequence 93, Application PC/TUS9103680

GENERAL INFORMATION:
APPLICANT: Matteucci, Mark D.
APPLICANT: Krawczyk, Steven
TITLE OF INVENTION: SEQUENCE-SPECIFIC NONPHOTOACTIVATED
TITLE OF INVENTION: DUPLEX DNA
TITLE OF INVENTION: DUPLEX DNA
NUMBER OP SEQUENCES: 158
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mortison & Poerster
STREET: 545 Middlefield Road, Suite 200
CITY: Mail Park
STATE: California
                                                                                                                                                                                                         ô
                                                                                                                                                                                                         .
0
                                                                                                                                               11.0%; Score 8; DB 1; Length 12; 100.0%; Pred. No. 2.8e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/03680
FILING DATE: 19910524
FLING DATE: 19910524
CLASSITICATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4610-0011.40
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEX: 706141
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTER: STATOS
LENGTH: 12 base pairs
TYPE: NUCLEIC ACLD
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "5-methylcytosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "5-methylcytosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
FEATURE:
NAME/KEY: modified_base
LOCATION: 2
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 3
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "5-methyl
FEATURE: modified_base
LOCATION: 6
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LOCATION: 8
OTHER INFORMATION: /mod_base= OTHER
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                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                 908 TITICITI 915
                                                                                                                                                  Query Match
Best Local Similarity
Matches 8; Conserv
                                    ; TYPE: DNA; ORGANISM: human US-09-475-947A-19
         LENGTH: 12
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Gaps
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Pred. No. 2.8e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Alexander-Bridges, Maria C.
APPLICANT: Alexander-Bridges, Maria C.
APPLICANT: Alexander-Bridges, Maria C.
TITLE OF INVENTION: INFIBITION OF INSULIN-INDUCED TITLE OF INVENTION: ADIPOSIS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE-FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIPICATION S14
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/242,409
FILING DATE:
CLASSIPICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           00786/238001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-242-409-2; Sequence 2, Application US/08242409; Patent No. 5496831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Fish & Richardson
225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.7%;
81.8%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 81.8
Matches 9; Conservative
          12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    929 TATCCCTCCTC 939
                                    ; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US95-03602-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 Trrccccccrc 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 510
US-08-049-283A-2/c
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PCT-US95-01602-1/C
; Sequence 3, Application PC/TUS9503602
; Sequence 3, Application
; TITLE OF APPLICANT: Research Corporation Technologies, Inc.
; TITLE OF INVENTION: STEM-LOOP AND CIRCULAR OLIGONUCLEOTIDES
; WUMBER OF SEQUENCES:
; RORRESPONDENCE ADDRESS:
; CORRESPONDENCE ADDRESS:
; STREET: 400 Garden City Plaza
CITY: Garden City
; STATE: New York
; COMPTRY: US.A.
; COMPTRY: N.S.A.
; COMPTRY: READABLE FORM:
; MEDLUM TYPE: Floppy disk
; COMPTRE: Ploppy disk
; COMPTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                  COUNTRY: U.S.A.

ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03602
FILING DATE: 21-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 11.0%; Score 8; DB 1; L. Best Local Similarity 62.5%; Pred. No. 2.88+02; Matches 5; Conservative 3; Mismatches 0
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                             FILING URB:
ATTORNEY/AGENT INFORMATION:
NAME: Didsglo, Frank 31,346
REGISTRATION NUMBER: 31,346
REGISTRATION NUMBER: 9373
TELECOMMUNICATION INFORMATION:
TELEFAX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERRINCE/DOCKET NUMBER: 9373
TELECOMMUNICATION INFORMATION:
TELERRY: (516) 742-4343
TELERRY: (516) 742-4346
TELERX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   931 TCCCTCCT 938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
PCT-US95-03602-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
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Sequence 13, Application US/08196103A

Sequence 13, Application US/08196103A

Patent No. 5672472

GENERAL INFORMATION:

APPLICANT: Excker, David J.

APPLICANT: Bruice, Thomas A.

APPLICANT: Davis, Peter

APPLICANT: Hancack, Ronnie C.

APPLICANT: Watt, Jaqueline

TITLE OF INVENTION: Synthetic Unrandomization of Oligomer

TITLE OF INVENTION: Synthetic Unrandomization of Oligomer

TITLE OF INVENTION: Fragments

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS: 21

ADDRESSEB: Woodcock Washburn Kurtz Mackiewicz and No. 5672472ris

STREET: One Liberty Place - 46th Ploor

GITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cuery Match
10.7%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: FINITIAL STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/196,103A
FILING DATE: February 22, 1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/196,103A
FILING DATE: Z3-AUG-1991
ATILING DATE: Z3-AUG-1991
ATILING DATE: Z3-AUG-1991
ATILING BATE: Z3-AUG-1991
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage COMPUTER: IBM COMPAtible OPERATING SYSTEM: IBM P.C. DOS (Version 5.0) SOFTWARE: Worderfect (Version 5.1) SOFTWARE: Worderfect (Version 5.1) CURRENT APPLICATION DATA: BAPLICATION NUMBER: US/08/435,350 FILING DATE: 05-MAY-1995 CLASSIPICATION: 514 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/936,531 FILING DATE: AUGUST 26, 1992 ATTORNEY/AGENT INFORMATION: NAME: Warburg Richard J. REGISTRATION NUMBER: 197/245 TELECOMMUNICATION INFORMATION: TELECHONE: (213) 489-1600 TELEFAX: (213) 955-0440 TELEFAX: (213) 955-0440 INFORMATION PRESENCE CHARACTERISTICS: BENGTH: 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               916 GGTCTTTGCCT 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-435-350-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 GGACTTGGCCT 1
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US-08-196-103A-13
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                        APPLICANT: Tenen, Daniel G.
APPLICANT: Pahl, Heike L.
APPLICANT: Burn, Timothy C.
TITLE OF INVENTIORS: 34
CORRESPONDENCE ADDRESS: 34
ADDRESSEB: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: TWO Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 11;
                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: PLOPBY disk
MONDUTER: IBM PC compatible
OOMPUTER: IBM PC compatible
OOMPUTER: IBM PC compatible
OOMPUTER: IBM PC compatible
OOMPUTER: IBM PC compatible
OURRANT APPLICATION DATA:
APPLICATION NUMBER: US/08/049,283A
FILING DATE: 14-APR.1993
FILING DATE: 19-FEB-1993
CLASSIFICATION OATA:
APPLICATION NUMBER: 08/020,465
FILING DATE: 19-FEB-1992
CLASSIFICATION 435
PRIOR APPLICATION 435
PRIOR APPLICATION: 435
ATRONEY/AGENT INFORMATION:
MANNE: BROOK, DAVIG E.
REGISTRATION NUMBER: 22,592
REGISTRATION NUMBER: 22,592
REGISTRATION NUMBER: 22,592
REGISTRATION NUMBER: 22,592
REGISTRATION NUMBER: B1H91-03'A
TELEPRANE (617) 861-6240
TELECOMMUNICATION INFORMATION:
TELEPRANE (617) 861-6540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENNATH: 11 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 511

US-08-435-350-109/C
; Sequence 109, Application US/08435350
; Patent No. 5599704
; GENERAL INFORMATION:
APPLICANT: James D. Thompson
APPLICANT: Genes D. Thompson
APPLICANT: MEMBER OF SEQUENCES:
TITLE OF INVENTION: TREATMENT OF BREAST CANCER
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STRTET: Gall West Sixth Street
COUNTRY: USA
ZIP: 90017
COMPUTER T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 10.7%; Score 7.8; DB 1; Best Local Similarity 81.8%; Pred. No. 2.8e+02; Matches 9; Conservative 0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: DNA (genomic)
US-08-049-283A-2
                                                                                                                                                                                                               STREET: Two Militia Dr
CITY: Lexington
STATE: Massachusetts
CCUNTRY: USA
ZIP: 02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            919 CTTTGCCTTTT 929
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             GENERAL INFORMATION:
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932 CCCTCCTCTTC 942
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US-08-314-309A-34/C
; Sequence 34, Application US/08314309A
; Patent No. 56/7141
; GENERAL INFORMATION:
APPLICANT: ISOGAL, TAKAO
; APPLICANT: FUKAGWA, MASAO
; APPLICANT: FUKAGWA, MASAO
; APPLICANT: TRAMONI, ICHIRO
; APPLICANT: TRAMONI, ICHIRO
; APPLICANT: KOJO, HITOSHI
; TITLE OF INVENTION: PROCESS FOR PRODUCING 7-AMINOCEPHEM
TITLE OF INVENTION: COMPOUND OR SALTS THEREOF
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 10.7%; Score 7.8; DB 1; Length 11; Similarity 54.5%; Pred. No. 2.8e+02; 6; Conservative 3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:

ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
MEDIUM TYEE: Floppy disk
MEDIUM TYEE: BAC compatible
MEDIUM SYSTEM: PC-DOS/MS-DOS
MOSTWARE: Datentin Release #1.0, Version #1.25
MEDIUM TAPLICATION DATA:
MAPPLICATION NUMBER: US/08/314,309A
FILING DATE: 30-SEP-1994
FILING DATE: 37-SEP-1994
FILING DATE: A35
MATA:
MA
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ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/631,906
FILING DATE: 21-DEC-1990
ATTORNEY/AGENT INFORMATION: NAME: Oblon, No. 5677141man F. REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-863-0 CONT TELEFAX: (703) 413-220
TELEFAX: (703) 413-220
TELEFAX: 248855 OPAT UR
INFORMATION FOR SEQ 1D NO: 34: SEQUENCE CHARACTERISTICS: SEQ
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: ISIS-0678
TELECOMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEPHONE: 215-568-3439
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGYTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: synthetic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
US-08-196-103A-13
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TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       932 CCCTCCTCTTC 942
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Best Local Similarity
Matches 6; Conserva
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: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-314-309A-34
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COUNTRY:
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0
                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Watt, Jacquelline
APPLICANT: Wogesh S. Sanghvi
TITLE OF INVENTION: Improved Methods for Synthetic Unrandomization
TITLE OF INVENTION: of Oligomer Fragments
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5698391ris
STREET: One Liberty Place - 46th Floor
                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
Score 7.8; DB 1; Length 11; Pred, No. 2.8e+02; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 7.8; DB 1; Length 11
Pred. No. 2.8e+02;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: PA
COMPRES U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BE PC compatible
COMPUTER: BE PC compatible
COMPUTER: BE PC compatible
SOFTWARE: Patentil Release #1.0, Version #1.25
CURRENT APPLICATION DATA: NA
APPLICATION NUMBER: US/08/357,396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISIS-1745
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CLASSTFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 749,000
FILING DATE: 23-AUC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 196,103
FILING DATE: 22-FEB-1994
ATVONEY/AGENT INFORMATION:
NAME: RAIDH, Rebecca L.
REGISTRATION NUMBER: 35,152
                                                                                                                                                                                                        RESULT 514
US-08-357-396-13
; Sequence 13, Application US/08357396
; Patent No. 5698391
; GENERAL INPORMATION:
APPLICANT: Philip Dan Cook
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: IS:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                     Philip Dan Cook
Ecker, David J.
Anderson, Kevin
Bruice, Thomas A.
Davis, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanecak, Ronnie C
Vickers, Timothy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: RNA (genomic) US-08-357-396-13
                                                                                                                                                                                                                                                                                                                                                                                                                                         Driver, Vickie
Freier, Susan, M.
Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
                                                                                           958 CGCTACCAACG 968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
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SEE: PROFILE DIAGNOSTIC SCIENCES, INC., 1 S10 EAST 73RD STREET, NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            932 CCCTCCTCTTC 942
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                                                                    NEW YORK
                                                                                            USA
                                                                                       COUNTRY: U
       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-173-489C-60
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                                                                                                                                                                          APPLICANT: Ecker, David J.
APPLICANT: Ecker, David J.
APPLICANT: Davis, Peter
APPLICANT: Davis, Peter
TITLE OF INVENTION: COMBINATORIAL OLIGOMER
TITLE OF INVENTION: IMMUNOABSORBANT SCREENING ASSAY FOR TRANSCRIPTION
TITLE OF INVENTION: FACTORS AND OTHER BIOMOLECULE BINDING
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz and
ADDRESSE: No. 5747253ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Pred. No. 2.8e+02;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 516
US-08-173-489C-60
S-08-173-489C-60
Sequence 60, Application US/08173489C
Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/386,141
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/032,852
FILING DATE: 16 WAR 1993
APPLICATION NUMBER: US/07/749,000
FILING DATE: 23-A0C-1991
ATTORNEY/AGENT INFORMATION:
NAME: Gaumond, Rebecca R.
REGISTRATION NUMBER: 151S-0653
REFERENCE/DOCKET NUMBER: 151S-0653
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION 13:
TELEFORMUNICATION 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDENNES: single
                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTER: PC-DOS/MS-DOS
OPERATING PAPENTIN Release #1.0, V
                                                                                                            Sequence 13, Application US/08386141 Patent No. 5747253 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear; MOLECULE TYPE: RNA (genomic)
US-08-386-141-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       932 CCCTCCTCTTC 942
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       1 CCCUMCCCUMC 11
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       В
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Length 11;
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US-08-173-489C-138

Sequence 138, Application US/08173489C

Patent No. 5861244

GENERAL INFORMATION:
APPLICANT: WANG, C. -G.

TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365

CORRESPONDENCE ADDRESS:
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET; STO EAST 73RD STREET,
CITY: NEW YORK

STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 7.8; DB 1; Length 11 Pred. No. 2.8e+02; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TODGLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from HER-2
DESCRIPTION: sequence region in Seq ID No. 586124459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 : FROM 1 TO 11
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM FOLYNTYT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION NUMBER: US/08/13,489C
FILING DATE: 29 DEC 1993
CLASSIFICATION NUMBER: US/08/136
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: US/28-179
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REFERENCE/DOCKET NUMBER: US/18-6
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 bases
TYPE: Nucleic Acid
STRANDEDURSS: single stranded
STRANDEDURSS: single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 10021.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
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Gaps ö

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TOPOLOGY: linear MOLECULE TYPE: other mucleic acid DESCRIPTION: third strand derived from Hepatitis B DESCRIPTION: isolate ayw sequence region in Seq ID No. 5861244149 HYPOTHETICAL: yes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
DESCRIPTION: 23s rRNA gene from Escherichia coli
DESCRIPTION: (Accession # M25458) nucleotides 982 to 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 7.8; DB 1; Length 11;
Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
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Sequence 221, Application US/08173489C

Pacent No. 5861244

GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANT: HERBURN, A. G.

TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: no'
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 150 :FROM 1 TO 11
US-08-173-4805-150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROFILE DIAGNOSTIC SCIENCES, INC.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: 18 PC/XT/AT

COMPUTER: 18 PC/XT/AT

COMPUTER: 18 PC/XT/AT

COMPUTER: 18 PC/XT/AT

COPERATING SYSTEM: MS-DOS version 6.2

SOFTWARE: Wordperfect Version 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/173,489C

FILING DATE: 22 DEC 1993

CLASSIFICATION 1435

PROM APPLICATION DATA:

APPLICATION NUMBER: US 07/968,436

FILING DATE: 29 OCT 1992

ATOMNEY AGENT INFORMATION:

NAME: Handelman, Joseph H.

REGISTRATION NUMBER: 26,179

REGISTRATION NUMBER: 26,179

REGISTRATION NUMBER: 26,179

REGISTRATION NUMBER: U9518-6

TELEPHONE: (ALTOMNATION:

TELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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TELEFAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 221:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANBDNESS: double stranded
                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 510 EAST 73RD STREET
NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Escherichia coli
STRAIN: MRECOO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
                                    SEQUENCE CHARACTERISTICS:
LENGTH: 11 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     931 TCCCTCCTTT 941
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MEDIUM TYPE: 3.5 incl
COMPUTER: IBM PC/XT//
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid STRANDENDESS: single stranded STRANDENDESS: single stranded TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: third strand derived from Hepatitis B DESCRIPTION: isolate adr sequence region in Seq ID No. 5861244137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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10.7%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.8e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 150, Application US/08173489C

Patent No. 5861244

GENERAL INFORMATION:
APPLICANT: HEPBURN, A. G.
ITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
ITLE OF INVENTION: TRIPLE-STRAND FORMATION:
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSEE: RROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 138 :FROM 1 TO 11
US-08-173-489C-138
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handedlman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: U9518-6
TELECPHONE: (attorney) (212) 708-1880
TELEFAX: (attorney) (212) 246-8959
INFORMATION POR SEQ ID NO: 138:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 bases
LENGTH: 11 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: 1BM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/436
FILING DATE: 29 OCT 1992
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
APPLICATION NUMBER: US 07/968,436
FILING DATE: 20 CT 1992
APPLICATION NUMBER: US 07/968,436
FILING DATE: 20 CT 1992
APPLICATION NUMBER: US 07/968,436
FILING DATE: 20 CT 1992
APPLICATION NUMBER: US 180
TELEFONMUNICATION INFORMATION:
TELEFONMUNICATION INFORMATION:
TELEFONMUNICATION INFORMATION:
TELEFONMUNICATION OF SEQ ID NO: 150:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (attorney)
TELEFAX: (attorney) (2
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                926 TITIAICCIC 936
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US-08-173-489C-150
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PUBLICATION
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JOURNAL:
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Patent No. 5861244

GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANTON: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 3.65
CORRESPONDENCE ADDRESS:
ADDRESSEE: PROPILE DIAGNOSTIC SCIENCES, INC.,
STREET: SID EAST 73RD STREET,
COMPUTER: NEW YORK
COUNTRY: USA
COMPUTER: INP PC/XY/AT
COMPUTER: 120 DCC 1993
COMPUTER: 120 DCC 1993
CLASSIFICATION NUMBER: US 07/968,436
FILING DATE: 22 DCC 1993
CLASSIFICATION NUMBER: US 07/968,436
FILING DATE: 22 DCT 1992
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 20 OCT 1992
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: US 07/968,436
TELECOMMUNICATION INFORMATION:
REGISTRATION NUMBER: US 07/968,436
TELECOMMUNICATION INFORMATION:
REGISTRATION NUMBER: US 07/968,436
TELECOMMUNICATION INFORMATION:
REGISTRATIC ACTORNEY) (212) 708-1880
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: US 07/968,436
TELECOMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 7.8; DB 1; Length 11; Pred. No. 2.8e+02; 0; Mismatches 2; Indels
                                          Machatt, M, A,
Edwards, K, Koessel,
                                                                                                                                        Primary and secondary structures of Escherichia coli MRE 600 238 structures of Escherichia coli MRE 600 238 ribosomal RNA Comparison with models of secondary structure for maize chloroplast 238 rRNA and for large portions of mouse and human 168 mitochondrial rRNAs ... Nucleic Acids Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from H. morrhuae
DESCRIPTION: 23s region in Seq ID No. 5861244225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221 :FROM 1 TO 11
PUBLICATION INPORMATION:
AUTHORS: Branlant, C, Krol, A, Ma. AUTHORS: Pouyet, J, Ebel, J P, E. AUTHORS: H.
TITLE: Primary and secondary
TITLE: ribosomal RNA Comparison with
                                                                                                                                                                                                                                                                                                                                                                                                                                             DATE: 1981
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-173-489C-221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 81.8%;
Matches 9; Conservative
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ANTI-SENSE: n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 520
US-08-173-489C-226
                                                                                                                                                                                                                                        TITLE: SETITLE: TRITLE: 16
JOURNAL: 9
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19. ORELICATION NO. 126; FROM 1 TO 11

OBS. ORELICATION REGIONS 118 OF THE SERVENT TO 11

OBS. OF THE SERVENT REGIONS 118 OF THE SERVENT TO 12

OBS. ORGANIZATION 10 77; SCOTO 7.5; DB 1; Length 11;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 905 TOATHTTOTH 315

US-08-173-480-265. Application US/08173489C

SEQUENCE 55. Application US/08173489C

SECTION THE PRINCE CONTRIBUTION: TRIPLE-STRAND PORMATION.

NUMBER OF SEGUENCES 356

TITLE OF INVESTION: TRIPLE-STRAND PORMATION.

NUMBER OF SEGUENCES 356

TITLE OF INVESTION: TRIPLE-STRAND PORMATION.

NUMBER OF SEGUENCES 356

TITLE OF INVESTION: TRIPLE-STRAND PORMATION.

NUMBER OF SEGUENCES 356

TITLE OF INVESTION: TRIPLE-STRAND PORMATION.

NUMBER OF SEGUENCES 356

TITLE OF INVESTION GREET: STRAND PORMATION.

NUMBER OF SEGUENCES 356

TITLE NOT TRIPLE STRAND 11.4440 SCOTES; INC., CONTRY. USA

SEGUENCE STRAND STREAM 11.4440 SCOTES 357

TITLE OF INVESTION WAS 357

TITLES OF SEGUENCES 356

SEGUENCES APPLICATION NUMBER: US/08/173,485C

TITLES NOT THE SEGUENCE STRAND STREAM SEGUENCES 367

SEGUENCE CHARACTERISTICS: Seguence 37

SEGUENCES APPLICATION NUMBER: US/08/173,485C

TITLES NUMBER: US/08/173,485C

SEGUENCES APPLICATION NUMBER: US/08/173,485C

TITLES NUMBER: US/08/173,485C

TITLES NUMBER: US/08/173,485C

TITLES NUMBER: US/08/173,485C

SEGUENCES CHARACTERISTICS:

SEGUENCES CHARACTERISTICS:

SEGUENCES CHARACTERISTICS:

SEGUENCES CHARACTERISTICS:

SEGUENCES CHARACTERISTICS:

SEGUENCES CHARACTERISTICS:

SEGUENCES SEGUENCES SEGUENCES SEGUENCES SEGUENCES SEGUENCES SEGUENCES SEGU
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Gaps ; 0

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Sequence 18, Application US/08227180B
Patent No. 586698
GENERAL INPORMATION:
FILLE OF INVENTION: Modulation of Gene Expression
TITLE OF INVENTION: Through Interference with RNA Secondary Structure
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSED: Jane Massey Licata, Esq.
STREET: 210 Lake Drive East, Suite 201
Score 7.8; DB 1; Length 11; Pred. No. 2.8e+02; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 7.8; DB 1; Length 11;
Pred. No. 2.8e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: NJ
COUNTRY: USA
ZIP: 08002
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IRM 486
COMPUTER: IRM 486
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in., DS, 1.4 MB
                                                                                                                                                                                                                                                       Patent No. 5864031

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sandra E. Russo-Rodriguez
APPLICANT: Tepper M. Koga
TITLE OF INVENTION: 5'-Dithio-Modified
TITLE OF INVENTION: 01/gonucleotides
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Amgen Inc.
STREET: 1840 Dehavilland Dr.
CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh OS 7.0
SOFTWARE: Microsoft Word Version 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/282,383
FILING DATE: 29JUL1994
CLASSIFICATION: 536
CLASSIFICATION: 536
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.7%;
81.8%;
  Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 81.8
Best Local 9; Conservative
                                                                                                   935 TCCTCTTCATT 945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 rrrargererr 11
                                                                                                                                                11 recerrent 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Thousand Oak
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 11 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-227-180B-18
                                                                                                                                                                                                                                          US-08-282-383-2
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MOLECULE TYPE: genomic DNA
DESCRIPTION: (16s rMA gene from Chlamydia psittaci
DESCRIPTION: (Accession # M13769) nucleotides 203 to 213
                                                                                                      10.7%; Score 7.8; DB 1; Length 11; 81.8%; Pred. No. 2.8e+02; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                RESULT 522
US-08-173-489C-295/c
US-08-173-489C-295/c
Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANT: HEPBURN, A. G.
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
TITLE OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295 :FROM 1 TO 11
                                     265 : FROM 1 TO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Woese, C.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC., STREET: 510 EAST 73RD STREET, CITY: NEW YORK STATE: NEW YORK COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USD.

ZIP: 10021.

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: 1BM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
FRIOR APPLICATION: 107/968,436
FILING DATE: 29 OCT 1992
ATTORNEY, AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: U9518-6
FELECOMMUNICATION INFORMATION:
FELEFRANCE/DOCKET NUMBER: U9518-6
FELECOMMUNICATION INFORMATION:
FELEFRANCE/DOCKET NUMBER: U9518-0
FELEFRAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 295:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
FYPE: nucleic acid
STRANDEDNESS: double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Chlamydia psittaci
DUBLICATION INFORMATION:
AUTHORS: Weisburg, W G, Hatch, T P,
TITLE: Eubacterial Origin of
TITLE: Chlamydiae
JOURNAL: Journal of Bacteriology
VOLUME: 167
         ; DATE: 1988
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-173-489C-265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; RELEVANT RESIDUES IN SEQ ID NO: US-08-173-489C-295
                                                                                                        Query Match
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                     929 TATCCCTC 939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: no
ORIGINAL SOURCE:
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                                                                                                                                                                                                             Score 7.8; DB 1; Length 11;
Pred. No. 2.8e+02;
0; Mismatches 2; Indels
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Pred. No. 2.8e+02;
0; Mismatches 2; Indels
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US-09-105-515-3
; Sequence 3, Application US/09105515
                                                                                                                                                                                                             Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
               ; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: Nucleic acid
; STRANDEDNESS: Single
; MOLECULE TYPE: DNA
US-08-991-830A-6
                                                                                                                                                                                                                                                                                                              928 TTATCCTCCT 938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             928 TTATCCTTCT 938
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APPLICANT: Chang, Esther H.
APPLICANT: Chang, Esther H.
APPLICANT: Chang, Esther H.
APPLICANT: Chang, Esther H.
APPLICANT: Patonlo, Rathleen F.
TITLE OF INVENTION: Compositions and Methods for Reducing Radiation and Drug Resis NUMBER OF SEQUENCES: 9
CORRESPONDENCE S.
ADDRESSEE: Sana A. Pratt
STREET: 10821 Hillbrooke Lane
CITY: Potomac
STREET: Potomac
STREET: Login Hillbrooke Lane
CITY: Potomac
STREET: Login Hillbrooke Lane
CITY: Potomac
STREET: Maryland
COUNTRY: USA
ZIP: 20854
COMPUTER: Repapy disk
COMPUTER: Repapy disk
COMPUTER: Repaphe Macintosh
COMPUTER: Repaphe Macintosh
COMPUTER: Apple Macintosh
COMPUTER: App
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SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/227,180B
FILING DATE: APT1113, 1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/0518,929
FILING DATE: May 4, 1990
APPLICATION NUMBER: PCT/081/02588
FILING DATE: No. 5866598mber 20, 1991
ATTORNEY/ACENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: 32,257
REFERENCE/DOCKET NUMBER: 32,257
TELECOMMUNICATION INPORMATION:
TELEBRAIN: (215) 568-3439
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE: NUMBER: 18:
LELBRAI: 11
TELEBRAI: 11
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TELEBRAI: 11
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REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 294-9171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
NATI SENSE: yes
US-08-227-180B-18
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Sequence 9, Application US/09487130

Factor No. 6362210

Factor No. 6362210

Factor No. 6362210

Factor No. 6362210

Factor No. 63623210

FILE REPRENCE 3156/6638510

TITLE OF INVENTION: CONVERSION OF A WATSON-CRICK DNA TO A HOOGSTEEN-PAIRED

TITLE OF INVENTION: UNDER 110/6638510

CURRENT FILING DATE: 2000-01-19

FRIOR PEDICATION NUMBER: US/09/487,130

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin Ver. 2.1

LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
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11 TCTTTTGTCAT 1
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Matches
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US-08-679-493A-67/C

| Sequence 67, Application US/08679493A
| Patent No. 6303295
| GENERAL INFORMATION:
| APPLICANT: TAYLOR, Ethan W.
| TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS
| FILE REPERENCE: 55-95
| CURRENT APPLICATION NUMBER: US/08/679,493A
| CURRENT PLILING DATE: 1996-07-12
| PRIOR FILING DATE: 1995-07-14
| PRIOR APPLICATION NUMBER: 60/001203
| PRIOR FILING DATE: 1995-09-01
| NUMBER OF SEQ ID NOS: 216
| NUMBER OF SEQ ID NOS: 216
| OCT NOS: 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                    COUNTY: US
COUNTY: US
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,515
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: RNA
ORGANISM: Human immunodeficiency virus type 1
    Patent No. 6113913
GENERAL INFORMATION:
APPLICANT: BROUGH, DOUGLAS E.
TITLE OF INFORTION: RECOMBINANT ADENOVIRUS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                         ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.
STREET: TWO PRUDENTIAL PLAZA, SUITE 4900
CITY: CHICAGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: KILYK JR., JOHN
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 8382
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5600
TELEPHAX: 312-616-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 312-616-5700 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
EDNESS: unknown
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Best Local Similarity
Matches 9; Conserv
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US-09-487-130-11

is Sequence 11, Application US/09487130

is Sequence 11, Application US/09487130

is Patent No. 61562322

is GENERAL INFORMATION:
is APPLICAMY: GAY, DONALD M.
is TITLE OF INVENTION: DUPLEX
is TITLE OF DATE: 2000-01-19
is CURRENT APPLICATION NUMBER: US/09/487,130
is CURRENT APPLICATION NUMBER: US/09/487,130
is TILLE OF SEQ ID NOS: 17
is SEQ ID NO 11
is SEQ ID NO 11
is LENGTH: 11
is CENTRALE IN OUR IN ö Gaps CTHER INFORMATION: Description of Artificial Sequence: synthetic; CTHER INFORMATION: nucleic acid US-09-487-130-11 ö Score 7.8; DB 1; Length 11; Pred. No. 2.8e+02; 5; Mismatches 2; Indels 1 mucucccuuc 11

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Gaps

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911 TCTTTGGTCTT 921

RESULT 531

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Query Match 10.7
Best Local Similarity 81.8
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
                                                                                                         LENGTH: 11
TYPE: DNA
ORGANISM: human
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                                                                          APPLICANT: DUTA, Sukanta K.
APPLICANT: DUTA, Sukanta K.
APPLICANT: DUTA, Sukanta K.
APPLICANT: DUTA, Sukanit
APPLICANT: DUTA, Sukanit
APPLICANT: PRIMAS, Biswajit
APPLICANT: VEWULAPALLI, Kamesh
TITLE OF INVENTION: A SIZE-VARIABLE STRAIN-SPECIFIC PROTECTIVE ANTIGEN FOR
TITLE OF INVENTION: POTOMAC HORSE FEVER
FILE REPERBOYE: 8172-9016
CURRENT APPLICATION NUMBER: US/09/157,257
CURRENT APPLICATION NUMBER: 60/059,252
EARLIER PILING DATE: 1997-09-18
SARLIER FILING DATE: 1997-09-18
SOFTWARE: PATENTING ONS: 48
SOFTWARE: PATENTING ONS: 48
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Pred. No. 2.8e+02;
0; Mismatches 2; Indels
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Sequence 167, Application US/09475947A

Sequence 167, Application US/09475947A

Setent No. 6472154

GRNERAL INFORMATION:
APPLICANT: Wren, Jonathan D.
APPLICANT: Wren, Jonathan D.
APPLICANT: Minna, John D.
TITLE OF INVENTION: Polymorphic Repeats in Human Genes
FILE REFERENCE: UTSD0667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Brough, Douglas E.
TITLE OF INVENTION: Recombinant Cell Line;
FILE REPERENCE: 207952
CURRENT FILING DATE: 207952
CURRENT FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-24
PRIOR FILING DATE: 1999-06-26
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver: 2.0
SERNOTH: 11
                  Sequence 39, Application US/09157257
Patent No. 6375954
GENERAL INFORMATION:
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Best Local Similarity 81.8%;
Matches 9; Conservative
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81.8%;
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Ehrlichia risticii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Adenovirus type 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 10.7
Best Local Similarity 81.6
Matches 9; Conservative
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US-09-157-257-39/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 7.8; DB 1; Length 11;
Pred. No. 2.8e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.7%; Score 7.8; DB 1; Length 11; Best Local Similarity 81.8%; Pred. No. 2.8e+02; Matches 9; Conservative 0; Mismatches 2; Indels
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APPLICANT: Berghammer, Andreas J.
APPLICANT: Berghammer, Andreas J.
APPLICANT: Rlingler, Martin
TITLE OF INVENTION: Universal markers of Transgenesis
FILE REFERENCE: EX.W199-0014
CURRENT FILING DATE: 1999-08-12
NUMBER OF SEQ ID NOS: 444
SEQ ID NO 14
SEQ ID NO 14
LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Garner, Harold R. APPLICANT: Wren, Jonathan D. APPLICANT: Wren, John D. APPLICANT: Minna, John D. TITLE OF INVENTION: Polymorphic Repeats in Human Genes FILE REPERRICE: USDGGGE: USDGGGF: USDGGGF: USDGGGF: USDGGGF: USGGGF: USGGG
CURRENT APPLICATION NUMBER: US/09/475,947A CURRENT FILING DATE: 1999-12-31 NUMBER OF SEQ ID NOS: 346 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 231, Application US/09475947A Patent No. 6472154 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-373-129A-14
; Sequence 14, Application US/09373129A
; Patent No. 6518481
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.7%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
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Gaps

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10.7%; Score 7.8; DB 1; Length 11; 81.8%; Pred. No. 2.8e+02; tive 0; Mismatches 2; Indels
Pred. No. 2.8e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Alexander-Bridges, Maria C.
APPLICANT: Alexander-Bridges, Maria C.
TITLE OF INVENTION: INHIBITION OF INSULIN-
TITLE OF INVENTION: INNUCED ADIPOSIS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
COMPUTER: How PS/2 Model 50Z or 55SX
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PALOR APPLICATION DATA:
PAPLICATION NUMBER: 08/242,409
FILING DATE: 13 May 1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
FELCOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELESTHONE: (617) 542-5070
TELESTAX: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT-US95-09475-2
| Sequence 2, Application PC/TUS9509475
| GENERAL INFORMATION:
| TITLE OF INVENTION: 5'-Dithio-Modified:
| TITLE OF INVENTION: 01/gonucleotides:
| TITLE OF INVENTION: 01/gonucleotides: 01/gonucleotides: 01/gonucleotides: 01/gonucleotides: 01/gonucleotides: 01/gonucleot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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          Best Local Similarity 81.8
Matches 9; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 81.8 Matches 9; Conservative
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                                                                                                                                                             935 TCCTCTTCATT 945
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 rrrccccccrc 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US95-05835-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT-US95-05835-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
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APPLICANT: LU, CHANGDE

TITLE OF INVENTION: ANTI-HBV

CURRENT APPLICATION NUMBER: US/09/529,812A

CURRENT APPLICATION NUMBER: PCT/CN98/00248

PRIOR FILING DATE: 1998-10-19

PRIOR FILING DATE: 1998-10-19

PRIOR FILING DATE: 1997-10-21

NUMBER OF SEQ ID NOS: 18

SEQ ID NO S: 20F-MARKE: PATE-MARKE: PATE-MARKE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                     RESULT 536
US-09-395-017B-48

/Sequence 48, Application US/09395017B
/Sequence 48, Application US/09395017B
/Sequence 40. 642014
/Setent No. 6642014
/GENERAL INFORMATION:
/APPLICANT: Pedersen, Henrik
/APPLICANT: Kjems, Jorgen
/APPLICANT: Lund, Mette
/TITLE OF INVENTION: Busyme Activity Screen With Direct
/TITLE OF INVENTION NUMBER: US/09/395,017B
/PRIOR APPLICATION NUMBER: PA 1998 01106
/PRIOR FILING DATE: 1998-09-13
/PRIOR FILING DATE: 1998-09-08-19
// NUMBER OF SEQ ID NOS: 49
// SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/09529812A
Patent No. 6682930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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Best Local Similarity 81.8%;
Matches 9; Conservative
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , OTHER INFORMATION: Primer US-09-395-0178-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      935 TCCTCTTCATT 945
                                                                         941 TCATTGGTTTA 951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Sequence 4, Application US/07990297

Sequence 4, Application US/07990297

GENERAL INFORMATION:

APPLICANT: GROSZ, ROW

APPLICANT: GROSZ, ROW

TITLE OF INVENTION: IMPROVED METHOD FOR

TITLE OF INVENTION: SEGMENTS OF NUCLEIC ACID USING

TITLE OF INVENTION: NESTED POLYMERASE CHAIN REACTION

TORRESPONDENCE ADDRESS:

ADDRESSEE: B. I. du Pont de Nemours and Company

STREET: 1007 Market Street

CITY: Wilmington

STREET: 1007 Market Street

COMPUTER: Macintosh

COMPUTER: Macintosh

OCHRANDIEN READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB

COMPUTER: Macintosh

OCHRANDIEN RACHOSHER: US/07/990,297

FILING DATE: 19921209

SOFTWARE: 19921209

SOFTWARE: 19921209

FILING DATE: 19921209

FILING DATE: 19921209

TELECOMMUNICATION INFORMATION:

NAME: GRISTATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION NUMBER: 35,880

REFERENCE/DOCKET NUMBER: MACING ASSERTION NUMBER: SEQUENCE CHARACTERISTICS:

TELECHANGE ASSERTION NUMBER: SEQUENCE CHARACTERISTICS:

TELECHANGE ASSERTICE:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:
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STATE:

COUNTRY:

LOUNTRY:

LOUNTRY:

STADABLE FORM:

MEDIUM TYPE: Diskette, 3.5 in., DS, 1.4 MB
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 in., DS, 1.4 MB
COMPUTER:

COPERATING SYSTEM: Macintosh OS 7.0

SOFTWARE: Microsoft Word Version 5.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/09475

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION:

PRIOR APPLICATION:

PRIOR APPLICATION DATA:

APPLICATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 bases

TYPE: nucleic acid

STRANDEDNESS: single

"OPPLICATION FOR SEQ ID NO: 2:

STRANDEDNESS: single

"OPPLICATION FOR SEQ ID NO: 2:

STRANDEDNESS: single

"OPPLICATION FOR SEQ ID NO: 2:

STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 7.8; DB 1;
Pred. No. 2.8e+02;
0; Mismatches 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 12 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          911 TCTTTGGTCTT 921
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US-07-990-297-4/C
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                                                                         10.7%; Score 7.8; DB 1; Length 12; ilarity 81.8%; Pred. No. 3e+02; Conservative 0; Mismatches 2; Indels
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10.7%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                          US-08-242-409-1/c
Sequence 1, Application US/08242409
Fatent No. 549681
GENERAL INFORMATION:
APPLICANT: Alexander-Bridges, Maria C.
APPLICANT: Alexandres: 12
CORRESPONDENCE BLODERSS:
ADDRESSE: Fish & Richardson
STREET: 25: Franklin Street
CITY: BOSCON
STREET: 25: Franklin Street
COUNTRY: U.S.A.
ZIP: O2110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55sX
OPPRATING SYSTEM: MS-DOS (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242,409
FILING DATE:
ATCHARLY AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 30,162
TELEPHONE: (617) 542-8906
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-235-503B-22/c
; Sequence 22, Application US/08235503B
; Patent No. 5563036
GENERAL INFORMATION;
APPLICANT: Peterson, Michael G
; MOLECULE TYPE: DNA (genomic) US-07-990-297-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 12
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                              950 TAATGTATCGC 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         929 TATCCCTCCTC 939
                                                                                                                                                                                                                                  12 TACGGTATCGC
                                                                         Query Match
Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                            RESULT 541
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Gaps
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Sequence 13, Application US/08110158

Sequence 13, Application US/08110158

Patent No. 5605821

APPLICANT: McEver, Rodger P.
APPLICANT: Pan, Juniang

TITLE OF INVENTION: Expression Control Sequences of the TITLE OF SEQUENCES: 17

CORRESPONDENCES: 17

AUTHOR SEQUENCES: 17

CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst

ADDRESSEE: Patrea L. Pabst

CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

10.7%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 81.8%; Pred. No. 3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CUMPARY: USA

ZIP: 30309-4530

COMPUTER READBABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/110,158
FILING DATE: 19930820
CLASSIFICATION NUMBER: US 07/320,408
FILING DATE: 08-MAR-1989
ATTONREY/AGENT INPOWMATION:
NAME: Pabbet, Patrea L.
REGISTRATION NUMBER: 31,284
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44683
TELECOMMUNICATION INFORMATION:
TELEPACK: 212-977-9550
TELEPACK: 212-977-9550
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base palrs
TENER: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION TELEPHONE: (404)-815-6508
                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-242-664-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR ESC
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                           932 CCCTCCTCTTC 942
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 3e+0
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPER: 3.5 inch 1.44Mb
COMPUTER: 1BM PC COMPAIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242,664
FILING DATE: May 12, 1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           May 12, 1994 M.: 514
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944 TTGGTTTAATG 954

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10.7%; Score 7.8; DB 1; Length 12; ilarity 81.8%; Pred. No. 3e+02; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WESSEL SECTION STATE OF THE OF
                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44Mb
COMPUTER: 1BW PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURERNT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,138
FILING DATE: June 7, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P. B. REFERENCE/DOCKET NUMBER: 44683-Z/JPW/MJG
TELEPOWNICTATION INFORMATION:
TELEPOWNICTATION INFORMATION:
TELEPOWNICTATION INFORMATION:
TELEPOWNICTATION INFORMATION:
TELEPOWE: 212-977-9550
INFORMATION POR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTY: U.S.A.

ZIP: 19898
COMPUTER READABLE FORM:
MADIUM TYPE: FLOPPY DISK
COMPUTER: MACINTOSH
OPERATING SYSTEM: MACINTOSH
OSOFWARE: MICROSOFT WORD 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/586,120
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GEIGER, KATHLEEN W.
REGISTRATION NUMBER: 35,880
REFERENCE/DOCKET NUMBER: MD-1068
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic) US-08-484-138-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            932 CCCTCCTCTTC 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 cerrerrerre 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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Best Local Similarity
Matches 9; Conserv
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     New York
: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
                                COUNTRY: U. ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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Best Local Similarity 81.8%; Pred. No. 3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 546
US-08-484-138-13/C
US-08-484-138-13/C
Sequence 13. Application US/08484138
Fatent No. 5652350
GENERAL INFORMATION:
APPLICANT: Watanabe, Kyoichi A.
APPLICANT: Ren, Wu-Yun
FAPLICANT: Weil, Roger
TITLE OF INVENTION: Complementary DNA and Toxins
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          949 TTAATGTATCG 959
2 TIGGTTTTAAG 12
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APPLICANT: PURGGAMA, MASAO
APPLICANT: FURAGAWA, MASAO
APPLICANT: IWAMI, MORITA
APPLICANT: ARANORI, ICHIRO
APPLICANT: ARANORI, ICHIRO
APPLICANT: ARANORI, ICHIRO
APPLICANT: ACAO, HITOSHI
TITLB OF INVENTION: COMFOUND OR SALIS THEREOF
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                       3: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
3: P.C.
1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.7%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                              SIREAL: 1.75 S. CELLEIBON DAVIS FIGURARY, STICE TO COMPUTE. Virginia COMPUTE. U.S.A.

ZIP: 2202
ZONTONEN: U.S.A.
ZONTONER: PLOPY disk
COMPUTER: PLOPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PEATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/314,309A
FILING DATE: 30-SEP-1994
CLASSIFICATION NUMBER: US 07/631,906
FILING DATE: 21-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5677141man F.
REFERENCS/OCKET NUMBER: 18-863-0 CONT
TELECOMMUNICATION NUMBER: 18-863-0 CONT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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Patent No. 5693508
GENERAL INFORMATION:
APPLICANT: CHANG, LUNG-JI
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: synthetic DNA
                                                                                                                                     Sequence 28, Application US/08314309A Patent No. 5677141 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (703) 413-3000
(703) 413-2220
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
950 TAATGTATCGC 960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-336-132-9/c
                                                                                                                          US-08-314-309A-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
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                                                                                                                                                                                                                                                10.7%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 3e+02;
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                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 548
US-08-254-355-5/c
; gequence 5, Application US/08254355
; Patent No. 5660981
; GENERAL INFORMATION:
APPLICANT: GROSZ, RONALD
APPLICANT: GROSZ, RONALD
TITLE OF INVENTION: SELECTION OF DIAGNOSTIC
TITLE OF INVENTION: GENERICAL MARKERS IN
TITLE OF INVENTION: OF A SPECIFIC MARKER
TITLE OF INVENTION: SALMONELA
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS
ADDRESSEE: AND COMPANY
STREET: ILOY MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 3e+0
0; Mismatches
                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: MACINTOSH
OPERATING SYSTEM: MACINTOSH SYSTEM 6.0
SOFTWARE: MICROSOSPT WORD 4.0
CURRENT APPLICATION DATA:
APPLICATION: NUMBER: US/08/254,355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35,880
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TELECOMMUNICATION INFORMATION
TELEPHONE: 302-892-8112
TELEPAX: 302-892-7949
                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-586-120-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: GEIGER, KATHLEEN W
REGISTRATION NUMBER: 35,8
                   INFORMATION FOR SEQ ID NO: E SEQUENCE CHARACTERISTICS:
LENGTH: 12 base --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 835420
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
    302-892-8112
                                                                                                                                                                                                                              Query Match
Best Local Similarity 81.0.
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 10.7
Best Local Similarity 81.8
Matches 9, Conservative
                                                                                                    LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                   950 TAATGTATCGC 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                        12 TACGGTATCGC 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 19898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WILMINTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE
    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-254-355-5
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US-08-411-727-6/c

| Sequence 6, Application US/08411727 |
| Patent No. 5705161 |
| Pa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.7%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 3e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CUDULKY: U.S.A.

CUDULKY: U.S.A.

CUDULKY: U.S.A.

CUDITKY: U.S.A.

MEDIUM TYPE: Flopy disk

MEDIUM TYPE: Flopy disk

COMPTUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/411,727

FILING DATE: 01-MAY-1995

CLASSIFICATION DATA:

APPLICATION NUMBER: ND 9201716

FILING DATE: 02-OCT-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/NL93/00163

FILING DATE: 30-OLL-1993

ATTORNEY/AGENT INFORMATION:

NAME: PATCH, Andrew J.

REGISTRATION NUMBER: BO 38275

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                WO PCT/NL93/00163
                                                                             FILING DATE: 30-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32925
REFERENCE/DOCKET NUMBER: BO 38:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION STELL 2297
ITELERAX: 703-685-673
TELERAX: 703-685-673
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
IYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-411-727-5
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 10.7
Best Local Similarity 81.8
Matches 9; Conservative
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                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
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JOS-08-411.72.7-5

JOS-08-411.72.7-6

JOS-08-411.72.7-6

JOS-08-411.72.7-6

JOS-08-411.72.7-7

JOS-08-411.72.
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CORRESPONDENCE ADDRESS:
ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER: EADABLE FORM:
MEDLUM TYEE: Floppy disk
COMPUTER: IBM PC compatible-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,132
FILING DATE: 07-07-1994
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
FILING DATE: 32,837
REGISTRATION NUMBER: 32,837
RESERRENCE/DOCKET NUMBER: CHANG-00817
TELEPHONE: (415) 397-8338
INFORMATION FOR SED ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
INFORMATION FOR SED ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPPOLOGY: linear y MOLECULE TYPE: DNA (genomic) US-08-336-132-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 81.8
Matches 9; Conservative
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US-08-411-727-5
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA A
REFERENCE/DOCKET NUMBER: MD1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8374
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   950 TAATGTATCGC 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 TACGGTATCGC 2
                                                                                                                                                                                                                                                               CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D.C.
: U.S.A.
                           US-08-608-881A-18/c
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US-08-360-125-41/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
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                                                                                                                                                                                                                                                                                                                                              Sequence 24, Application US/08484334

PREFER NO. 5733779

GENERAL INFORMATION:
APPLICANT: REFF, Mitchell E.
TITLE OF INVENTION: IMPARED DOMINANT SELECTABLE MARKER
TITLE OF INVENTION: SEQUENCE AND INTRONIC INSERTION STRATEGIES FOR ENHANTITLE OF INVENTION: SEQUENCE AND INTRONIC INSERTION SYSTEMS COMPRISING SAME
NUMBER OF INVENTION: SYSTEMS COMPRISING SAME
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                         Score 7.8; DB 1; Length 12;
Pred. No. 3e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Flappy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,334
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: P.O. BOX 1404
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/147,696
APPLICATION NUMBER: US 07/977,691
PRIOR APPLICATION NUMBER: US 07/977,691
APPLICATION NUMBER: US 07/977,691
ATTORNEY AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 131712-162
TELECOMMUNICATION:
TELEPHONE: (703) 836-6620
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: DIMA (genomic)
US-08-411-727-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 24:
                                                                                                                           10.7%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                         Query Match
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                          959 GCTACCAACGG 969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Conservative
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                                                                                                                                                                                                                                              12 GGTACGAACGG 2
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Best Local Similarity
Matches 9; Conserv
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US-08-484-334-24/c
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PROGRESS 1813-18 (CONTINUE OF INVESTIGATION (CONTINUE) OF
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Sequence 2; Application US/08545785
Patent No. 577013
GENERAL INPORMATION:
ABPLICANT: Embod and Rayner
TITLE OF INVENTION: And Method Of Preparation
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5770713ris LLP
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Croin, Mark
APPLICANT: Croin, Maureen T.
APPLICANT: Fodor, Stephen P.A.
APPLICANT: Podor, Stephen P.A.
APPLICANT: Hubbell, Earl A.
APPLICANT: Hubbell, Earl A.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Morris, Macdonald S.
APPLICANT: Morris, Macdonald S.
APPLICANT: Sheldon, Edward L.
TITLE OF INVENTION: Biological Chips
NUMBER OF SEQUENCES: 360
CORRESPONDENCE ADDRESS: 360
CORRESPONDENCE ADDRESS: ADDRESSE: Townsend and Crew Lip
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                          CTAIR:
CTAIR:
CTAIR:
CUNTRY: U.S.A.

ZDP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
CCMPUTER: IBM PC compatible
OPERATING STERM:
PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,785
FILING DATE: 17-74M-1996
CLASSIFICATION: 536
ATTORNEY/GRAFT INFORMATION:
NAME: JOSEPH LACCI
REGISTRATION NUMBER: 33,307
REGISTRATION INFORMATION:
TELEPHONE: 215-568-3100
INFORMATION FOR SEQ 1D NO: 2:
SEQUENCE CHARACTERISTICS:
TEMMENT: 12 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-441-887A-71
; Sequence 71, Application US/08441887A
Patent No. 5837832
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       926 TITIATCCCTC 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 12 bases
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                            RESULT 556
US-08-545-785-2
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STRAIL...
STRAIL...
STRAIL ISOLATE:
DEVELOPMENTAL STAGE:
HARLOPMENTAL STAGE:
HARLOPMENTAL STAGE:
HARLOPMENTAL STAGE:
TISSUB TYPE:
CELL LINE:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FRATURE:
FRATURE:
CHROMOSOME/SEGMENT:
UNITS:
FRATURE:
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10.7%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordberfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,125
                                                                                                  FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
PILING DATE:
TILING DATE:
APPLICATION NUMBER: 07/905,534
APPLICATION NUMBER:
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: WASTERN TORNEY:
TELEFRICE/DOCKET NUMBER: 33,367
TELEFRING DATE:
TELEFRINGEN: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE:
JOUGNAL:
VOLUME:
SSUE:
FRAGES:
DATE:
POCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-41
                                                                                                                                                                                                                                                                                                                                                                                                                                 41:
                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 12 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
LOCATION:
LOCATION:
DENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATICN:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       905 TCATTTTCTTT 915
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ANTI-SENSE:
RAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
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APPLICANT: Croin, Maureen T.
APPLICANT: Croin, Maureen T.
APPLICANT: Huang, Xiaohua X.
APPLICANT: Huang, Xiaohua X.
APPLICANT: Hubbli, Earl A.
APPLICANT: Hubbli, Earl A.
APPLICANT: Lobban, Peter E.
APPLICANT: Lobban, Peter E.
APPLICANT: Marchand S.
APPLICANT: Mariay of Nucleic Acid Probes on TITLE OF INVENTION: Arrays of Nucleic Acid Probes on TITLE OF INVENTION: Biological Chips NUMBER OF SEQUENCES: 360
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and CITW.
STREET: TWO FT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.7%; Score 7.8; DB 1; Length 12;
81.8%; Pred. No. 3e+02;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC comparatible
COMPUTER: IEM PC comparatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,887A
FILING DATE: 16-MAY-1995
CLASSIPICATION: 435
                                                            PUCASIFICATION DATA:
APPLICATION NUMBER: US 08/143,312
FILING DATE: 26-OCT-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/082,937
CLASSIFICATION NUMBER: US 08/082,937
FILING DATE: 25-UTN-1993
ATTORNEY AGENT INFORMATION:
NAME: Liebeschuetz, Joseph O.
RESTRANION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 018547-004160US
TELEPHONE: 650-326-2402
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGRANDER: ABS DE DE NO: 91:
SEQUENCE CHARACTERISTICS:
LENGRANDER: ABS DE DE NO: 91:
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: US/08/441,887A
FILING DATE: 16-MAY-1995
CLASSIFICATION: 435
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APPLICATION NUMBER: US 08/143,312
FILING DATE: 26-0CT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (probe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 81.8
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 rrrccccrcc 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cronin, Maureen T.
APPLICANT: Cronin, Maureen T.
APPLICANT: Fodor, Stephen P.A.
APPLICANT: Hubbell, Earl A.
APPLICANT: Hubbell, Earl A.
APPLICANT: Libenuz, Robert J.
APPLICANT: Libenuz, Peter E.
APPLICANT: Morris, Macdonald S.
APPLICANT: Sheldon, Earl A.
TITLE OF INVENTION: Arrays of Nucleic Acid Probes on MINDER OF INVENTION: Biological Chips
                                                               COMPUTER REALBLE FORM:
COMPUTER: TEM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPETATION PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,887A
FILING APPLICATION 1435
RIOR APPLICATION NUMBER: US/08/143,312
FILING DATE: 26-OCT-1993
CLASSIFICATION NUMBER: US 08/082,937
FILING DATE: 25-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Liebsechuetz, Joseph O.
REFERENCE/DOCKET NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 37,505
REFERENCE/DOCKET NUMBER: US 08547-004160US
TELEPHONE: 650-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEE: Townsend and Townsend and Crew LLP
: Two Embarcadero Center, 8th Floor
San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 650-326-2422
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (probe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 81.8
Matches 9; Conservative
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                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Ca
          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cronin, Maureen T.
APPLICANT: Cronin, Maureen T.
APPLICANT: Fodor, Stephen P.A.
APPLICANT: Hubbell, Riebhua X.
APPLICANT: Hubbell, Rarl A.
APPLICANT: Lipshutz, Robert J.
APPLICANT: Loban, Peter E.
APPLICANT: Macdonald S.
APPLICANT: Sheldon, Edward L.
APPLICANT: Sheldon, Edward L.
APPLICANT: Sheldon, Arrays of Nucleic Acid Probes on TITLE OF INVENTION: Allohomics 360
CORRESPONDENCE: Johnsen.
STREET: TOWNSENTESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,887A
FLING DATE: 16-MAY-1995
CLASSIPICATION: 435
FROM APPLICATION DATA:
APPLICATION NUMBER: US 08/143,312
FILING DATE: 26-CT-1993
CLASSIPICATION DATA:
APPLICATION NUMBER: US 08/082,937
FILING DATE: 25-UN-1993
ATTORNEY/AGENT INFORMATION:
NAMME: Liebeschuetz, Joseph O.
REGISTRATION NUMBER: 018547-004160US
TELECOMMUNICATION INFORMATION:
MAME: Liebeschuetz, Joseph O.
REGISTRATION NUMBER: 018547-004160US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Townsend and Townsend and Crew STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco STARE: California COUNTRY: USA
                                                                            LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLCGY: linear
MOLECULE TYPE: DNA (probe)
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TELEFAX: 650-326-2422
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERLSTICS:
TRNGTH: 12 base pairs
                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
             650-326-2422
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STRANDEDNESS: single
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             TELEFAX:
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Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cronin, Maureen T.
APPLICANT: Cronin, Maureen T.
APPLICANT: Fodor, Stephen P.A.
APPLICANT: Hubbell, Earl A.
APPLICANT: Macdonald S.
APPLICANT: Morris, Macdonald S.
APPLICANT: Marrays of Nucleic Acid Probes on TITLE OF INVENTION: Biological Chips
NUMBER OF SEQUENCES: 360
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Embarcadero Center, 8th Floor
CITY: San Francisco
COUNTY: USA
ZIP: 94111
COMPUTER: EADABLE FORM:
MEDIT STATE: California
CONPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAREATION DATA:
APPLICATION NUMBER: US/08/441,887A
FILING DATE: 26-OCT-1993
CLASSIFICATION NUMBER: US 08/082,937
FILING DATE: 25-UNA-1993
ATTORNEY/AGENT NUMBER: USSEPHOR.
REGISTRATION NUMBER: USSEPHOR.
REFERENCE/LOSTERNIN NUMBER: 108847-004160118
REFERENCE/LOSTERNIN NUMBER: 108847-004160118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
APPLICATION NUMBER: US 08/082,937
FILING DATE: 25-UN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Liabeschuetz, Joseph O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 018547-004160US
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFAX: 650-326-2400
TELEFAX: 650-326-2400
TELEFAX: 650-326-2400
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNES: single
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; Sequence 135, Application US/08441887A
; Parent No. 5837832
; GENERAL INFORMATION:
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ELECOMMUNICATION INFORMATION:
TELEPHONE: 650-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative (
                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: DNA (probe)
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Sequence 14, Application US/08661330A

Patent No. 5849485

Patent No. 5849485

GENERAL INFORMATION:
APPLICANT: Sladek, Frances M.
APPLICANT: Shong, Weimin JG., James F.
TITLE OF INTENTION: LIVER ENRICHED TRANSCRIPTION FACTOR
NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:
ADDRESSE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Hackensack
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
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MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elba PC Compatible
COPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: D4-JUN-1996
FILING DATE: 14-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: AGCKSON ESG., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REFERENCE/POCKET UNMBER: 600-1-030A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 7.8; DB 1;
Pred. No. 3e+02;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-578-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                                                                        UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
AUTHORS:
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                                                                                       CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                            VOLUME:
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                                                                                                                                                                                                                                                                                   Sequence 41, Application US/08450578
Sequence 41, Application Sequence Application Sequence Applicant: Saixo HOSOKAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: Yoko HIRAKAWA
TITLE OF INVENTION: Human Monoclonal Antibody
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer TITLE OF INVENTION: Call Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                                                                            .
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                                                                                            Gaps
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                                             Query Match
10.7%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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CELL TYPE: Hybridoma producing human antibody 1-3-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER FALBABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/450,578 FILING DATE: May 25, 1995 CLASSIFICATION 1435 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/360,125 FILING DATE: December 20, 1994 PRIOR APPLICATION NUMBER: 08/360,125 FILING DATE: December 20, 1994 PRIOR APPLICATION NUMBER: 07/905,534 FILING DATE: JUNE 29, 1992 ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367 REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850 TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41:
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SEQUENCE CHARACTERISTICS:
LENCTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                         934 CTCCTCTTCAT 944
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INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: "STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: cDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                      RESULT 562
US-08-450-578-41/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U
       US-08-441-887A-334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE:
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TYPE: nucleic acid
STRANDEDNESS: double stranded
       909 TITCTTTGGTC 919
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 647-651
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MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from
DESCRIPTION: retinoblastoma sequence region in Seq ID No. 586124483
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.7%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 3e+02; tive 0; Mismatches 2; Indels
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| Sequence 84, Application US/08173489C |
| Sequence 84, Application US/08173489C |
| Sequence 84, Application US/08173489C |
| Sequence 84, Application |
| Applicant: Wang, C. -G. |
| APPLICANT: Wang, C. -G. |
| TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA |
| TITLE OF INVENTION: TRIPLE-STRAND FORMATION. |
| NUMBER OF SEQUENCES: 3 |
| ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC., STREET, CITY: NEW YORK |
| STREET | SOURCES |
| SOURCES |
| SOURCES 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ANTI-SENSE: NO
; PUBLICATION INFORMATION;
; RELEVANT RESIDUES IN SEQ ID NO: 84 :FROM 1 TO 12
US-08-173-489C-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: User

ZIP: 10021.
COMPUTER READBALE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XI/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REPERENCE/DOCKET NUMBER: 26,179
REPERENCE/DOCKET NUMBER: 26,179
TELEPHONE: (attorney) (212) 708-188C
TELEFAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 bases
TYPE: Nucleic Acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
                                                                                                                                    MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "HNF-4 Consensus"
US-08-661-330A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 10.7
Best Local Similarity 81.8
Matches 9; Conservative
12 base pairs
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                                  TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                      linear
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LENGTH:
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Gaps
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RESULT 565
US-08-173-489C-119
US-08-173-489C-119
Sequence 119, Application US/08173489C
Parent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANT: HEPBURN, A. G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
DESCRIPTION: beta-globin gene (accession # V00499)
DESCRIPTION: nucleotides 1284 to 1295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DATE: 1980
RELEVANT RESIDUES IN SEQ ID NO: 119 :FROM 1 TO 12
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                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 ESST 73RD STREET,
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                      COUNTRY: New ALCOLD
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch;
COMPUTER: 18M PC/XT/AT
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 29 OCT 1993
CLASSITCATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: HANGHOMMER: 26,179
REFERENCE/DOCKET NUMBER: U9518-6
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (attorney) (212) 246-8959
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TVDF: NUCLE: 2016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: no ORIGINAL SOURCE: ORIGINAL SOURCE: ORANISM: Homo sapiens PUBLICATION INFORMATION: AUTHORS: C, Maniatis, T TITLE: The nucleotide sequence of JOURNAL: Cell
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12 CCTTTCACCCC 2

RESULT 567

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MOLECULE TYPE: genomic DNA
DESCRIPTION: 23s rRNA gene from Bscherichia coli
DESCRIPTION: (Accession # M25458) nucleotides 785 to 796
HYPOTHETICAL: no
ANTI-SENSE: no
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10.7%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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ribosomal RNA Comparison with models of
secondary structure for maize chloroplast 23S
TRNA and for large portions of mouse and human
16S mitochondrial rRNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUBLICATION INFORMATION:
AUTHORS: Branlant, C, Krol, A, Machatt, M, A,
AUTHORS: Pouyet, J, Ebel, J P, Edwards, K, Koessel,
AUTHORS: H.
                                   Sequence 219, Application US/08173489C
Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANT: HEPBURN, A. G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                              ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC., STREET; 510 EAST 73RD STREET, CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: 1BM PC/XT/AT
COMPUTER: 1BM PC/XT/AT
COMPUTER: 1BM PC/XT/AT
COMPUTER: 1BM PC/XT/AT
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSITE CATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: HANGELMAN, JOSEPH H.
REGISTRATION NUMBER: 26,179
REFERENCE/OCKET NUMBER: 26,179
REFERENCE/OCKET NUMBER: 19518-6
TELECOMUNICATION INFORMATION:
TELECAX: (attorney) (212) 708-1880
TELERAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 219:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDENNESS: double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primary and secondary
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                                                                                                                                                                                                                                                                                                                                                                STATE: NEW YORK
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RESULT 566
US-08-173-489C-219/c
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Pred. No. 3e+02;
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Sequence 292, Application US/08173489C
Sequence 292, Application US/08173489C
Patent No. 5861241
Patent INCRATION:
APPLICANT: WANG, C. -G.
APPLICANT: HERBURN, A. G.
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
US-08-133-489C-246

US-08-133-489C-246

Sequence 246, Application US/08173489C

Sequence 246, Application US/08173489C

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DESCRIPTION: third strand derived from M. luteus
DESCRIPTION: 23s region in Seq ID No. 5861244245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: NEW YORK
COUNTRY: USA
ZIP: 10021.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XI/AT
OPERATING SYSTEM: M9-DOS version 6.2
SOFTWARE: WORDERFECT VERSIOn 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT IRFORMATION:
NAME: Handelman, JOSEPH H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Handelman, Joseph H. REGISTRATION NUMBER: 26,179 REFERENCE/DOCKET NUMBER: U9518-6 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        510 EAST 73RD STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
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PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         905 TCATTTTCTT 915
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NEW YORK
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Patent No. 2871697
GENERAL INFORMATION:
APPLICANT: Rothberg, Jonathan
APPLICANT: Deem, Michael
APPLICANT: Simpson, John
TITLE OF INVENTION: Method for the Determination and
TITLE OF INVENTION: Classification of DNA Sequences in a Sample Without
TITLE OF INVENTION: Sequencing
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from C.
DESCRIPTION: pasteurianum 16s region in Seq ID No. 5861244291
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; PUBLICATION INFORMATION:
; FELEWANT RESIDUES IN SEQ ID NO: 292 :FROM 1 TO 12
US-08-173-489C-292
NUMBER OF SEQUENCES: 365
CORRESPONDENCE PADRESS:
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                  ZIP: 10021.

COMPUTER READABLE FORM:

MEDLUM TYPE: 3.5 inch, 1.44Mb storage MEDLUM TYPE: 3.5 inch, 1.44Mb storage COMPUTER: 18M PC/XT/AT

OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 2.2 DEC 1993
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 2.9 OCT 1992
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: US 07/968,436
FILING DATE: 2.9 OCT 1992
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: US-180
TELEPHONE: (attorney) (212) 708-1880
TELEPHONE: (attorney) (212) 246-8959
SEQUENCE CHARACTERISTICS:
LENGTH: 12 bases
TYPE: nucleic acid
STRANDEDNESS: single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.7%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 81.8
Matches 9; Conservative
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US-08-547-214-13
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Sequence 27, Application US/08761243C
Patent No. 5879879
GENERAL INFORMATION:
TITLE OF INVENTION: No. 5879879el Cis-Acting Element In The Human LDL Receptor Pro-
NUMBER OF SEQUENCES: 28
CORRESPONDENCES: 28
CORRESPONDENCESS:
ADDRESSEE: Benjamin Aaron Adler, Ph.D.,J.D.
STREET: 8011 Candle Lane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
TLING DATE: 24-OCT-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leelie
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 19,872
REJERANCE/DOCKET NUMBER: 7934-015-999
TELEFAX: (212)-790-9090
TELEFAX: (212)-790-9090
TELEFAX: (212)-790-9084
TELEFAX: (212)-699-8844
TELERA: (212)-699-8844
TELERA: CALA PENNIE
INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
TYPE: MISSIEM SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/761,243C
FILING DATE: December 6, 1996
CLIASSIFICTATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler; Ph.D., J.D.
REGISTRATION NUMBER: D5956
TELEFONMUNICATION INFORMATION:
TELEFONMUNICATION INFORMATION:
TELEFONMUNICATION INFORMATION:
TELEFANK: 713-777-6908
INFORMATION FOR SEQ ID NO: 27:
SEMENCE.
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LENGTH: 12 bp
LENGTH: 12 bp
TYPE: nucleic acid
STRANDEDNESS: single-stranded
STRANDENESS: single-stranded
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.7%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 81.5-
These 9; Conservative
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STATE: Texas
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: li:
; MOLECULE TYPE:
US-08-547-214-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-761-243C-27/c
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APPLICANT: Simpson, John
TITLE OF INVENTION: GLASSIFYING, OR QUANTIFYING DIA SEQUENCES IN A SAMPLE
TITLE OF INVENTION: WITHOUT SEQUENCING
TITLE OF INVENTION: WITHOUT SEQUENCING
NUMBER OF SEQUENCES: 77
CORRESPONDENCE 17
CORRESPONDENCE 2: 77
CORRESPONDENCE 3: 64
ADDRESSES: ADDRESS: 65
ADDRESSES: Pennie and edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
STATE: New York
STATE: New York
COUNTRY: USA
STREET: 118P PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION HATA:
APPLICATION NUMBER: US/08/63,823B
FILING DATE: 14-Unne-1996
CLASSIFICATION NUMBER: 18,872
ATTORNEY AGENT INFORMATION:
NAME: Misrock, S. Leale
REGISTRATION NUMBER: 7934-033
TELEPONUMICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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GENERAL INFORMATION:

APPLICANT: HORATION:

APPLICANT: HORATAWA, Toshiaki

APPLICANT: HORATAWA, Yoko

APPLICANT: HORATAWA, Yoko

APPLICANT: HORATAWA, Yoko

APPLICANT: INO NO. 5927ihiko

APPLICANT: NAGAIKE, Kazuhiro

TITEE OF INVENTION: WITHOR MONOCICUAL ANTIBODY SPECIFICALLY BIND)

TITEE OF INVENTION: SUFFEC ANTIGEN OF CANCER CELL MEMBRANE

FILE REFERENCE: 177/22736.IKH

CURRENT APPLICATION NUMBER: US/09/017,628

CURRENT APPLICATION NUMBER: 08/360,125

EARLIER FILING DATE: 1994-112-20

NUMBER OF SEQ ID NOS: 42

SOFTWARE: PALENTIN VEY: 2.0

SEQ ID NO 41

LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
OTHER INFORMATION: Hybridoma producing human antibody 1-3-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
10.7%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 41, Application US/09017628
Patent No. 5990287
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (212) 869-9741/886
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  943 ATTGGTTTAAT 953
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-017-628-41/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-663-823B-13
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                                                                     Score 7.8; DB 1; Length 12;
Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.7%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 3e+02;
                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL MAINT
APPLICANT: HAZEL, JAMES WILLIAM
APPLICANT: HAZEL, JAMES WILLIAM
TITLE OF INVENTION: GENERAL OF LISTERIA
TITLE OF INVENTION: THE DETECTION OF LISTERIA
TITLE OF INVENTION: MONOCYTOGENES AND LISTERIA SPP.
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEEE: E. I. DU PONT DE NEMOURS AND COMPANY 1. 1007 MARKET STREET WILMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.

ZIP: 19998
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.50 INCH DISKETTE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: MICROSOFT WORD 2.0C
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/745,228
FILING DATE: NOVEMBER 8, 1996
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD. LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERRNCE/POCKET NUMBER: MD-1065-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 30.892-8112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 572
US-08-663-823B-13
; Sequence 13, Application US/08663823B
; Patent No. 5972693
; PAPERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan
                                                                                                                                                                                                                                                                                           RESULT 571

US-08-766-439-4/c

; Sequence 4, Application US/08766439

; Patent No. 5922538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-766-439-4
                                                                   10.7%;
illarity 81.8%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 81.8
Matches 9; Conservative
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                                                                                                                                                                       923 GCCTTTTATCC 933
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                                                                        Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: DELAWARE
; ORIGINAL SOURCE:
US-08-761-243C-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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Sequence 24, Application US/09013092

Sequence 24, Application US/09013092

Patent No. 6017733

GENERAL INFORMATION

TO SEQUENCE TITLE OF INVENTION: SEQUENCE AND INTENDIC INSERTION STRATEGIES FOR ENHANCEMENT

TITLE OF INVENTION: SEQUENCE AND INTENDIC INSERTION STRATEGIES FOR ENHANCEMENT

TITLE OF INVENTION: SYSTEMS COMPRISING SAME

TITLE OF INVENTION: SYSTEMS COMPRISING SAME

NUMBER OF SEQUENCES: 32

ADDRESSEONDENCE ADDRESS:

ADDRESSEE: BUNNS, DOANE, SWECKER & MATHIS
                  Score 7.8; DB 1; Length 12;
Pred. No. 3e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT ARPLICATION DATA:
APPLICATION UNDER: US/08/822,586
APPLICATION UNDER: US/08/822,586
FILING DATE: MARCH 20, 1997
ATTORNEY/AGENT INFORMATION:
NAME: ELIZABETH A. BOGGGIAN
REGISTRATION NUMBER: 39,911
REPERENCE/DOCKET NUMBER: 96700/437
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 286-0854 or 286-0082
TELEFAX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 other nucleic acid
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ilarity 81.8%;
Conservative
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COUNTRY: United States
ZIP: 22313-140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      915 TGGTCTTTGCC 925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 resecarrece 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-013-092-24/c
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SEQUENCE ALL ADDICATION:
SEQUENCE ALL ADDICATION:
SEQUENCE ALL ADDICATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
SEQUENCE ANTION OF CANCER CELL MEMBRANE
TITLE OF INVENTION:
SECONDESSEE: Wandersh, Lind & Ponack, L.L.P.
SCHEEFE: John SEGUENCES:
SCHEEFE: Doing X Street, N.W., #800
STREET: JOHN STREET: DOING STREET:
                                                                                                      ô
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                                                                                                      Gaps
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                                                 Score 7.8; DB 1; Length 12;
Pred. No. 3e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CELL TYPE: Hybridoma producing human antibody 1-3-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.7%; Score 7.8; DB 1;
81.8%; Pred. No. 3e+02;
iive 0; Mismatches 2
                                            Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                                                905 TCATTTTCTTT 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      905 TCATTTTCTT 915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA ORIGINAL SOURCE:
US-09-017-628-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-014-880-41
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Gaps

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Sequence 84, Application US/08874825
Sequence 84, Application National Applicant: National Applicant: Raight, James Thrie OF INVENTION: PROTEIN INTERACTIONS THAT OCCUR IN POPULATIONS TITLE OF INVENTION: AND IDENTIFICATION OF INHIBITORS OF THESE INTERACTORS NUMBER OF SEQUENCES: 122
CORRESPONDED ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Pred. No. 3e+02;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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10.7%; Score 7.8; DB 1;
Best Local Similarity 81.6%; Pred. No. 3e+02;
Matches 9; Conservative 0; Mismatches
                                                                                                                                                                     MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "HNF-4 Consensus"
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READBLE ECONO.

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
CORPUTER: IBM Compatible
CORPUTER: IBM Compatible
CORPUTER: SetSEQ Version 2.0
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/874,825
FILING DATE: 13-UN-1997
CLASSIFICATION NUMBER: 08/663,824
APPLICATION NUMBER: 08/663,824
FILING DATE: 14-UN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Lealie
REGISTRATION NUMBER: 18,972
REFERENCE/DOCKET NUMBER: 7934-045
FILERPHONE: 212-790-9090
TELEEPHONE: 212-790-9090
TELEEPHONE: 212-869-864
TELERY: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 84:
**CHARACTERISTICS:

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                       10.7%;
                                                                                                                                                                                                                                                                                                                                           Ouery Match 10.7
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    934 CTCCTCTTCAT 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         915 TGGTCTTTGCC 925
                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 TGRMCYTWGCM 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
                                                                                                                                            linear
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                                                                                                                                                                                                                                                                               US-09-038-217A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-874-825-84
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US-09-038-217A-14/C
US-09-038-217A-14/C
Sequence 14. Application US/09038217A
Sequence 14. Application US/09038217A
Retent No. 6025196
GENERAL INFORMATION:
APPLICANT: Sladek, Frances M.
APPLICANT: Zhong, Weimin
APPLICANT: Darnell, Jr., James F.
TITLE OF INVENTION: LIVER ENRICHED TRANSCRIPTION FACTOR
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 7.8; DB 1; Length 12;
Pred. No. 3e+02;
0; Mismatches 2; Indels
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COMPUTE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PatentIn Pelease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,217A
FILING DATE: March 11, 1998
CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/013,092
                                                                                                                                                                                                                                 FILLING DALE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/147,696
FILLING DATE: 03-NOV-1993
APPLICATION NUMBER: US 07/977,691
FILING DATE: 13-NOV-1992
ATTONEN'AGENT INFORMATION:
NAME: TESKIN, ROBIN L.
REGISTATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-010
TELECOMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-5021
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH 12 DASE PAIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 201-343-1684
INFORMATION FOR SEQ 1D NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: DNA (genomic) US-09-013-092-24
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81.8%;
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Best Local Similarity 81.8
Matches 9; Conservative
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EDNESS: single
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STATE: New Jersey
COUNTRY: USA
ZIP: 07601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
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10.7%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 38+02;
Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                   ZIF: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/884,324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                         CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                           Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: Genomic I
ORIGINAL SOURCE:
ORGANISM: human
TISSUE TYPE: placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: exon
; LOCATION: 1..87
; IDENTIFICATION METHOD:
US-08-884-324-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   933 CCTCCTCTTCA 943
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                                                                               PESULT 579
US-06-814-825-85
US-06-814-825-85
PGGENERAL INFORMATION:
Sequence 85, Application US/08874825
PSTEATEN OF 6057101
PGENERAL INFORMATION:
APPLICANT: Nandabalan, Kriehnan
APPLICANT: Yang, Weijia
APPLICANT: Weijid. Johathan
APPLICANT: Kaight, James
ANDIBESOB: PENNES: 12
ANDIBESOB: PENNES: 13
ANDIBESOB: PENNES: 14
ANDIBESOB: PENNES: 13
ANDIBESOB: PENNES: 14
ANDIBESOB: PENNES: 14
ANDIBESOB: PENNES: 14
ANDIBESOB: PENNES: 14
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| Sequence 6, Application US/08884324
| Patter No. 6060283
| Patter No. 6060283
| GENERAL INFORMATION:
| APPLICANT: Takanori OKURA
| APPLICANT: Maschi TORIGOS
| APPLICANT: Maschi KURIMOTO
| TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE
| TITLE OF INVENTION: OF INDUCING THE PRODUCTION OF INTERFERON-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   934 CTCCTCTTCAT 944
1 CGCGTCTTCAT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 cragicircar 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 9; Conserv
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Patent No. 6083693

GENERAL INFORMATION:
APPLICANT: Nandabalan, Krishnan
APPLICANT: Nandabalan, Krishnan
APPLICANT: Nathberg, Jonathan
TITLE OF INVENTION: INFERTIFICATION AND COMPARISON OF PROTEIN-PROTEIN
TITLE OF INVENTION: INFERTIFICATIONS THAT OCCUR IN POPULATIONS
FILE REFERENCE: 7934-006
CURRENT APPLICATION NUMBER: US/08/663,824
CURRENT FILING DATE: 1996-06-14
NUMBER OF SEQ ID NOS: 118
SEQ ID NO 85
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Nandabalan, Krishnan
APPLICANT: Nandabalan, Krishnan
APPLICANT: Rothberg, Jonathan
TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN
TITLE OF INVENTION: INTERACTIONS THAT OCCUR IN POPULATIONS
FILE REFERENCE: 7934-006
CURRENT APPLICATION NUMBER: US/08/663,824
CURRENT FILING DATE: 1996-06-14
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                           ; LOCATION: 4.9"
; OTHER INFORMATION: /note= "Portion of the germline; OTHER INFORMATION: gene incorporated into the CDR3 construct"
15.08-881-037-79
                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: Description of Artificial Sequence: linker US-08-663-824-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: linker US-08-663-824-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 7.8; DB 1; Length 12;
Pred. No. 3e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                              10.7%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 84, Application US/08663824
Patent No. 6083693
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                               FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 81..

Best Local Similarity 61..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              955 TATCGCTACCA 965
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      12 base pairs
                                 TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 cecercricar 11
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US-08-663-824-85
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NATURE:
NATURE:
NATURE:
LOCATION: 1..12
LOCATION: 1..12
OTHER INFORMATION: /note= "Adapter sequence results
OTHER INFORMATION: from oligonucleotide duplex formation with nucleotides 5-16
OTHER INFORMATION: SEQ ID NO: 16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Pred. No. 3e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:

COUNTRY: USA

ZIP: 94304-1018

CONDUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM FC compatible
COMPUTER: ISM PC compatible
COMPUTER: DATE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/881,037
FILING DATE: 23-UN-1997
FILING DATE: 18-MAY-1995
CLASSIFICATION 1906
FILING DATE: 18-MAY-1995
CLASSIFICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION NUMBER: 34,202
REPERBENCE/DOCKET NUMBER: 34,202
REPERBENCE/DOCKET NUMBER: 203442110710
TELECOMMUNICATION INFORMATION:
TOTAL TOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 79, Application US/08881037
Fatent No. 6080588
GENERAL INFORMATION:
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Poerster
CITY: Palo Alto
APPLICATION.

FILING DATE: 07-UN-10-1

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: POPOVICH, Thomas E

REGISTRATION NUMBER: 30,099

REFERENCE/DOCKET NUMBER: MED1003USD4

TELECOMMUNICATION INFORMATION:

TELEPROME: 612-334-8991

TELEPRAX: 612-334-8991

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 12 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TYPE: nucleic acid

STRANDEDNESS: double

"NAM (SYRTHELIC)

"NAM (SYRTHELIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.7%;
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Best Local Similarity
Matches 9; Conserv
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US-08-881-037-79
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US-08-484-408A-15
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Fatent No. 6117653
GENERAL INFORMATION:
TITLE OF INVENTION: HEPATITIS B SURFACE ANTIGEN VACCINE
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
GORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
COUNTRY: Winneapolis
STATE: WN
COUNTRY: USA
Score 7.8; DB 1; Length 12;
Pred. No. 3e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.7%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 3e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Robert S. Matson
APPLICANT: Robert S. Matson
ITILE OF INVENTION: USE OF URACIL-DNA GLYCOSYLASE
TITLE OF INVENTION: USE OF URACIL-DNA GLYCOSYLASE
TITLE OF INVENTION: IN GENETIC ANALYSIS
NUMBER OF SEQUENCES: 10
CORRESSEE: Beckman Instruments, Inc.
STREET: 2500 Harbor Boulevard
CITY: Fulletron
STREET: ABLORME: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER READABLE
OFFRATING SYSTEM: WINDOWS 95 - WORDPERPECT 7.0
SOFTWARE: BM COMPATION
SOFTWARE: ASCII (DOS) TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/959,853
FILING DATE: Harder
NAME: P. R. Harder
NAME: P. R. Harder
NAME: P. R. Harder
NAME: P. R. HARDER: ASCII (NOS)
REFERENCE/DOCKET NUMBER: 20,022
                                                                                                                                                                                                                                        RESULT 585
US-08-959-883-8/c
; Sequence 8, Application US/08959853
; Patent No. 6090553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-959-853-8
Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (714) 773-7936
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Conservative
                                                                                                        934 CICCICITCAT 944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                           1 cragrerrear 11
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Best Local Similarity
Matches 9; Conserv
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US-08-484-408A-15
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NAME/KEY: misc_feature
LOCATION: 1..12
OTHER INFORMATION: /note= "Adapter sequence results
OTHER INFORMATION: from oligonucleotide duplex formation with nucleotides 5-16 o
OTHER INFORMATION: SEQ ID NO: 16"
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/942,406
FILING DATE: 01-Oct-1997
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.7%; Score 7.8; DB 1; Length 12; ilarity 81.8%; Pred. No. 3e+02; Conservative 0; Mismatches 2; Indels
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TITLE OF INVENTION: Method for the Determination and NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC-DOS/MS-DOS
COPTWARE: PatentIn Release #1.0, Version #1.30
SUSTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/484,408A
FILING DATE: 07-JUN 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: POPOVICH, Thomas E
REGISTRATION NUMBER: 30,099
REFERENCE/DOCKET NUMBER: MED1003USD4
TELEPRATION NUMBER: 30,099
REFERENCE/DOCKET NUMBER: MED1003USD4
TELEPRATION FORMATION:
TELEPRATION FORMATION:
TELEPRATION FORMATION:
TELEPRATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: mucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOMECULE TYPE: DNA (Synthetic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7914-015-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
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FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rothberg, Jonathan
Deem, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/08942406; Patent No. 6141657; GENERAL INFORMATION:
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Best Local Similarity
Matches 9; Conserv
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schultz1-899.rni

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TOPOLOGY: linear MOLECULE TYPE: DNA
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COUNTRY: USA
ZIP: 10036-2711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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US-09-280-999-24/c

i Sequence 24, Application US/09280999

j Patent No. 6129730

GENERAL INFORMATION:

APPLICANT: REFF, Mitchell E.

ITILE OF INVENTION: IMPALRED DOMINANT SELECTABLE MARKER

ITILE OF INVENTION: SEQUENCE AND INTRONIC INSERTION STRATEGIES FOR ENHANCEMEN

ITILE OF INVENTION: SYSTEMS COMPRISING SAME

ITILE OF INVENTION: SYSTEMS COMPRISING SAME

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: P.O. BOX 1404

CITY: Wirthia
                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                       Score 7.8; DB 1; Length 12;
Pred. No. 3e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/280,999
                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-08-942-406-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-010
TELECOMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-2021
INFORMATION FOR SEQ ID NO: 24:
FROMMER: FRANCIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
APPLICATION NUMBER: US/08/147,696
FILING DATE: 03-NOV-1993
APPLICATION NUMBER: US 07/977,691
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
                  TELEPHONE: (212)-790-9090
TELEFAX: (212)-869-8864
TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/013,092
                                                                                                                                                                                                                                                                                                       10.7%;
81.8%;
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                                                                                                                                                                                                                                                                                                     Query Match 10.7
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 12 base pairs
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US-09-281-418-71/c
| Sequence 71, Application US/09281418
| Sequence 71, Application US/09281418
| Setent No. 6287769
| GENERAL INCRMATION:
| APPLICANT: Incue, Takakazu
| TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA Fr
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                                             Gaps
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Score 7.8; DB 1; Length 12;
Pred. No. 3e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/09/322,617
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 7.8; DB 1;
Pred. No. 3e+02;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Pennie and Edmonus
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                  Sequence 13, Application US/09322617
; Sequence 13, Application US/09322617
; Patent No. 6231812
; GENERAL INFORMATION:
APPLICANT: Deem, Michael
APPLICANT: Deem, Michael
APPLICANT: Simpson, John
TITLE OF INVENTION: Method for the Det
TITLE OF INVENTION: Sequencing
NUMBER OF INVENTION: Sequencing
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/547,214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7934
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)-790-9990
TELEFAX: (212)-865-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18,872
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INFORMATION FOR SEQ 1D NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
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                                                                                          949 TTAATGTATCG 959
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                                                                                                                                   12 TTAATTAATCG 2
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APPLICANT: Scherman, Daniel
APPLICANT: Scherman, Daniel
APPLICANT: Wils, Pierre
APPLICANT: Blanche, Francis
TITLE OF INVENTION: PURPERCATION OF A TRIPLE HELIX FORMATION WITH AN
TITLE OF INVENTION: PURPERCATION OF A TRIPLE HELIX FORMATION WITH AN
TITLE OF INVENTION: IMMOBILIZED OLIGONUCLEOTIDE
FILS REFERENCE: 03804.0138-01
CURRENT FILING DATE: 1050-06-09
PRIOR FILING DATE: 1997-06-09
PRIOR FILING DATE: 1995-11-08
NUMBER OF SEQ ID NOS: 36
SOUTHARE: Patentin Ver. 2.1
SEQ ID NO 28
LENGTH: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.7%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) OTHER INFORMATION: Description of Artificial Sequence:
, OTHER INFORMATION: binding region
US-08-849-567A-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: ; OTHER INFORMATION: oligonucleotide US-09-580-923-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: JOYCE, Gerald F.
APPLICANT: JOYCE, Gerald R.
TITLE OF INVENTION: ENZYMATIC DNA MOLECULES
FILE REFERENCE: SCR19438
CURRENT PAPLICATION NUMBER: US/08/849,567A
CURRENT FILING DATE: 1997-08-25
RRIOR APPLICATION NUMBER: PCT/US95/15580
PRIOR APPLICATION NUMBER: O8/12,194
RRIOR APPLICATION NUMBER: 08/12,194
RRIOR APPLICATION NUMBER: 08/12,194
RRIOR PILING DATE: 1995-06-07
PRIOR PILING DATE: 1995-06-07
PRIOR FILING DATE: 1994-12-02
NUMBER OF SEQ ID NOS: 101
SSQ ID NO 42
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-849-567A-42; Sequence 42, Application US/08849567A; Patent No. 6326174
                                                                                                                            RESULT 592
US-09-580-923-28
Sequence 28, Application US/09580923
Patent No. 6319672
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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      12 CCTTACCTTTT
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Best Local Similarity
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US-03-417-455-28/C
US-03-417-455-28/C
Sequence 28, Application US/09417455
PATENT NO. 6294655
GENERAL INFORMATION:
APPLICANT: Perch, John
APPLICANT: Perch, John
TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
FILE REFERENCE: 28110/36328
CURRENT APPLICATION NUMBER: US/09/417,455
CURRENT PILING DATE: 1999-01-0.3
FRIOR FILING DATE: 1999-04-05
PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: US 09/287,210
PRIOR APPLICATION NUMBER: US 09/287,210
PRIOR APPLICATION NUMBER: US 09/287,210
PRIOR PRIOR APPLICATION NUMBER: US 09/229,591
PRIOR PLING DATE: 1999-04-05
PRIOR PLING DATE: 1999-04-05
PRIOR PLING DATE: 1999-04-05
PRIOR PLING DATE: 1999-04-05
PRIOR PLING DATE: 1998-06-19
PRIOR PLING DATE: 1998-06-10
PRIOR PLI
TITLE OF INVENTION: agment, Method of Assaying Microorganisms, Method of Analyzing I
TITLE OF INVENTION: nisms and Method of Assaying Contaminant
FILLE REFERENCE: 9982.7
CURRENT APPLICATION NUMBER: US/09/281,418
CURRENT FILING DATE: 1999-03-30
EARLIER APPLICATION NUMBER: UP/1998/87651
EARLIER FILING DATE: 1999-03-16
EARLIER FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 216
LENGTH: 12
LENGTH: 12
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Pred. No. 3e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 7.8; DB 1; Length 12;
Pred. No. 3e+02;
0; Mismatches 2; Indels
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81.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
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Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Primer US-09-281-418-71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: TBD
US-09-417-455-28
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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Sequence 84, Application US/09231303
; Sequence 84, Application US/09231303
; Patent No. 6395476
; GENERAL INFORMATION:
    APPLICANT: Nandabalan, Krishnan
    APPLICANT: Nandabalan, Krishnan
    APPLICANT: Nandabalan, Krishnan
    APPLICANT: Rothberg, Jorathan
    TITLE OF INVENTION: IDENTIFICATION AND COMPARISON OF PROTEIN-PROTEIN
    TITLE OF INVENTION: IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS
    FILE REFERENCE: 7934-087
    CURRENT APPLICATION NUMBER: US/09/231,303
    CURRENT APPLICATION NUMBER: US/09/231,303
    CURRENT FILING DATE: 1999-01-12
    EARLIER FILING DATE: 1996-06-14
    NUMBER OF SEQ ID NOS: 118
    SOFTHARE: PATENTIN UNE: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) TYPE: DNA
) ORGANISM: Artificial Sequence
) FEATURE:
) PEATURE:
) OTHER INFORMATION: Description of Artificial Sequence: linker
US-09-231-303-84
                                                                                                                                                Score 7.8; DB 1; Length 12;
Pred. No. 3e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.7%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Nathery Jonathan M
PAPLICANT: Nathery Girish N
APPLICANT: Nathery Girish N
APPLICANT: Hu, Xinghua
TITLE OF INVENTION: Methods and Devices for Measuring
TITLE OF INVENTION: Differential Gene Expression
FILE REFERENCE: 7934-052
CURRENT APPLICATION NUMBER: US/09/203,231B
CURRENT FILING DATE: 1998-12-02
FRIOR FILING DATE: 1997-12-03
NUMBER OF SEQ ID NOS: 88
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/09203231B Patent No. 6355423 GENERAL INFORMATION:
                                                                                                                                                Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 81.0
Best Local 9; Conservative
                                                                                                                                                                                                                                                                          919 CTTTGCCTTTT 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTHER INFORMATION: Primer US-09-203-231B-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              943 ATTGGTTTAAT 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AGTGGCTTAAT 11
                                                                                                                                                                                                                                                                                                              12 CCTTACCTTT 2
                                                       ; OTHER INFORMATION: TBD US-09-348-942-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-09-203-231B-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-231-303-84
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LENGTH: 12
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US-09-348-942-28/C
is Sequence 28, Application US/09348942
is Patent No. 6337072
is GENERAL INFORMATION:
APPLICANT: John FOR AND ADDIAGE INTERLEUXIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
ITILE OF INVENTION: A NOVEL INTERLEUXIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
ITILE OF INVENTION: A NOVEL INTERLEUXIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
ITILE OF INVENTION: A NOVEL INTERLEUXIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
ITILE OF INVENTION: UNMBER: US/09/348,942
CURRENT FILING DATE: 1999-07-07
REALIER APPLICATION NUMBER: US 09/291,10
REALIER FILING DATE: 1999-04-05
REALIER FILING DATE: 1999-04-05
REALIER FILING DATE: 1999-01-13
REALIER APPLICATION NUMBER: US 09/29,591
REALIER FILING DATE: 1998-05-13
REALIER APPLICATION NUMBER: US 09/099,818
REALIER FILING DATE: 1998-05-13
REALIER FILING DATE: 1998-05-13
REALIER FILING DATE: 1998-05-13
REALIER FILING DATE: 1998-05-13
REALIER FILING DATE: 1998-05-15
REALIER PADE SOR 1D NOS: 30
REALIER FOR SOR 1D NOS: 30
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GENERAL INFORMATION:
APPLICANT: Bloch, William
APPLICANT: Benolm, Michael
APPLICANT: Benolm, Michael
APPLICANT: Benolm, Michael
APPLICANT: Merrer, William E.
APPLICANT: Benolm, Michael
APPLICANT: Mores, Rene L.
TITLE OF INVENTION: Compositions of Solvents and High
TITLE OF INVENTION: Compositions of Nucleic Acid Analogs
FILE REPERENCE: 4444
CURRENT APPLICATION NUMBER: US/09/311,079
CURRENT PILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 12;
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Indels
7
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Best Local Similarity 81.8%; Pred. No. 3e+02;
Matches 9; Conservative 0; Mismatches
Mismatches
                                                                                                                                                                                                                                                                       ; Sequence 6, Application US/09311079; Patent No. 6331618
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9; Conservative
                                                              952 ATGIATCGCIA 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 907 ATTTTCTTTGG 917
                                                                                                                      2 ATGTGACGCTA 12
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                                                                                                                                                                                                                  RESULT 594
US-09-311-079-6/c
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Matches
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10.7%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 3e+02;
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hansburg, Daniel
REGISTRATION NUMBER: 36156
REFERENCE/DOCKET NUMBER: 7991-010-999
TELECOMMUNICATION INFORMATION:
TELEFAX: 215-504-4444
                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 12 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 81.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                             926 TTTTATCCCTC 936
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US-08-927-165A-16
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US-09-751-561-13
                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-751-561-13
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                                                                                                                                                      Sequence 85, Application US/09231303
| Sequence 85, Application US/09231303
| Patent No. 6395478
| GENERAL INFORMATION:
| APPLICANT: Nandabalan, Krishnan
| APPLICANT: Nandabalan, Krishnan
| APPLICANT: Nathberg, Jonathan AND COMPARISON OF PROTEIN-PROTEIN
| TITLE OF INVENTION: IDENTIFICATION FRAT OCCUR IN POPULATIONS AND
| TITLE OF INVENTION: IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS
| TITLE OF INVENTION: IDENTIFICATION OF INHIBITORS OF THESE INTERACTIONS
| CURRENT APPLICATION NUMBER: US/09/231,303
| CURRENT FILING DATE: 1999-01-12
| EARLIER FILING DATE: 1996-06-14
| NUMBER OF SEQ ID NOS: 118
| SEQ ID NO 85
| LENGTH: 12
                                Gaps
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 Score 7.8; DB 1; Length 12;
Pred. No. 3e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kniec, Eric B.
APPLICANT: Rice, Michael C.
APPLICANT: Rice, Michael C.
APPLICANT: Shu, Zhigang
ITILE OF INVENTION: Mammalian and Human Rec2
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,165A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-927-165A-16/c
; Sequence 16, Application US/08927165A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 18940
COMPUTER REDABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATINE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Kimeragen, Inc. STREET: 300 Pheasant Run
 10.7%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                9; Conservative
                                                              934 CTCCTCTTCAT 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              934 CTCCTCTTCAT 944
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                     1 CGCGTCTTCAT 11
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 Query Match
Best Local Similarity
Matches 9; Conserv
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                                                                                                                                      RESULT 598
US-09-231-303-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-231-303-85
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Sequence 41, Application US/08450363

Sequence 41, Application US/08450363

Patent No. 6436434

Patent No. 6436434

APPLICANT: Salko HOSOKAWA

APPLICANT: Yoko HIRAKAWA

APPLICANT: No. 6436434 hiko ITO

APPLICANT: Nazuhiro NAGAIKE

TITLE OF INVENTION: Human Monoclonal Antibody

TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer

TITLE OF INVENTION: Call Membrane

NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 7.8; DB 1; Length 12;
Pred. No. 3e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7934-015-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)-999-9090
TELEFAX: (212)-869-8864
                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/724,385
FILING DATE: 28-NO. 6432361-2000
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/322,617
FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: WordPerfect.5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/450,363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3: Wenderoth, Lind & Ponack
805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                        ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.7%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 81.8
Matches 9; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Distributer
                                                 CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               943 ATTGGTTTAAT 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AGTGGCTTAAT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-724-385-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF FILE REFERENCE: 28110/36010

CURRENT PAPLICATION NUMBER: US/09/457,626

CURRENT FILING DATE: 1999-10-13

EARLIER PAPLICATION NUMBER: US 09/417,455

EARLIER FILING DATE: 1999-10-13

EARLIER FILING DATE: 1999-10-13

EARLIER FILING DATE: 1999-0-0-05

EARLIER FILING DATE: 1999-0-0-05

EARLIER FILING DATE: 1999-0-0-05

EARLIER FILING DATE: 1999-0-1-05

EARLIER PAPLICATION NUMBER: US 09/251,370

EARLIER PAPLICATION NUMBER: US 09/251,370

EARLIER PAPLICATION NUMBER: US 09/25,591

EARLIER PAPLICATION NUMBER: US 09/229,591

EARLIER PAPLICATION NUMBER: US 09/229,591

EARLIER PAPLICATION NUMBER: US 09/229,591

EARLIER PAPLICATION NUMBER: US 09/099,818

EARLIER FILING DATE: 1998-07-31

EARLIER FILING DATE: 1998-05-13

EARLIER FILING DATE: 1998-05-15

EARLIER FILING DATE: 1998-05-16

EARLIER FILING DATE: 1998-05-1
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                          Score 7.8; DB 1; Length 12;
Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Simpson, John TITLE OF INVENTION: Method for the Determination and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 7.8; DB 1;
Pred. No. 3e+02;
                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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US-09-724-385-13
; Sequence 13, Application US/09724385
; Patent No. 6422361
; GENERAL INFORMATION:
; APPLICANT: Rothberg, Jonathan
Deem, Michael
                                                                                                                                                                                                                                                                          RESULT 601
US-09-457-626-28/C
US-09-457-626-28/C
Patent No. 6426191
GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Pace, Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.7%;
81.8%;
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CORRESPONDENCE ADDRESS:
Ouery Match
Best Local Similarity 81.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 81.0
                                                                                                                                         943 ATTGGTTTAAT 953
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US-09-457-626-28
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COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/757,528
FILING DATE: 10-Jan-2001
FILING DATE: 10-Jan-2001
FILING DATE: 10-Jan-2001
PRIOR APPLICATION NUMBER: 08/547,214
PRIDRE APPLICATION NUMBER: 08/547,214
PRIDRE MARE: Misrock, S. Leslie
REGISTRATION NUMBER: 18/872
REFERENCE/DOCKET NUMBER: 7934-015-999
TELEFAX: (212)-790-9090
TELEFAX: (212)-790-9090
TELEFAX: (212)-790-9090
TELEFAX: (212)-790-9090
TELEFAX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 Dase pairs
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US-09-059-625-31/c
; Sequence 31, Application US/09059625
; Patent No. 6486303
; GENERAL INFORMATION:
APPLICANT: Moyle, William R
; TITLE OF INVENTION: Improved Method For Making Hormone;
ITILE OF INVENTION: Heterodimers
NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
ADDRESSE: Richard R. Muccino
STREET: 758 Springfield Avenue
COUNTRY: US
; COUNTRY: US
; COUNTRY: US
; COUNTRY: US
; COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 10.7%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 3e+02; Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                APPLICANT: Rothberg, Jonathan
Deem, Michael
Simpson, John
TITLE OF INVENTION: Method for the Determination and
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear

MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-757-528-13
                    Sequence 13, Application US/09757528
Patent No. 6453245
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  943 ATTGGTTTAAT 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AGTGGCTTAAT 11
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10.7%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL ITYPE:
FILING DATE: May 25, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA.
APPLICATION NUMBER: 08/360,125
FILING DATE: December 20, 1994
PRIOR APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
ATTORNEY AGENT INFORMATION:
NAME: WARTEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELEPHONE: 202-371-8850
TELERA:
TELEPHONE: 202-371-8850
TELEX:
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDRESS: double
TOPOLOGY: linear
MOLECTUE TYPE: CDNA
HYPOTHETICAL:
ANTI-SENSE:
RAGGMENT TYPE:
ORGANISM:
ORGANISM:
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RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBATALICATION IN GENOME:
CLOUB:
CLROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INPORMATION:
AUTHORS:
AUTHORS:
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MMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-450-363-41
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VOLUME:
ISSUE:
PAGES:
DATE:
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Gaps

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RESULT 604 US-09-757-528-13

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Patent No. 6500672

GENERAL INFORMATION:
APPLICANT: Sladek, Frances M.
Zhong, Weimin
Darnell, Jr., James F.

TITLE OF INVENTION: LIVER ENRICHED TRANSCRIPTION FACTOR
NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PIPLICATION NUMBER: US/09/447,034
FILING DATE: 22-No. 6500672-1999
CLASSIFICATION: «Unknown»
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/038,217
FILING DATE: March 11, 1998
ATTORNEY/AGENT INFORMATION:
NAME: JGACKON ESG., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-030B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 7.8; DB Pred. No. 3e+02 0; Mismatches
                                                                           FILING DATE: 14-APR-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Muccino, Richard R
REGISTRATION NUMBER: 32,538
REFERENCE/DOCKET NUMBER: UMD1-040
TELECHONE: 908-273-4988
TELEFAN: 908-273-4988
TELEFAN: 908-273-4679
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                           JMBER: US/09/059,625
14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                   DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                        LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               948 TTTAATGTATC 958
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                                                                                                                                                                                                                                                                                                                                                                                            unknown
                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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US-09-059-625-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 606
US-09-447-034-14/c
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APPLICANI: Pace, Ann
TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
FILE REPRENCE: 20110/36456
CURRENT APPLICATION NUMBER: US/09/576,008
CURRENT FILING DATE: 2000-03-10
FRICH APPLICATION NUMBER: US 09/427,626
FRICH APPLICATION NUMBER: US 09/427,626
FRICH APPLICATION NUMBER: US 09/427,626
FRICH APPLICATION NUMBER: US 09/417,455
FRICH FILING DATE: 1999-10-13
FRICH FILING DATE: 1999-10-13
FRICH FILING DATE: 1999-10-13
FRICH RELING DATE: 1999-04-05
FRICH FILING DATE: 1999-03-13
FRICH FILING DATE: 1999-05-10
FRICH APPLICATION NUMBER: US 09/099,818
FRICH FILING DATE: 1998-05-10
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10.7%; Score 7.8; DB 1; Length 12;
Best Local Similarity 54.5%; Pred. No. 3e+02;
Matches 6; Conservative 4; Mismatches 1; Indels
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TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "HNF-4 Consensus"
HYPOTHETICAL: YES
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 28, Application US/09576008
Patent No. 6541623
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ford, John APPLICANT: Ho, Alice Suk-Yue
                                                                                                                                                                                                                                                                                                                                                                                                                                       915 TGGTCTTTGCC 925
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                                                                                                                                                                                                       US-09-447-034-14
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12 ccrraccrrrr 2

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APPLICANT: ELEMIN ALERED S.
APPLICANT: ELEMIN LYNN C.
APPLICANT: ELEMIN LYNN C.
APPLICANT: GRAW, LYNN C.
TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES
THE REPERBENCE: 4300.014100
CURRENT APPLICATION NUMBER: 06/063,667
PRIOR PILING DATE: 1998-04-21
PRIOR PILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 66/046,147
PRIOR APPLICATION NUMBER: 66/044,492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
10.7%; Score 7.8; DB 1; Length 12;
Best Local Similarity 63.6%; Pred. No. 3e+02;
Matches 7; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMPROVED METHOD FOR
AMPLIFICATION OF
TARGETED SEGMENTS OF
NUCLEIC ACID USING
NESTED POLYMERASE CHAIN
REACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (). ()
; OTHER INFORMATION: SYNTHETIC OLIGONUCLECTIDE US-09-814-601-137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh 6.0
SOFTWARE: PATENTIN RELEASE #1.0,
SOFTWARE: VERSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11702
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: IMPROVED METHOD F
TITLE OF INVENTION: TARGETED SEGMENTS
TITLE OF INVENTION: TARGETED SEGMENTS
TITLE OF INVENTION: NUCLEIC ACID USIN
TITLE OF INVENTION: NESTED POLYMERABE
TITLE OF INVENTION: REACTION
NUMBER OF SEQUENCES: 22
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 4, Application PC/TUS9311702
; GENERAL INFORMATION:
; APPLICANT:
Application US/09874601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     961 TACCAACGGTG 971
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: RNA
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Patent No. 6632057

GENERAL INFORMATION:

APPLICANT: ELWIN, ALFRED S.

APPLICANT: GRANT: MARIA B.

TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES

FILER REFERENCE: 4300.01410

CURRENT APPLICATION NUMBER: 09/09/874,601

CURRENT PILING DATE: 1998-04-21

PRIOR PILING DATE: 1998-04-21

PRIOR FILING DATE: 1997-06-09

PRIOR FILING DATE: 1997-06-09

PRIOR FILING DATE: 1997-04-21

PRIOR FILING DATE: 1997-04-21

NUMBER OF SEQ ID NOS: 182

SOFTWARE: PatentIn version 3.0

LENGTH: 12
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10.7%; Score 7.8; DB 1; Length 12;
Best Local Similarity 63.6%; Pred. No. 3e+02;
Matches 7; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 7.8; DB 1; Length 12;
Pred. No. 3e+02;
0; Mismatches 2; Indels
                                                                                                 Sequence 57, Application US/09512563C
Fatent No. 657906
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Goodpasture Binding Protein
FILLE REFRENCE: 98-733-A
FURRENT APPLICATION NUMBER: US/09/512,563C
CURRENT FILING DATE: 2000-02-24
FRICA APPLICATION NUMBER: 60/121,483
FRICA APPLICATION NUMBER: 60/121,483
FRICA APPLICATION UNMBER: 60/121,483
FRICA APPLICATION UNMBER: 60/121,483
FRICA FRICATION UNMBER: 1999-02-24
NUMBER OF SEQ ID NOS: 63
SOFFWARE: Patentin Ver. 2.0
SED ID NOS: 57
LENGTH: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
                                                                                        US-09-512-563C-57/c
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US-09-874-601-137
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Best Local Similarity 81.8%;
Matches 9; Conservative C
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        929 TATCCCTCCTC 939
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STATE:
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Sequence 22, Application PC/TUS9505265

Sequence 22, Application PC/TUS9505265

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TORRESPONDENCES: 74

CORRESPONDENCES: 74

CORRESPONDENCES: 74

CORRESPONDENCES: 74

CORRESPONDENCES: 74

CORRESPONDENCES: 74

CORPUTE: An Francisco Center, Suite 3400

CITY: San Francisco

CITY: San Francisco

COUNTY: Usa Francisco

CONTY: 9411-4187

COMPUTER: READABLE FORM:

MOMPUTER: Floppy disk

COMPUTER: Floppy disk

COMPUTER: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: PCT/US95/05265
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Pred. No. 3e+02;
4; Mismatches 1; Indels
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CLASIPECATION:
PRICA APPLICATION NUMBER: US 08/235,503
FILING DATE: 29-APP-1994
FILING DATE: 29-APP-1994
ATTORNEY/AGBNT INFORMATION:
NAME: Osman, Richard A
REJERRINGLE/DOCKET NUMBER: 36,605
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application PC/TUS9505835
Sequence 1, Maphication PC/TUS9505835
SEREAL INFORMATION:
APPLICANT: Alexander-Bridges, Maria C.
APPLICANT: Zhao, Hui-Fen
TITLE OF INVENTION: INHIBITION OF INSULIN-
TITLE OF INVENTION: INDUCED ADIPOSIS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
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54.5%;
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(415) 398-3249
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Best Local Similarity 54.5
Matches 6; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                915 TGGTCTTTGCC 925
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12 TACGGTATCGC 2
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PCT-US95-05835-1/c
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Pred. No. 3e+02;
0; Mismatches 2; Indels
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Sequence 13, Application PC/TUS9506379
GENERAL INFORMATION:
APPLICANT: Watanabe, Kyoichi A.
APPLICANT: Wali, Roger
APPLICANT: Wali, Roger
ITLE OF INVENTION: Complementary DNA and Toxins
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSE: Cooper & Dunham LLP
STREET: New York
CITY: New York
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMEUTER: 1BM PS/2 Model 502 or 555X OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: Wordberfect (Version 5.1) CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/05835 FILING DATE:
                                                                                                                                                                       FILING APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/242,409
FILING DATE: 13 May 1994
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, Paul T.
REGISTRAITON NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/238001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: New JOIN
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44Mb
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
RPLING DATE: May 13, 1994
CLASSIFICATION:
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NAME: White, John P.
REGISTRATTON NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 446
TELECOMMUNICATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 212-391-0526
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Search completed: October 18, 2004, 14:27:52 Job time : 3 secs
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5212296-13/c
5212296-13/c
Fatent No. 5212296
Fatent No. 5212296
FATELICANT: DEAN, CAROLINE, HARDER, PATRICIA A., LETO, KENNETH
70. FOREYER, JAMES P.; OMER, CHARLES A., ROMESSER, JAMES A.
71TEPPERMAN, JAMES M.
71TLE OF INVENTION: EXPRESSION OF HERBICIDE METABOLIZING
                                                                                          Query Match 10.7%; Score 7.8; DB 1; Length 12; Best Local Similarity 81.8%; Pred. No. 3e+02; Matches 9; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.7%; Score 7.8; DB 1; Length 12; 81.8%; Pred. No. 38+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    SELECTION OF DIAGNOSTIC GENETIC MARKERS IN MICROORGANISMS AND USE OF A SPECIFIC MARKER FOR DETECTION OF SALMONELLA
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
TITLE OF INVENTION: SELECTION OF DIAGNO
TITLE OF INVENTION: MICROGRAMISMS AND
TITLE OF INVENTION: MICROGRAMISMS AND
TITLE OF INVENTION: OF A SPECIFIC MARKE
TITLE OF INVENTION: OF A SPECIFIC MARKE
TITLE OF INVENTION: SALMONELLA
NUMBER OF SEQUENCES: 22
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: MACINTOSH
OPERATING SYSTEM: MACINTOSH, 6.0
SOFTWARE: MICROSOFT WORD, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/569,781
FILING DATE: 23-AUG-1990
PRIOR APPLICATION NUMBER: 464,499
FILING DATE: 12-JAN-1990
APPLICATION NUMBER: 405,605
FILING DATE: 11-SEP-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: GEIGER, KATHLEEN W.
REGISTRATION NUMBER: 35,880
REFERENCE/DOCKET NUMBER: MD-1068
INFORMATION FOR SEQ ID NO; 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDENNES: single
                                                                                                                                                                                                                                                                                           RESULT 615
PCT-US95-06704-5/c
; Sequence 5, Application PC/TUS9506704
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US95-06704-5
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US95-06379-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 81.8
Matches 9; Conservative
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10.7%; Score 7.8; DB 1; Length 12;
Best Local Similarity 81.8%; Pred. No. 3e+02;
Matches 9; Conservative 0; Mismatches 2; Indels
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;SEQ ID NO:13:
;
LENGTH: 12
5212296-13
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